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(71) Applicant (for all designated States except US): GENE  
LOGIC, INC. [US/US]; 708 Quince Orchard Road,  
Gaithersburg, MD 20878 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): MENDRICK,

Donna [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). PORTER, Mark [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). JOHNSON, Kory [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). HIGGS, Brandon [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). CASTLE, Arthur [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US). ELASHOFF, Michael [US/US]; 708 Quince Orchard Road, Gaithersburg, MD 20878 (US).

(74) Agents: TUSCAN, Michael, S. et al.; Morgan, Lewis &amp; Bockius LLP, 1111 Pennsylvania Avenue, NW, Washington, DC 20004 (US).

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(54) Title: MOLECULAR TOXICOLOGY MODELING

(57) Abstract: The present invention is based on the elucidation of the global changes in gene expression and the identification of toxicity markers in tissues or cells exposed to a known renal toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The invention includes a database of genes characterized by toxin-induced differential expression that is designed for use with microarrays and other solid-phase probes.

## MOLECULAR TOXICOLOGY MODELING

**INVENTORS: Donna MENDRICK, Mark PORTER, Kory JOHNSON, Brandon HIGGS, Arthur CASTLE, and Michael ELASHOFF**

### RELATED APPLICATIONS

- This application claims priority to U.S. Provisional Applications 60/292,335; 60/297,523; 60/298,925; 60/303,810; 60/303,807; 60/303,808; 60/315,047; 60/324,928; 60/330,867; 60/330,462; 60/331,805; 60/336,144; 60/340,873; 60/357,843; 60/357,842; 5 60/357,844; 60/364,134; 60/370,206; 60/370,247; 60/370,144; 60/371,679; and 60/372,794, all of which are herein incorporated by reference in their entirety. This application is also related to U.S. Application Nos. 09/917,800 and 10/060,087, both of which are also herein incorporated by reference in their entirety.

### SEQUENCE LISTING SUBMISSION ON COMPACT DISC

- 10 The Sequence Listing submitted concurrently herewith on compact disc is herein incorporated by reference in its entirety. Four copies of the Sequence Listing, one on each of four compact discs are provided. Copy 1, Copy 2 and Copy 3 are identical. Copies 1, 2, and 3 are also identical to the CRF. Each electronic copy of the Sequence Listing was created on May 22, 2002 with a file size of 3088 KB. The file names are as  
15 follows: Copy 1- gl5089wo.txt; Copy 2- gl5089wo.txt; CRF- gl5089wo.txt.

### BACKGROUND OF THE INVENTION

- The need for methods of assessing the toxic impact of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism has led to the development of procedures which utilize living organisms as biological monitors.
- 20 The simplest and most convenient of these systems utilize unicellular microorganisms such as yeast and bacteria, since they are the most easily maintained and manipulated. In addition, unicellular screening systems often use easily detectable changes in phenotype to monitor the effect of test compounds on the cell. Unicellular organisms, however, are inadequate models for estimating the potential effects of many compounds on complex  
25 multicellular animals, as they do not have the ability to carry out biotransformations.
- The biotransformation of chemical compounds by multicellular organisms is a significant factor in determining the overall toxicity of agents to which they are exposed. Accordingly, multicellular screening systems may be preferred or required to detect the

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toxic effects of compounds. The use of multicellular organisms as toxicology screening tools has been significantly hampered, however, by the lack of convenient screening mechanisms or endpoints, such as those available in yeast or bacterial systems. Additionally, previous attempts to produce toxicology prediction systems have failed to provide the necessary modeling data and statistical information to accurately predict toxic responses (e.g., WO 00/12760, WO 00/47761, WO 00/63435, WO 01/32928, and WO 01/38579).

#### SUMMARY OF THE INVENTION

The present invention is based on the elucidation of the global changes in gene expression in tissues or cells exposed to known toxins, in particular renal toxins, as compared to unexposed tissues or cells as well as the identification of individual genes that are differentially expressed upon toxin exposure.

In various aspects, the invention includes methods of predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, and predicting the renal toxicity of a compound. The invention also includes methods of identifying agents that modulate the onset or progression of a toxic response. Also provided are methods of predicting the cellular pathways that a compound modulates in a cell. The invention also includes methods of identifying agents that modulate protein activities.

In a further aspect, the invention includes probes comprising sequences that specifically hybridize to genes in Tables 1-5. Also included are solid supports comprising at least two of the previously mentioned probes. The invention also includes a computer system that has a database containing information identifying the expression level in a tissue or cell sample exposed to a renal toxin of a set of genes comprising at least two genes in Tables 1-5.

#### DETAILED DESCRIPTION

Many biological functions are accomplished by altering the expression of various genes through transcriptional (e.g. through control of initiation, provision of RNA precursors, RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death, are often characterized by the variations in the expression levels of groups of genes.

Changes in gene expression are also associated with the effects of various chemicals, drugs, toxins, pharmaceutical agents and pollutants on an organism or cell. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes after exposure to an agent could lead to tumorigenesis or hyperplastic growth of cells (Marshall (1991), *Cell* 64: 313-326; Weinberg (1991), *Science* 254: 1138-1146). Thus, changes in the expression levels of particular genes (e.g. oncogenes or tumor suppressors) may serve as signposts for the presence and progression of toxicity or other cellular responses to exposure to a particular compound.

Monitoring changes in gene expression may also provide certain advantages during drug screening and development. Often drugs are screened for the ability to interact with a major target without regard to other effects the drugs have on cells. These cellular effects may cause toxicity in the whole animal, which prevents the development and clinical use of the potential drug.

The present inventors have examined tissue from animals exposed to known renal toxins which induce detrimental kidney effects, to identify global changes in gene expression induced by these compounds. These global changes in gene expression, which can be detected by the production of expression profiles (an expression level of one or more genes), provide useful toxicity markers that can be used to monitor toxicity and/or toxicity progression by a test compound. Some of these markers may also be used to monitor or detect various disease or physiological states, disease progression, drug efficacy, and drug metabolism.

#### *Identification of Toxicity Markers*

To evaluate and identify gene expression changes that are predictive of toxicity, studies using selected compounds with well characterized toxicity have been conducted by the present inventors to catalogue altered gene expression during exposure *in vivo* and *in vitro*. In the present study, cephaloridine, cisplatin, puromycin aminonucleoside (PAN), bromoethylamine hydrobromide (BEA), gentamicin, ifosfamide, cyclophosphamide, carboplatin, AY-25329, indomethacin, acyclovir, citrinin, mercuric chloride, diflunisal, cidofovir, pamidronate, lithium, hydralazine, colchicine, sulfadiazine, and adriamycin were selected as known renal toxins.

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Cephaloridine is an amphoteric, semi-synthetic, broad-spectrum cephalosporin derived from cephalosporin C. Cephalosporins are  $\beta$ -lactam-containing antibiotics which prevent bacterial growth by inhibiting polymerization of the peptidoglycan bacterial cell wall. The linear glycan chains (composed of N-acetylglucosime and N-acetylmuramic acid) are cross-linked to each other by the coupling of short chains of several amino acids, the coupling resulting from the action of a transpeptidase. It is believed that cephalosporins act by blocking the activity of the transpeptidase (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., J.G. Hardman *et al.* Eds., McGraw Hill, New York, 1996, pp. 1074-1075, 1089-1095).

Cephaloridine is administered intramuscularly and is used to treat infections of the respiratory tract, gastrointestinal tract and urinary tract, as well as infections of soft tissue, bones and joints. Noted adverse effects include hypersensitivity reactions (such as anaphylactic shock, urticaria and bronchospasm), gastrointestinal disturbances, candidiasis, and cardiovascular and blood toxicity, in particular, toxicity to the hematopoietic system (cells responsible for the formation of red and white blood cells and platelets).

Although cephaloridine may be nephrotoxic at high dosages, it is not as harmful to the kidneys as are the aminoglycosides and polymyxins. High dosages of cephaloridine may cause acute renal tubular necrosis (Cecil Textbook of Medicine, 20<sup>th</sup> ed., part XII, p. 586, J. C. Bennett and F. Plum Eds., W. B. Saunders Co., Philadelphia, 1996) or drug-induced interstitial nephritis, which is accompanied by elevated IgE levels, fever, arthralgia and maculopapular rash. Renal biopsy demonstrates edema and interstitial inflammatory lesions, mainly with lymphocytes, monocytes, eosinophils and plasma cells. Vasculitis of small vessels may develop, leading to necrotising glomerulonephritis (G. Koren, "The nephrotoxic potential of drugs and chemicals. Pharmacological basis and clinical relevance.," *Med Toxicol Adverse Drug Exp* 4(1):59-72, 1989).

Cephaloridine has also been shown to reduce mitochondrial respiration and uptake of anionic succinate and carrier-mediated anionic substrate transport (Tune *et al.* (1990), *J Pharmacol Exp Ther* 252: 65-69). In a study of oxidative stress and damage to kidney tissue, cephaloridine depleted reduced glutathione (GSH) and produced oxidized glutathione (GSSG) in the renal cortex. This drug also inhibited glutathione reductase

and produced malondialdehyde and conjugated dienes (Tune *et al.* (1989), *Biochem Pharmacol* 38: 795-802). Because cephaloridine is actively transported into the proximal renal tubule, but slowly transported across the luminal membrane into the tubular fluid, high concentrations can accumulate and cause necrosis. Necrosis can be prevented by administering inhibitors of organic anion transport, although such treatment may be counterproductive, as cephaloridine is passed in and out of the kidney by the renal organic anion transport system (Tune *et al.* (1980), *J Pharmacol Exp Ther* 215: 186-190).

Cisplatin ( $\text{Pt}(\text{NH}_3)_2(\text{Cl})_2$ ), a broad-spectrum anti-tumor agent, is commonly used to treat tumors of the testicles, ovaries, bladder, skin, head and neck, and lungs (PDR 47<sup>th</sup> ed., pp. 754-757, Medical Economics Co., Inc., Montvale, NJ, 1993; Goodman & Gilman's *The Pharmacological Basis of Therapeutics* 9<sup>th</sup> ed., pp. 1269-1271, J.G. Hardman *et al.* Eds., McGraw Hill, New York, 1996). Cisplatin diffuses into cells and functions mainly by alkylating the N<sup>7</sup> of guanine, a highly reactive site, causing interstrand and intrastrand crosslinks in the DNA that are lethal to cells. The drug is not sensitive to the cell cycle, although its effects are most pronounced in S phase.

Because the drug is cleared from the body mainly by the kidneys, the most frequent adverse effect of cisplatin usage is nephrotoxicity, the severity of which increases with increasing dosage and treatment terms. Other adverse effects include renal tubule damage, myelosuppression (reduced numbers of circulating platelets, leukocytes and erythrocytes), nausea and vomiting, ototoxicity, serum electrolyte disturbances (decreased concentrations of magnesium, calcium, sodium, potassium and phosphate, probably resulting from renal tubule damage), increased serum concentrations of urea and creatinine, and peripheral neuropathies.

In one study on rats (Nonclercq *et al.* (1989), *Exp Mol Pathol* 51: 123-140) administration of cisplatin or carboplatin induced renal injury, carboplatin causing less damage than cisplatin. The most prominent injury was to the straight portion of proximal renal tubule.

In another rat study (Goldstein *et al.* (1981), *Toxicol Appl Pharmacol* 60: 163-175) animals injected with cisplatin displayed decreased food intake as drug dosage increased. On day 2, the high-dose groups (10-15 mg/kg) exhibited a six or seven-fold elevation in BUN. On day 4, BUN elevation was noted in the 5mg/kg group. An

increase in urine volume was observed beginning on days 3-4, along with decreased urine osmolality in the low-dose groups (2.5 or 5 mg/kg). Another experiment on rats (Agarwal *et al.* (1995), *Kidney Int* 48: 1298-1307) showed that cisplatin treatment produced elevations in serum creatinine levels, which began on day 3 and progressed for the duration of the study.

PAN ( $C_{22}H_{29}N_7O_5$ ), an antibiotic produced by *Streptomyces alboniger*, inhibits protein synthesis and is commonly used experimentally on rats to mimic human minimal change disease. One study showed that PAN-injected rats demonstrated an increase in levels of serum non-esterified fatty acids, while the serum albumin concentration was negatively affected (Sasaki *et al.* (1999), *Adv Exp Med Biol* 467: 341-346).

In another rat study, an adenosine deaminase inhibitor prevented PAN nephrotoxicity, indicating that PAN toxicity is linked to adenosine metabolism (Nosaka *et al.* (1997), *Free Radic Biol Med* 22: 597-605). Another group showed that PAN, when administered to rats, led to proteinuria, a condition associated with abnormal amounts of protein in the urine, and renal damage, *e.g.* blebbing of glomerular epithelial cells, focal separation of cells from the glomerular basement membrane, and fusion of podocytes (Olson *et al.* (1981), *Lab Invest* 44: 271-279). In another study on rats, administration of PAN induced glomerular epithelial cell apoptosis in a dose- and time-dependent manner (Sanwal *et al.* (2001), *Exp Mol Pathol* 70: 54-64).

One study with PAN-injected rats (Koukouritaki *et al.* (1998), *J Investig Med* 46: 284-289) examined the changes in the expression of the proteins paxillin, focal adhesion kinase, and Rho, all of which regulate cell adhesion to the extracellular matrix. Paxillin levels increased steadily, peaked at day 9 after PAN injection, and then remained elevated even after proteinuria resolved. There was no observed change in expression of either focal adhesion kinase or Rho.

BEA, ( $C_2H_6BrN.HBr$ ), is commonly used experimentally on rats to induce papillary necrosis and renal cortex damage, which is similar to human analgesic nephropathy. BEA-induced papillary necrosis in rats eventually leads to the onset of focal glomerular sclerosis and nephrotic proteinuria (Garber *et al.* (1999), *Am J Kidney Dis* 33: 1033-1039). Even at low doses (50 mg/kg), BEA can induce an apex limited renal papillary necrosis (Bach *et al.* (1983), *Toxicol Appl Pharmacol* 69: 333-344). In male Wistar rats, BEA administered at 100 mg/kg was shown to cause renal papillary

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necrosis within 24 hours (Bach *et al.* (1991), *Food Chem Toxicol* 29: 211-219). Additionally, Bach *et al.* showed that there was an increase in urinary triglycerides, and lipid deposits were seen by Oil Red O lipid staining in the cells of the collecting ducts and hyperplastic urothelia adjacent to the necrosed region.

- 5 It has also been shown that succinate and citrate concentrations are significantly lower in the urine of BEA-treated rats (Holmes *et al.* (1995), *Arch Toxicol* 70: 89-95). Moreover, BEA treatment induced glutaric and adipic aciduria, which is symptomatic of an enzyme deficiency in the acyl CoA dehydrogenases. The same study examined urinary taurine levels in desert mice, and in BEA-treated desert mice there was an  
10 increase in the urinary taurine level which is indicative of liver toxicity.

Another study on BEA-treated rats showed that there was an increase in the concentrations of creatine in the renal papilla and glutaric acid in the liver, renal cortex, and renal medulla as soon as 6 hours post-treatment (Garrod *et al.* (2001), *Magn Reson Med* 45: 781-790).

- 15 Discovered and purified in the early 1960's, gentamicin is a broad-spectrum aminoglycoside antibiotic that is cidal to aerobic gram-negative bacteria and commonly used to treat infections, *e.g.*, those of the urinary tract, lungs and meninges. As is typical for an aminoglycoside, the compound is made of two amino sugar rings linked to a central aminocyclitol ring by glycosidic bonds. Aminoglycosides are absorbed poorly  
20 with oral administration, but are excreted rapidly by the kidneys. As a result, kidney toxicity is the main adverse effect, although ototoxicity and neuromuscular blockade can also occur. Gentamicin acts by interfering with bacterial protein synthesis. This compound is more potent than most other antibacterial inhibitors of protein synthesis, which are merely bacteriostatic, and its effects on the body are, likewise, more severe  
25 (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., pp. 1103-1115, J.G. Hardman *et al.* Eds., McGraw Hill, New York, 1996).

- Aminoglycosides work rapidly, and the rate of bacterial killing is concentration-dependent. Residual bactericidal activity remains after serum concentration has fallen below the minimum inhibitory concentration (MIC), with a duration that is also  
30 dosage/concentration-dependent. The residual activity allows for once-a-day administration in some patients. These drugs diffuse into bacterial cells through porin channels in the outer membrane and are then transported across the cytoplasmic

membrane via a membrane potential that is negative on the inside (Goodman & Gilman, supra).

Kidney damage, which can develop into renal failure, is due to the attack of gentamicin on the proximal convoluted tubule, particularly in the S1 and S2 segments.

- 5 The necrosis, however, is often patchy and focal (Shanley *et al.* (1990), *Ren Fail* 12: 83-87). A rat study by Shanley *et al.* showed that superficial nephrons are more susceptible to necrosis than juxtamedullary nephrons, although the initial segment of the superficial nephrons is remarkably resistant to necrosis.

- Reported enzymatic changes upon gentamicin treatment are increased activities  
10 of N-acetyl-beta-D-glucosaminidase and alkaline phosphatase and decreased activities of sphingomyelinase, cathepsin B,  $\text{Na}^+/\text{K}^+$ -ATPase, lactate dehydrogenase and NADPH cytochrome C reductase, along with decreased protein synthesis and alpha-methylglucose transport (Monteil *et al.* (1993), *Ren Fail* 15: 475-483). An increase in gamma-glutamyl transpeptidase activity in urine has also been reported (Kocaoglu *et al.* (1994), *Arch*  
15 *Immunol Ther Exp (Warsz)* 42: 125-127), and the quantification of this enzyme in urine is a useful marker for monitoring gentamicin toxicity.

- One source of renal pathology resulting from gentamicin treatment is the generation of reactive oxygen metabolites. Gentamicin has been shown, both *in vitro* and *in vivo*, to be capable of enhancing the production of reactive oxygen species. Iron,  
20 a necessary co-factor that catalyzes free-radical formation, is supplied by cytochrome P450 (Baliga *et al.* (1999), *Drug Metab Rev* 31: 971-997).

- A gene delivery experiment in rats, in which the human kallikrein gene was cloned into an adenovirus vector and the construct then co-administered with a gentamicin preparation, showed that kallikrein can protect against gentamicin-induced  
25 nephrotoxicity. Significantly increased renal blood flow, glomerular filtration rates and urine flow were observed, along with decreased renal tubular damage, cellular necrosis and luminal protein casts. Kallikrein gene delivery also caused a decrease in blood urea nitrogen levels and increases in urinary kinin and nitrite/nitrate levels. This study provides evidence that the tissue kallikrein-kinin system may be a key pathway that is  
30 perturbed during the induction of nephrotoxicity by gentamicin (Murakami *et al.* (1998), *Kidney Int* 53: 1305-1313).

Ifosfamide, an alkylating agent, is commonly used in chemotherapy to treat testicular, cervical, and lung cancer. Ifosfamide is slowly activated in the liver by hydroxylation, forming the triazene derivative 5-(3,3-dimethyl-1-triazeno)-imidazole-4-carboxamide (DTIC) (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., p.1235, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). Cytochrome P450 activates DTIC via an N-demethylation reaction yielding an alkylating moiety, diazomethane. The active metabolites are then able to cross-link DNA causing growth arrest and cell death. Though ifosfamide is therapeutically useful, it is also associated with nephrotoxicity, urotoxicity, and central neurotoxicity.

Mesna, another therapeutic, is often administered concomitantly to prevent kidney and bladder problems from arising (Brock and Pohl (1986), *IARC Sci Publ* 78: 269-279). However, there are documented cases in which tubular toxicity occurred and elevated urinary levels of alanine aminopeptidase and N-acetyl-beta-D-glucosaminidase were found in patients even though mesna was administered alongside ifosfamide (Goren *et al.* (1987), *Cancer Treat Rep* 71: 127-130).

One study examined 42 patients that had been administered ifosfamide to treat advanced soft-tissue sarcoma (Stuart-Harris *et al.* (1983), *Cancer Chemother Pharmacol* 11: 69-72). The ifosfamide dosage varied from 5.0 g/m<sup>2</sup> to 8.0 g/m<sup>2</sup>, and all of the patients were given mesna to counteract the negative effects of ifosfamide. Even so, nausea and vomiting were common to all of the patients. Out of the 42 patients, seven developed nephrotoxicity, and two of the cases progressed to fatal renal failure.

In another clinical study, renal tubular function was monitored in 18 neuroblastoma patients (Caron *et al.* (1992), *Med Pediatr Oncol* 20: 42-47). Tubular toxicity occurred in at least 12 of the patients, and seven of those patients eventually developed Debre-de Toni-Fanconi syndrome, although in 3 cases the syndrome was reversible.

Fanconi syndrome is a disorder marked by dysfunction of the proximal tubules of the kidney. It is associated with aminoaciduria, renal glycosuria, and hyperphosphaturia. Ifosfamide is often used experimentally on rats to induce Fanconi syndrome. In one study, rats that were administered 80 mg/kg of ifosfamide had significantly lower body weight and hematocrit than control rats (Springate and Van Liew (1995), *J Appl Toxicol* 15: 399-402). Additionally, the rats had low-grade glucosuria, proteinuria, and

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phosphaturia. In a mouse study, ifosfamide induced elevated serum creatinine and urea levels and decreased the clearance rate of creatinine (Badary (1999), *J Ethnopharmacol* 67: 135-142).

Cyclophosphamide, a nitrogen mustard and alkylating agent, is highly toxic to  
5 dividing cells and is commonly used in chemotherapy to treat malignant lymphomas, such as non-Hodgkin's lymphomas and Burkitt's lymphoma, multiple myeloma, leukemias, neuroblastomas, ovarian adenocarcinomas and retinoblastomas, as well as breast and lung cancer (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., pp.1234, 1237-1239, J.G. Hardman *et al.*, eds., McGraw Hill, New  
10 York, 1996; Physicians Desk Reference, 47<sup>th</sup> ed., pp. 744-745, Medical Economics Co., Inc., Montvale, NJ, 1993). Additionally, cyclophosphamide is used as an immunosuppressive agent in bone marrow transplantation and following organ transplantation. Although cyclophosphamide is therapeutically useful against certain types of cancer, it is also associated with cardiotoxicity, nephrotoxicity (including renal  
15 tubular necrosis), hemorrhagic cystitis, myelosuppression, hepatotoxicity, impairment of male and female reproductive systems, interstitial pneumonitis and central nervous system toxicity.

Once in the liver, cyclophosphamide is hydroxylated by the cytochrome P450 mixed function oxidase system, producing the active metabolites phosphoramidate mustard  
20 and acrolein, which cross-link DNA and cause growth arrest and cell death. These metabolites, however, are highly toxic and cause adverse effects in the other organs into which they are transported, such as the kidneys. Acrolein is removed from the kidneys by secretion into the urine, resulting in cystitis (inflammation of the bladder), often hemorrhagic cystitis.

25 In the kidney, cyclophosphamide induces necrosis of the renal distal tubule. Cyclophosphamide, which is structurally similar to the anti-cancer drug ifosfamide, does not induce damage to the renal proximal tubule nor does it induce Debre-de Toni-Fanconi syndrome (Rossi *et al.* (1997), *Nephrol Dial Transplant* 12: 1091-1092).

One clinical trial of patients being treated with cyclophosphamide showed that  
30 renal damage from the drug leads to a reduced biotransformation rate and low renal clearance of the drug, resulting in a build-up of toxic alkylating metabolic products (Wagner *et al.* (1980), *Arzneimittelforschung* 30: 1588-1592).

In a study of patients suffering from malignant lymphomas and mammary carcinomas, a direct relationship was found between the dose of cyclophosphamide used in treatment and the concentration of alkylating metabolites in the patients' urine. The upper limit of the dose was determined by the nature and degree of the toxic side effects, rather than by the rate at which the drug could be metabolized (Saul *et al.* (1979), *J Cancer Res Clin Oncol* 94: 277-286). It is the acrolein itself that is toxic, not the alkylating activity of cyclophosphamide (Brock *et al.* (1979), *Arzneimittelforschung* 29: 659-661). A study on rats also showed that acrolein from the kidneys can produce hemorrhagic cystitis and that the acrolein concentration is directly related to the frequency and severity of the cystitis (Chijiwa *et al.* (1983), *Cancer Res* 43: 5205-5209).

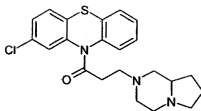
Carboplatin, a platinum coordination complex, is commonly used in chemotherapy as an anti-tumor agent. As a chemotherapeutic agent, carboplatin acts similarly to cisplatin. Carboplatin enters the cell by diffusion where it is activated by hydrolysis (Goodman & Gilman's *The Pharmacological Basis of Therapeutics* 9th ed., p. 1270-1271, J.G. Hardman *et al.* Eds., McGraw Hill, New York 1996). Once activated, the platinum complexes are able to react with DNA causing cross-linking to occur. One of the differences between carboplatin and cisplatin is that carboplatin is better tolerated clinically. Some of the side-effects associated with cisplatin, such as nausea, neurotoxicity, and nephrotoxicity, are seen at a lesser degree in patients administered carboplatin. Some other side-effects are hypomagnesaemia and hypokalaemia (Kintzel (2001), *Drug Saf* 24: 19-38).

In one study on male Wistar rats, carboplatin was administered at a dosage of 65mg/kg (Wolfgang *et al.* (1994), *Fundam Appl Toxicol* 22: 73-79). After treatment with carboplatin, CGT excretion was increased approximately two-fold.

Another study compared cisplatin and carboplatin when given in combination with vindesine and mitomycin C (Jelic *et al.* (2001) *Lung Cancer* 34: 1-13). The study showed that carboplatin administered with vindesine and mitomycin C was advantageous in terms of overall survival, although the regimen was more hematologically toxic than when cisplatin was given.

AY-25329, is a phenothiazine that has been shown to be mildly hepatotoxic and to induce nephrosis. Its structure is shown below.

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Phenothiazines are a class of psychoactive drugs. They have been used to treat schizophrenia, paranoia, mania, hyperactivity in children, some forms of senility, and anxiety (<http://www.encyclopedia.com/articlesnew/36591.html>). Some side effects associated with prolonged use of the drugs are reduced blood pressure, Parkinsonism, reduction of motor activity, and visual impairment.

Chlorpromazine (Thorazine or Largactil) is an aliphatic phenothiazine and is widely used for treating schizophrenia and manic depression. Prolactin secretion is increased while taking chlorpromazine, and galactorrhea and gynecomastia have both been associated with the drug (<http://www.mentalhealth.com/drug/p30-c01.html>). Trifluoperazine is another prescribed phenothiazine. It is used to treat anxiety, to prevent nausea and vomiting, and to manage psychotic disorders (<http://www.mentalhealth.com/drug/p30-s04.html>). Negative side-effects that have been associated with the drug are liver damage, bone marrow depression, and Parkinsonism.

Acyclovir (9-[(2-hydroxyethyl) methyl] guanine, Zovirax®), an anti-viral guanosine analogue, is used to treat herpes simplex virus (HSV), varicella zoster virus (VZV) and Epstein-Barr virus (EBV) infections. It is transported into cells by the nucleoside transporter that imports guanine, and acyclovir is phosphorylated by virally encoded thymidine kinase (TK). Other kinases convert acyclovir to its activated di- and triphosphate forms, which prevent the polymerization of viral DNA. Acyclovir triphosphate competes with dGTP for the viral polymerase, and acyclovir is preferentially incorporated, but as a monophosphate. As a result, chain elongation ceases (Fields Virology 3<sup>d</sup> ed., Fields *et al.*, eds., pp. 436-440, Lippincott-Raven Publishers, Philadelphia, 1996; Cecil Textbook of Medicine, 20<sup>th</sup> ed., part XII, p. 1742, J. C. Bennett and F. Plum Eds., W. B. Saunders Co., Philadelphia, 1996).

The pharmacokinetics of acyclovir show that it has a useful half-life of about three hours and that most of it is excreted in the urine largely unchanged (Brigden *et al.* (1985), *Scand J Infect Dis Suppl* 47: 33-39). Not surprisingly, the most frequent adverse

effect of acyclovir treatment is damage to various parts of the kidney, particularly the renal tubules. Crystalluria, or the precipitation of crystals (in this case, crystals of acyclovir), in the lumina of the renal tubules can occur (Fogazzi (1996), *Nephrol Dial Transplant* 11: 379-387). If the drug crystallizes in the renal collecting tubules,

- 5 obstructive nephropathy and tubular necrosis can result (Richardson (2000), *Vet Hum Toxicol* 42: 370-371). Tissues from biopsies of affected patients showed dilation of the proximal and distal renal tubules, with loss of the brush border, flattening of the lining cells and focal nuclear loss (Becker *et al.* (1993), *Am J Kidney Dis* 22: 611-615).

- Citrinin, a mycotoxin produced by the fungus *Penicillium citrinum*, is a natural  
10 contaminant of foods and feeds (Bondy and Armstrong (1998) *Cell Biol. Toxicol.* 14: 323-332). It is known that mycotoxins can have negative effects on the immune system, however citrinin-treated animals have been shown to stimulate responses against antigens (Sharma (1993) *J. Dairy Sci.* 76: 892-897). Citrinin is a known nephrotoxin, and in birds such as chickens, ducklings, and turkeys, it causes diarrhea, increased food  
15 consumption and reduced weight gain due to kidney degeneration (Mehdi *et al.* (1981) *Food Cosmet. Toxicol.* 19: 723-733; Mehdi *et al.* (1984) *Vet. Pathol.* 21: 216-223). In the turkey and duckling study, both species exhibited nephrosis with the occurrence of hepatic and lymphoid lesions (Mehdi *et al.*, 1984).

- In one study, citrinin was administered to rabbits as a single oral dose of either  
20 120 or 67 mg/kg (Hanika *et al.* (1986) *Vet. Pathol.* 23: 245-253). Rabbits treated with citrinin exhibited renal alterations such as condensed and distorted mitochondria, distended intercellular spaces of the medullary and straight cortical distal tubules, and disorganization of interdigitating processes. In another rabbit study, citrinin-administered rabbits displayed azotaemia and metabolic acidosis (Hanika *et al.* (1984)  
25 *Food Chem. Toxicol.* 22: 999-1008). Renal failure was indicated by decreased creatinine clearance and increased blood urea nitrogen and serum-creatinine levels.

- In the past, mercury was an important component of pharmaceuticals, particularly of antiseptics, antibacterials, skin ointments, diuretics and laxatives. Although, mercury has been largely replaced by more effective, more specific and safer compounds, making  
30 drug-induced mercury poisoning rare, it is still widely used in industry. Poisoning from occupational exposure and environmental pollution, such as mercury release into public water supplies, remains a concern as wildlife, domestic animals and humans are affected.

Because of their lipid solubility and ability to cross the blood-brain barrier, the most dangerous form of mercury is the organomercurials, the most common of which is methylmercury, a fungicide used for disinfecting crop seeds. In a number of countries, incidents involving large-scale illness and death from mercury poisoning have been reported when mercury-contaminated seeds were planted and the crops harvested and consumed. A second source of organic mercury poisoning results from industrial chemicals containing inorganic mercury, such as mercury catalysts, which form methylmercury as a reaction product. If this waste product is released into reservoirs, lakes, rivers or bays, the surrounding population can become sick or die, particularly those who eat local fish.

The inorganic salt mercuric chloride,  $\text{HgCl}_2$ , as well as other mercuric salts, are more irritating and more toxic than the mercurous forms. Mercuric chloride is used today in industry, for the manufacture of bleach, electronics, plastics, fungicides and dental amalgams. The main source of human exposure is industrial dumping into rivers (Goodman & Gilman's: The Pharmacological Basis of Therapeutics (9th ed.), pp. 1654-1659, McGraw-Hill, New York, 1996).

When inorganic mercury salts are ingested, about 10% of the mercuric ions are absorbed by the gastrointestinal tract, and a considerable portion of the  $\text{Hg}^{2+}$  can remain bound to the mucosal surfaces. The highest concentration of  $\text{Hg}^{2+}$  is found in the kidneys, as it is retained there longer than in other tissues. Consequently, the kidneys are the organ most adversely affected by inorganic mercury poisoning. The proximal tubules are the major site of damage, where tubular necrosis results. The mercury affects primarily the S2 and S3 portions of the proximal tubules, but, at high levels of mercury exposure, the S1 and distal portions of the tubules are also damaged. These regions of the nephrons are affected because they contain enzymes (such as gamma-glutamyltranspeptidase) and transport proteins (such as the basolateral organic anion transport system) involved in mercury uptake (Diamond *et al.* (1998), *Toxicol Pathol* 26: 92-103).

Urinary markers of mercury toxicity which can be detected in NMR spectra include elevated levels of lactate, acetate and taurine and decreased levels of hippurate (Holmes *et al.* (2000), *Chem Res Toxicol* 13: 471-478). Known changes in gene expression in kidneys exposed to  $\text{Hg}^{2+}$  include up-regulation of the heat-shock protein

hsp72 and of the glucose-regulated protein grp94. The degree of tissue necrosis and level of expression of these proteins is proportional to both the dose of mercury ( $Hg^{2+}$ ) and the length of the exposure time to mercury ( $Hg^{2+}$ ), with hsp72 accumulating in the renal cortex and grp94 accumulating in the renal medulla (Goering *et al.* (2000), *Toxicol Sci* 53: 447-457).

Diflunisal, a non-steroidal anti-inflammatory drug (NSAID), is a difluorophenyl derivative of salicylic acid (Goodman & Gilman's *The Pharmacological Basis of Therapeutics* 9<sup>th</sup> ed., p. 631, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). It is most frequently used in the treatment of osteoarthritis and musculoskeletal strains. NSAIDs have analgesic, antipyretic and anti-inflammatory actions, however hepatotoxicity is known to be an adverse side effect of NSAID treatment (Masubuchi *et al.* (1998) *J. Pharmacol. Exp. Ther.* 287: 208-213). Diflunisal has been shown to be less toxic than other NSAIDs, nevertheless over long periods of dosage it can lead to deleterious effects on platelet or kidney function (Bergamo *et al.* (1989) *Am. J. Nephrol.* 9: 460-463). Other side effects that have been associated with diflunisal treatment are diarrhea, dizziness, drowsiness, gas or heartburn, headache, nausea, vomiting, and insomnia (<http://arthritisinsight.com/medical/ meds/dolobid.html>).

Masubuchi *et al.* compared the hepatotoxicity of 18 acidic NSAIDs. In the study, diflunisal (administered at a concentration of 500  $\mu$ M) was shown to increase LDH leakage in rat hepatocytes, a marker for cell injury, when compared to the control sample. In addition, treatment with diflunisal led to decreased intracellular ATP concentrations.

One study compared the effects of diflunisal and ibuprofen when given to patients over a two week period (Muncie and Nasrallah (1989) *Clin. Ther.* 11: 539-544). In both the ibuprofen and the diflunisal group, two patients complained of abdominal cramping. The study indicated that even during short-term usage some gastrointestinal effects may occur. The toxic dose used in this study was chosen as one that did not induce significant gastric ulceration in rats. The group of rats given the high dosage of diflunisal had increased concentrations of creatinine which is consistent with renal injury, although dehydration may also cause increases in creatinine concentration.

Cidofovir (Vistide®) is an antiviral cytosine analog used in the treatment of viral infections such as herpesvirus, adenovirus, papillomavirus, poxvirus and hepadnavirus

(Goodman & Gilman's *The Pharmacological Basis of Therapeutics* 9<sup>th</sup> ed., p. 1216, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). It is also useful for the treatment of cytomegalovirus (CMV) infection, which is a type of herpesvirus.

Some mild side effects seen in patients receiving cidofovir are nausea, vomiting,  
5 and fever. The most serious reported side effect of the drug is kidney toxicity  
(<http://tthivclinic.com/cido.html>). In response to the threat of nephrotoxicity, it is  
necessary for patients receiving cidofovir to have their kidneys checked before treatment,  
and the patients must be monitored during treatment for early symptoms of kidney  
10 problems. In addition, cidofovir is given with fluids to help reduce the risk of kidney  
toxicity (<http://www.aidsinfonyc.org/network/simple/cido.html>). Probenecid, a drug  
that helps protect the kidneys, is normally administered concomitantly (Lalezari and  
Kuppersmann (1997) *J. Acquir. Immune Defic. Syndr. Hum. Retrovirol.* 14: S27-31).

One study compared the safety and efficacy of cidofovir in the treatment of CMV  
(Lalezari *et al.* (1998) *J. Acquir. Immune Defic. Syndr. Hum. Retrovirol.* 17: 339-344).  
15 Approximately 40% of the patients exhibited dose-dependent asymptomatic proteinuria  
and 25% of the patients had elevated serum creatinine levels.

Pamidronate (Aredia®) is a bisphosphonate drug that is clinically used to inhibit  
bone resorption and make bones more stable. It is used to treat hypercalcemia (too much  
calcium in the blood) that occurs with some types of cancer. Typically administered by  
20 intravenous injection, pamidronate is frequently used in patients with breast cancer or  
multiple myeloma whose disease has spread to the bones. Some side effects related to  
pamidronate treatment are abdominal cramps, chills, confusion, fever, muscle spasms,  
nausea, muscle stiffness, and swelling at the injection site ([http://www.nursing.  
uiowa.edu/sites/PedsPain/Adjuvants/PAMIDRnt.html](http://www.nursing.uiowa.edu/sites/PedsPain/Adjuvants/PAMIDRnt.html)). Patients with kidney problems  
25 may be prohibited from using pamidronate as it is excreted through the kidneys.

In one study, rats and mice were given varying doses of labeled pamidronate (Cal  
and Daley-Yates (1990) *Toxicology* 65: 179-197). Pamidronate treatment led to  
significant weight loss and a decrease in creatinine clearance. Morphological studies  
showed a loss of brush border membranes and the presence of focal proximal tubular  
30 necrosis.

Another study compared the tolerability of different treatments for hypercalcemia  
of malignancy by reviewing articles published between 1979 and 1998 (Zojer *et al.*

(1999) *Drug Saf.* 21: 389-406). The authors found that elevated serum creatinine level, nausea, and fever were reported following treatment with bisphosphonates such as pamidronate.

Markowitz *et al.* (2001, *J. Am. Soc. Nephrol.* 12: 1164-1172) tried to determine  
5 whether there was a correlation between pamidronate treatment and collapsing focal  
segmental glomerulosclerosis (FSGS). The authors examined the histories of seven  
patients who had developed collapsing FSGS, and they found that the only drug  
treatment in common was the administration of pamidronate. When given at the  
recommended dose of 90 mg per month, renal toxicity was rare. However, when  
10 pamidronate was given at higher doses nephrotoxicity occurred.

Lithium, an alkali metal, is the main pharmacological treatment for bipolar  
disorders. It is typically given as a salt, such as lithium carbonate or lithium citrate.  
Some common side effects of lithium treatment are an increase in urination, increase in  
drinking, dry mouth, weight gain, fine tremor, and fatigue. Some more serious side  
15 effects related to lithium treatment are blurred vision, mental confusion, seizures,  
vomiting, diarrhea, muscle weakness, drowsiness, and coarse tremor (Goodman &  
Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., p. 448, J.G. Hardman *et al.*,  
Eds., McGraw Hill, New York, 1996).

Since lithium is often used on a maintenance basis for a lifelong period,  
20 numerous studies have been performed to try and elucidate the effects of lithium on the  
kidney. One group administered lithium in daily doses within the human therapeutic  
range to male Wistar rats (Kling *et al.* (1984) *Lab Invest* 50: 526-535). Rats that were  
given lithium developed marked polyuria within three weeks of the initial dosing. The  
rats displayed elevated free water clearance and vasopressin-resistant diabetes insipidus.  
25 The cortical collecting tubules displayed morphological changes, *e.g.* dilation of the  
tubules, bulging cells lining the tubules, enlarged nuclei, following lithium treatment.

Another study examined a human population that had been given lithium for the  
treatment of bipolar disorder (Markowitz *et al.* (2000) *J. Am. Soc. Nephrol.* 11: 1439-  
1448). The patients had a mean age of 42.5 years and had been undergoing lithium  
30 treatment from 2 to 25 years (mean of 13.6 years). Approximately one fourth of the  
patients had nephrotic proteinuria, almost 90% of them had nephrogenic diabetes  
insipidus (NDI), and renal biopsies revealed a chronic tubulointerstitial nephropathy in

all of the patients. Following cessation of lithium treatment, seven of the patients proceeded to end-stage renal disease.

- Even though nephrotoxicity is a known side effect of lithium treatment, some studies have indicated that in actuality it is not all that common (Johnson (1998) *Neuropsychopharmacology* 19: 200-205). One study showed that the NDI-like effect in lithium treatment was easily overcome by increasing the levels of arginine vasopressin (AVP) (Carney *et al.* (1996) *Kidney Int* 50: 377-383). Other studies have suggested that patients with psychiatric disorders display certain defects in renal function without undergoing lithium treatment (Gitlin (1999) *Drug Saf* 20: 231-243).
- 10       Hydralazine, an antihypertensive drug, causes relaxation of arteriolar smooth muscle. Such vasodilation is linked to vigorous stimulation of the sympathetic nervous system, which in turn leads to increased heart rate and contractility, increased plasma renin activity, and fluid retention (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., p. 794, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996).
- 15       The increased renin activity leads to an increase in angiotensin II, which in turn causes stimulation of aldosterone and sodium reabsorption.

- Hydralazine is used for the treatment of high blood pressure (hypertension) and for the treatment of pregnant women suffering from high blood pressure (pre-eclampsia or eclampsia). Some common side effects associated with hydralazine use are diarrhea,
- 20       rapid heartbeat, headache, decreased appetite, and nausea. Hydralazine is often used concomitantly with drugs that inhibit sympathetic activity to combat the mild pulmonary hypertension that can be associated with hydralazine usage.

- In one hydralazine study, rats were fed hydralazine and mineral metabolism was monitored (Peters *et al.* (1988) *Toxicol Lett* 41: 193-202). Manganese and zinc
- 25       concentrations were not effected by hydralazine treatment, however tissue iron concentrations were decreased and kidney copper concentrations were increased compared to control groups.

- Another study compared the effects of hydrazine, phenelzine, and hydralazine treatment on rats (Runge-Morris *et al.* (1996) *Drug Metab Dispos* 24: 734-737).
- 30       Hydralazine caused an increase in renal GST-alpha subunit expression, although unlike hydrazine and phenelzine it did not alter renal cytochrome P4502E1 expression.

Colchicine, an alkaloid of *Colchicum autumnale*, is an antiinflammatory agent used in the treatment of gouty arthritis (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9<sup>th</sup> ed., p. 647, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996).

5        An antimitotic agent, colchicine binds to tubulin which leads to depolymerization and disappearance of the fibrillar microtubules in granulocytes and other motile cells. In doing so, the migration of granulocytes into the inflamed area is inhibited. Through a series of events, the inflammatory response is blocked.

10        Some common, mild side effects associated with colchicine treatment are loss of appetite and hair loss. More severe side effects that warrant cessation of treatment are nausea, vomiting, diarrhea, and abdominal pain. Colchicine overdose can induce multiorgan failure with a high incidence of mortality. In this setting, renal failure is multifactorial and related to prolonged hypotension, hypoxemia, sepsis, and rhabdomyolysis. In rats, less dramatic doses have been shown to inhibit the secretion of  
15        many endogenous proteins such as insulin and parathyroid hormone.

One study investigated the effects of colchicine on microtubule polymerization status and post-translational modifications of tubulin in rat seminiferous tubules (Correa and Miller (2001) *Biol Reprod* 64: 1644-1652). Colchicine caused extensive microtubule depolymerization, and total tubulin levels decreased twofold after colchicine  
20        treatment. The authors also found that colchicine treatment led to a decrease in tyrosination of the microtubule pool of tubulin which was associated with depolymerization of microtubules.

Sulfadiazine, a sulfonamide, is an antimicrobial agent. It is commonly used concomitantly with pyrimethamine to treat toxoplasmosis, an infection of the brain, in  
25        patient suffering from AIDS. These drugs are able to cross the blood-brain barrier and are used at relatively high doses. In addition, sulfadiazine has been shown to be effective at preventing certain types of meningococcal diseases and in treating urinary tract infections.

Sulfonamides in general are structural analogs of para-aminobenzoic acid  
30        (PABA). Because they are competitive antagonists of PABA, sulfonamides are effective against bacteria that are required to utilize PABA for the synthesis of folic acid

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(Goodman & Gilman's *The Pharmacological Basis of Therapeutics* 9<sup>th</sup> ed., p. 1058-1060, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996).

The main side effects associated with sulfadiazine treatment are fever and skin rashes. Decreases in white blood cells, red blood cells, and platelets, nausea, vomiting, and diarrhea are some other side effects that may result from sulfadiazine treatment. The most troublesome problem with this drug for HIV/AIDS patients is kidney toxicity. These patients tend to use these drugs for extended periods of time, which puts a constant strain on the kidneys. In addition, kidney stones tend to form in the bladder and ureter thereby blocking the flow of urine. Kidney damage may result, and if left untreated kidney failure may occur. Therefore, patients being treated with sulfadiazine are instructed to increase their fluid intake in order to prevent crystal formation in the kidneys.

One case study examined four HIV-positive patients who had been given sulfadiazine to treat toxoplasmosis (Crespo *et al.* (2000) *Clin Nephrol* 54: 68-72). All four of the patients, one of whom was a previously healthy person, developed oliguria, abdominal pain, renal failure, and displayed multiple radiolucent renal calculi in echography. Following extensive hydration and alcalinization, the renal function of the patients returned to normal.

Adriamycin, known generically as doxorubicin, is an anthracycline antibiotic produced by the fungus *Streptomyces peucetius*. It is an anti-tumor drug used in the treatment of breast, ovarian, bladder, and lung cancers as well as non-Hodgkin's lymphoma, Hodgkin's disease and sarcoma (Goodman & Gilman's *The Pharmacological Basis of Therapeutics* 9<sup>th</sup> ed., p. 1264-1265, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996).

Adriamycin has tetracycline ring structures with the sugar daunosamine attached by glycosidic linkage. It is able to intercalate with DNA, it affects DNA and RNA synthesis, and it can interact with cell membranes and alter their functions. Typically the drug is cell-cycle specific for the S phase of cell division. By binding to the cancer cells' DNA and blocking topoisomerase II, cancer cells are unable to divide and grow.

Some common side effects associated with adriamycin treatment are fatigue, a drop in white blood cell, red blood cell, or platelet count, hair loss, skin discoloration, and watery eyes ([www.cancerhelp.org.uk/help/default.asp?page=4025](http://www.cancerhelp.org.uk/help/default.asp?page=4025)). More serious

side effects include myocardial toxicity, ulceration and necrosis of the colon, and development of a second cancer.

Because of its utility in fighting cancer, numerous studies have been performed in attempts to further understand the mechanisms and effects of adriamycin. In one study, investigators injected mice with a single dose of adriamycin (Chen *et al.* (1998) *Nephron* 78: 440-452). The mice exhibited signs of combined glomerular albuminuria and immunoglobulinuria, progressively elevated levels of nitrite/nitrate in the urine, abnormal renal function, and other symptoms indicative of focal segmental glomerulosclerosis.

In another study, rats were given adriamycin and the effects on angiotensin converting enzyme (ACE) were monitored (Venkatesan *et al.* (1993) *Toxicology* 85: 137-148). The rats developed glomerular and tubular injury, and serum ACE levels were significantly elevated 20, 25, and 30 days post-treatment. A different study followed rabbits for up to one year that were treated with either adriamycin, nephrectomy, or combinations thereof (Gadeholt-Gothlin *et al.* (1995) *Urol Res* 23: 169-173). The rabbits that were treated with adriamycin exhibited signs of nephrotoxicity at relatively low doses.

#### *Toxicity Prediction and Modeling*

The genes and gene expression information, gene expression profiles, as well as the portfolios and subsets of the genes provided in Tables 1-5, may be used to predict at least one toxic effect, including the nephrotoxicity of a test or unknown compound. As used, herein, at least one toxic effect includes, but is not limited to, a detrimental change in the physiological status of a cell or organism. The response may be, but is not required to be, associated with a particular pathology, such as tissue necrosis.

Accordingly, the toxic effect includes effects at the molecular and cellular level.

Nephrotoxicity is an effect as used herein and includes but is not limited to the pathologies of nephritis, kidney necrosis, glomerular and tubular injury, and focal segmental glomerulosclerosis. As used herein, a gene expression profile comprises any quantitative representation of the expression of at least one mRNA species in a cell sample or population and includes profiles made by various methods such as differential display, PCR, hybridization analysis, etc.

In general, assays to predict the toxicity or nephrotoxicity of a test agent (or compound or multi-component composition) comprise the steps of exposing a cell

population to the test compound, assaying or measuring the level of relative or absolute gene expression of one or more of the genes in Tables 1-5 and comparing the identified expression level(s) to the expression levels disclosed in the Tables and database(s) disclosed herein. Assays may include the measurement of the expression levels of about  
5 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 50, 75, 100 or more genes from Tables 1-5.

In the methods of the invention, the gene expression level for a gene or genes induced by the test agent, compound or compositions may be comparable to the levels found in the Tables or databases disclosed herein if the expression level varies within a factor of about 2, about 1.5 or about 1.0 fold. In some cases, the expression levels are  
10 comparable if the agent induces a change in the expression of a gene in the same direction (e.g., up or down) as a reference toxin.

The cell population that is exposed to the test agent, compound or composition may be exposed *in vitro* or *in vivo*. For instance, cultured or freshly isolated renal cells, in particular rat renal cells, may be exposed to the agent under standard laboratory and cell culture conditions. In another assay format, *in vivo* exposure may be accomplished  
15 by administration of the agent to a living animal, for instance a laboratory rat.

Procedures for designing and conducting toxicity tests in *in vitro* and *in vivo* systems are well known, and are described in many texts on the subject, such as Loomis *et al.*, Loomis's Essentials of Toxicology, 4th Ed., Academic Press, New York, 1996; Echobichon, The Basics of Toxicity Testing, CRC Press, Boca Raton, 1992; Frazier,  
20 editor, *In Vitro* Toxicity Testing, Marcel Dekker, New York, 1992; and the like.

In *in vitro* toxicity testing, two groups of test organisms are usually employed: One group serves as a control and the other group receives the test compound in a single dose (for acute toxicity tests) or a regimen of doses (for prolonged or chronic toxicity  
25 tests). Because, in some cases, the extraction of tissue as called for in the methods of the invention requires sacrificing the test animal, both the control group and the group receiving compound must be large enough to permit removal of animals for sampling tissues, if it is desired to observe the dynamics of gene expression through the duration of an experiment.

30 In setting up a toxicity study, extensive guidance is provided in the literature for selecting the appropriate test organism for the compound being tested, route of administration, dose ranges, and the like. Water or physiological saline (0.9% NaCl in

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water) is the solute of choice for the test compound since these solvents permit administration by a variety of routes. When this is not possible because of solubility limitations, vegetable oils such as corn oil or organic solvents such as propylene glycol may be used.

- 5       Regardless of the route of administration, the volume required to administer a given dose is limited by the size of the animal that is used. It is desirable to keep the volume of each dose uniform within and between groups of animals. When rats or mice are used, the volume administered by the oral route generally should not exceed about 0.005 ml per gram of animal. Even when aqueous or physiological saline solutions are  
10       used for parenteral injection the volumes that are tolerated are limited, although such solutions are ordinarily thought of as being innocuous. The intravenous LD<sub>50</sub> of distilled water in the mouse is approximately 0.044 ml per gram and that of isotonic saline is 0.068 ml per gram of mouse. In some instances, the route of administration to the test animal should be the same as, or as similar as possible to, the route of administration of  
15       the compound to man for therapeutic purposes.

- When a compound is to be administered by inhalation, special techniques for generating test atmospheres are necessary. The methods usually involve aerosolization or nebulization of fluids containing the compound. If the agent to be tested is a fluid that has an appreciable vapor pressure, it may be administered by passing air through the  
20       solution under controlled temperature conditions. Under these conditions, dose is estimated from the volume of air inhaled per unit time, the temperature of the solution, and the vapor pressure of the agent involved. Gases are metered from reservoirs. When particles of a solution are to be administered, unless the particle size is less than about 2  $\mu$ m the particles will not reach the terminal alveolar sacs in the lungs. A variety of  
25       apparatuses and chambers are available to perform studies for detecting effects of irritant or other toxic endpoints when they are administered by inhalation. The preferred method of administering an agent to animals is via the oral route, either by intubation or by incorporating the agent in the feed.

- When the agent is exposed to cells *in vitro* or in cell culture, the cell population to  
30       be exposed to the agent may be divided into two or more subpopulations, for instance, by dividing the population into two or more identical aliquots. In some preferred embodiments of the methods of the invention, the cells to be exposed to the agent are

derived from kidney tissue. For instance, cultured or freshly isolated rat renal cells may be used.

The methods of the invention may be used generally to predict at least one toxic response, and, as described in the Examples, may be used to predict the likelihood that a compound or test agent will induce various specific kidney pathologies, such as nephritis, kidney necrosis, glomerular and tubular injury, focal segmental glomerulosclerosis, or other pathologies associated with at least one of the toxins herein described. The methods of the invention may also be used to determine the similarity of a toxic response to one or more individual compounds. In addition, the methods of the invention may be used to predict or elucidate the potential cellular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin (see Tables 5-5CC).

#### *Diagnostic Uses for the Toxicity Markers*

As described above, the genes and gene expression information or portfolios of the genes with their expression information as provided in Tables 1-5 may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or to identify or predict the toxic effects of a compound or agent. For instance, a tissue sample such as a sample of peripheral blood cells or some other easily obtainable tissue sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-5 may be compared to the expression levels found in tissues or cells exposed to the toxins described herein. These methods may result in the diagnosis of a physiological state in the cell or may be used to identify the potential toxicity of a compound, for instance a new or unknown compound or agent. The comparison of expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described below.

In another format, the levels of a gene(s) of Tables 1-5, its encoded protein(s), or any metabolite produced by the encoded protein may be monitored or detected in a sample, such as a bodily tissue or fluid sample to identify or diagnose a physiological state of an organism. Such samples may include any tissue or fluid sample, including urine, blood and easily obtainable cells such as peripheral lymphocytes.

*Use of the Markers for Monitoring Toxicity Progression*

As described above, the genes and gene expression information provided in Tables 1-5 may also be used as markers for the monitoring of toxicity progression, such as that found after initial exposure to a drug, drug candidate, toxin, pollutant, etc. For instance, a tissue or cell sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-5 may be compared to the expression levels found in tissue or cells exposed to the renal toxins described herein. The comparison of the expression data, as well as available sequence or other information may be done by a researcher or diagnostician or may be done with the aid of a computer and databases.

*Use of the Toxicity Markers for Drug Screening*

According to the present invention, the genes identified in Tables 1-5 may be used as markers or drug targets to evaluate the effects of a candidate drug, chemical compound or other agent on a cell or tissue sample. The genes may also be used as drug targets to screen for agents that modulate their expression and/or activity. In various formats, a candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of a drug's effects by looking at the number of markers which the drug induces and comparing them. More specific drugs will have less transcriptional targets. Similar sets of markers identified for two drugs may indicate a similarity of effects.

Assays to monitor the expression of a marker or markers as defined in Tables 1-5 may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

In one assay format, gene chips containing probes to one, two or more genes from Tables 1-5 may be used to directly monitor or detect changes in gene expression in the treated or exposed cell. Cell lines, tissues or other samples are first exposed to a test agent and in some instances, a known toxin, and the detected expression levels of one or more, or preferably 2 or more of the genes of Tables 1-5 are compared to the expression

levels of those same genes exposed to a known toxin alone. Compounds that modulate the expression patterns of the known toxin(s) would be expected to modulate potential toxic physiological effects *in vivo*. The genes in Tables 1-5 are particularly appropriate markers in these assays as they are differentially expressed in cells upon exposure to a known renal toxin. Tables 1 and 2 disclose those genes that are differentially expressed upon exposure to the named toxins and their corresponding GenBank Accession numbers. Table 3 discloses the human homologues and the corresponding GenBank Accession numbers of the differentially expressed genes of Tables 1 and 2.

In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the transcriptional regulatory regions of a gene in Tables 1-5 and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.* (1990), *Anal Biochem* 188: 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a gene identified in Tables 1-5. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time, and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.* (Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cells and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector) construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the gene products

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of Tables 1-5 fused to one or more antigenic fragments or other detectable markers, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may  
5 further comprise an immunologically distinct or other detectable tag. Such a process is well known in the art (see Sambrook *et al.*, *supra*).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an  
10 aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells are disrupted and the  
15 polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the agent-contacted sample is then compared with the control samples (no exposure and exposure to a known toxin) where only the excipient is contacted with the cells and an increase or  
20 decrease in the immunologically generated signal from the agent-contacted sample compared to the control is used to distinguish the effectiveness and/or toxic effects of the agent.

Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of a protein(s) encoded by the genes in Tables  
25 1-5. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the relative amounts of a protein (Tables 1-5) between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population and a cell population exposed to a known toxin may be assayed.  
30 In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates

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may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see G.A. Grant in: Molecular Biology and Biotechnology, Meyers, ed., pp. 659-664, VCH Publishers, New York, 1995). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

#### *Nucleic Acid Assay Formats*

The genes identified as being differentially expressed upon exposure to a known renal toxin (Tables 1-5) may be used in a variety of nucleic acid detection assays to detect or quantify the expression level of a gene or multiple genes in a given sample. The genes described in Tables 1-5 may also be used in combination with one or more additional genes whose differential expression is associate with toxicity in a cell or tissue. In preferred embodiments, the genes in Tables 1-5 may be combined with one or

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more of the genes described in prior and related applications 60/292,335; 60/297,523; 60/298,925; 60/303,810; 60/303,807; 60/303,808; 60/315,047; 60/324,928; 60/330,867; 60/330,462; 60/331,805; 60/336,144; 60/340,873; 60/357,843; 60/357,842; 60/357,844; 60/364,134; 60/370,206; 60/370,247; 60/370,144; 60/371,679; 60/372,794, 09/917,800  
5 and 10/060,087 all of which are incorporated by reference on page 1 of this application.

Any assay format to detect gene expression may be used. For example, traditional Northern blotting, dot or slot blot, nuclease protection, primer directed amplification, RT-PCR, semi- or quantitative PCR, branched-chain DNA and differential display methods may be used for detecting gene expression levels. Those  
10 methods are useful for some embodiments of the invention. In cases where smaller numbers of genes are detected, amplification based assays may be most efficient. Methods and assays of the invention, however, may be most efficiently designed with hybridization-based methods for detecting the expression of a large number of genes.

Any hybridization assay format may be used, including solution-based and solid  
15 support-based assay formats. Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, particles, beads, microparticles or silicon or glass based chips, etc. Such chips, wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755).

20 Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has  
25 an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000, 100,000 or 400,000 or more of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of about a square centimeter. Probes corresponding to the genes of Tables 1-5 or from the related applications described above may be attached  
30 to single or multiple solid support structures, e.g., the probes may be attached to a single chip or to multiple chips to comprise a chip set.

Oligonucleotide probe arrays for expression monitoring can be made and used

according to any techniques known in the art (see for example, Lockhart *et al.* (1996), *Nat Biotechnol* 14: 1675-1680; McGall *et al.* (1996), *Proc Nat Acad Sci USA* 93: 13555-13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described in Tables 1-5. For instance, such arrays may contain oligonucleotides that are complementary to or hybridize to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70, 100 or more of the genes described herein. Preferred arrays contain all or nearly all of the genes listed in Tables 1-5, or individually, the gene sets of Tables 5-5CC. In a preferred embodiment, arrays are constructed that contain oligonucleotides to detect all or nearly all of the genes in any one of or all of Tables 1-5 on a single solid support substrate, such as a chip.

The sequences of the expression marker genes of Tables 1-5 are in the public databases. Table 1 provides the GenBank Accession Number or NCBI RefSeq ID for each of the sequences (see [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)). Table 3 provides the LocusLink and Unigene names and descriptions for the human homologues of the genes described in Tables 1 and 2. The sequences of the genes in GenBank and/or RefSeq are expressly herein incorporated by reference in their entirety as of the filing date of this application, as are related sequences, for instance, sequences from the same gene of different lengths, variant sequences, polymorphic sequences, genomic sequences of the genes and related sequences from different species, including the human counterparts, where appropriate. These sequences may be used in the methods of the invention or may be used to produce the probes and arrays of the invention. In some embodiments, the genes in Tables 1-5 that correspond to the genes or fragments previously associated with a toxic response may be excluded from the Tables.

As described above, in addition to the sequences of the GenBank Accession Numbers or NCBI RefSeq ID's disclosed in the Tables 1-5, sequences such as naturally occurring variants or polymorphic sequences may be used in the methods and compositions of the invention. For instance, expression levels of various allelic or homologous forms of a gene disclosed in Tables 1-5 may be assayed. Any and all nucleotide variations that do not alter the functional activity of a gene listed in the Tables 1-5, including all naturally occurring allelic variants of the genes herein disclosed, may be used in the methods and to make the compositions (*e.g.*, arrays) of the invention.

Probes based on the sequences of the genes described above may be prepared by

any commonly available method. Oligonucleotide probes for screening or assaying a tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least about 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases, longer probes of at least 30, 40, or 50 nucleotides will be desirable.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described in Tables 1-5 refer to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequences of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

"Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (e.g., the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (e.g. probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes

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where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

The phrase "hybridizing specifically to" or "specifically hybridizes" refers to the binding, duplexing, or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is  
5 present in a complex mixture (*e.g.*, total cellular) DNA or RNA.

Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 different nucleic acid hybridizations.

As used herein a "probe" is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in probes may be  
10 joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.  
15

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."  
20

The terms "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.  
25

While the mismatch(es) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most  
30

likely to destabilize the duplex with the target sequence under the test hybridization conditions.

The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH.

Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M  $\text{Na}^+$  ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical submit (e.g. nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

#### *Probe design*

One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of test probes that specifically hybridize to the sequences of interest. Probes may be produced from any region of the genes identified in the Tables and the attached representative sequence listing. In instances where the gene reference in the

Tables is an EST, probes may be designed from that sequence or from other regions of the corresponding full-length transcript that may be available in any of the sequence databases, such as those herein described. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, any available software may be used to produce specific probe sequences, including, for instance, software available from Molecular Biology Insights, Olympus Optical Co. and Biosoft International. In a preferred embodiment, the array will also include one or more control probes.

High density array chips of the invention include "test probes." Test probes may be oligonucleotides that range from about 5 to about 500, or about 7 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 35 nucleotides in length. In other particularly preferred embodiments, the probes are 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences such as cDNA fragments. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using native nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes may fall into three categories referred to herein as 1) normalization controls; 2) expression level controls; and 3) mismatch controls.

Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample to be screened. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (*e.g.*, fluorescence intensity) read from all other probes in the array are divided by the signal (*e.g.*, fluorescence intensity) from the control probes thereby normalizing the measurements.

Virtually any probe may serve as a normalization control. However, it is

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recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base

- 5 composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (*i.e.*, no secondary structure) and do not match any target-specific probes.

- Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene
- 10 provides a suitable target for expression level controls. Typically expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

- Mismatch controls may also be provided for the probes to the target genes, for
- 15 expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize.
- 20 One or more mismatches are selected such that under appropriate hybridization conditions (*e.g.*, stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a 20 mer, a corresponding mismatch
- 25 probe will have the identical sequence except for a single base mismatch (*e.g.*, substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

- Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is
- 30 directed. For example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation, for instance, a mutation of

a gene in the accompanying Tables 1-5. The difference in intensity between the perfect match and the mismatch probe provides a good measure of the concentration of the hybridized material.

#### *Nucleic Acid Samples*

- 5 Cell or tissue samples may be exposed to the test agent *in vitro* or *in vivo*. When cultured cells or tissues are used, appropriate mammalian cell extracts, such as liver extracts, may also be added with the test agent to evaluate agents that may require biotransformation to exhibit toxicity. In a preferred format, primary isolates of animal or human renal cells which already express the appropriate complement of drug-  
10 metabolizing enzymes may be exposed to the test agent without the addition of mammalian kidney extracts.

- The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may or may not be cloned. The genes may or may not be amplified. The cloning and/or amplification do not appear  
15 to bias the representation of genes within a population. In some assays, it may be preferable, however, to use polyA+ RNA as a source, as it can be used with less processing steps.

- As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or  
20 process. Methods of isolating total mRNA are well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24, Hybridization With Nucleic Acid Probes: Theory and Nucleic Acid Probes, P. Tijssen, Ed., Elsevier Press, New York, 1993. Such samples include RNA samples, but  
25 also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates are used.

- 30 Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells. Frequently the sample will be a tissue or cell sample that has been exposed to a

compound, agent, drug, pharmaceutical composition, potential environmental pollutant or other composition. In some formats, the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to, sputum, blood, blood-cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom. Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

#### *Forming High Density Arrays*

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a single or on multiple solid substrates by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung, U.S. Patent No. 5,143,854).

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithographic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in PCT Publication Nos. WO 93/09668 and WO 01/23614. High density nucleic acid arrays can also be fabricated by depositing pre-made or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses

a dispenser that moves from region to region to deposit nucleic acids in specific spots.

### *Hybridization*

Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. See WO 99/32660. The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (e.g., low temperature and/or high salt) hybrid duplexes (e.g., DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus, specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e.g., higher temperature or lower salt) successful hybridization tolerates fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency.

In a preferred embodiment, hybridization is performed at low stringency, in this case in 6x SSPET at 37°C (0.005% Triton X-100), to ensure hybridization and then subsequent washes are performed at higher stringency (e.g., 1x SSPET at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (e.g., down to as low as 0.25x SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to various controls that can be present (e.g., expression level control, normalization control, mismatch controls, etc.).

In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash

stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

#### *Signal Detection*

- The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art. See WO 99/32660.

#### *Databases*

- The present invention includes relational databases containing sequence information, for instance, for the genes of Tables 1-5, as well as gene expression information from tissue or cells exposed to various standard toxins, such as those herein described (see Tables 5-5CC). Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information (see Tables 1 and 2), or descriptive information concerning the clinical status of the tissue sample, or the animal from which the sample was derived. The database may be designed to include different parts, for instance a sequence database and a gene expression database. Methods for the configuration and construction of such databases and computer-readable media to which such databases are saved are widely available, for instance, see U.S. Patent No. 5,953,727, which is herein incorporated by reference in its entirety.

- The databases of the invention may be linked to an outside or external database such as GenBank ([www.ncbi.nlm.nih.gov/entrez/index.html](http://www.ncbi.nlm.nih.gov/entrez/index.html)); KEGG ([www.genome.ad.jp/kegg](http://www.genome.ad.jp/kegg)); SPAD ([www.grt.kyushu-u.ac.jp/spad/index.html](http://www.grt.kyushu-u.ac.jp/spad/index.html)); HUGO ([www.gene.ucl.ac.uk/hugo](http://www.gene.ucl.ac.uk/hugo)); Swiss-Prot ([www.expasy.ch/sprot](http://www.expasy.ch/sprot)); Prosite ([www.expasy.ch/tools/scnpsit1.html](http://www.expasy.ch/tools/scnpsit1.html)); OMIM ([www.ncbi.nlm.nih.gov/omim](http://www.ncbi.nlm.nih.gov/omim)); and GDB ([www.gdb.org](http://www.gdb.org)). In a preferred embodiment, as described in Tables 1-5, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI) ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)).

- Any appropriate computer platform, user interface, etc. may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or information provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such as those available from Silicon Graphics. Client/server

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environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

The databases of the invention may be used to produce, among other things, electronic Northern blots that allow the user to determine the cell type or tissue in which a  
5 given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising one or more of the genes in Tables 1-5, comprising the step of comparing the expression level  
10 of at least one gene in Tables 1-5 in a cell or tissue exposed to a test agent to the level of expression of the gene in the database. Such methods may be used to predict the toxic potential of a given compound by comparing the level of expression of a gene or genes in Tables 1-5 from a tissue or cell sample exposed to the test agent to the expression levels found in a control tissue or cell samples exposed to a standard toxin or renal toxin such  
15 as those herein described. Such methods may also be used in the drug or agent screening assays as described herein.

#### *Kits*

The invention further includes kits combining, in different combinations, high-density oligonucleotide arrays, reagents for use with the arrays, protein reagents encoded  
20 by the genes of the Tables, signal detection and array-processing instruments, gene expression databases and analysis and database management software described above. The kits may be used, for example, to predict or model the toxic response of a test compound, to monitor the progression of renal disease states, to identify genes that show promise as new drug targets and to screen known and newly designed drugs as discussed  
25 above.

The databases packaged with the kits are a compilation of expression patterns from human or laboratory animal genes and gene fragments (corresponding to the genes of Tables 1-5). In particular, the database software and packaged information that may contain the databases saved to a computer-readable medium include the expression  
30 results of Tables 1-5 that can be used to predict toxicity of a test agent by comparing the expression levels of the genes of Tables 1-5 induced by the test agent to the expression levels presented in Tables 5-5CC. In another format, database and software information

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may be provided in a remote electronic format, such as a website, the address of which may be packaged in the kit.

The kits may be used in the pharmaceutical industry, where the need for early drug testing is strong due to the high costs associated with drug development, but where bioinformatics, in particular gene expression informatics, is still lacking. These kits will reduce the costs, time and risks associated with traditional new drug screening using cell cultures and laboratory animals. The results of large-scale drug screening of pre-grouped patient populations, pharmacogenomics testing, can also be applied to select drugs with greater efficacy and fewer side-effects. The kits may also be used by smaller biotechnology companies and research institutes who do not have the facilities for performing such large-scale testing themselves.

Databases and software designed for use with microarrays is discussed in Balaban *et al.*, U.S. Patent Nos. 6,229,911, a computer-implemented method for managing information, stored as indexed Tables 1-5, collected from small or large numbers of microarrays, and 6,185,561, a computer-based method with data mining capability for collecting gene expression level data, adding additional attributes and reformatting the data to produce answers to various queries. Chee *et al.*, U.S. Patent No. 5,974,164, disclose a software-based method for identifying mutations in a nucleic acid sequence based on differences in probe fluorescence intensities between wild type and mutant sequences that hybridize to reference sequences.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

## EXAMPLES

### Example 1: Identification of Toxicity Markers

- The renal toxins cephaloridine, cisplatin, puromycin aminonucleoside (PAN), bromoethylamine hydrobromide (BEA), gentamicin, ifosfamide, cyclophosphamide, carboplatin, AY-25329, indomethacin, acyclovir, citrinin, mercuric chloride, diflunisal, cidofovir, pamidronate, lithium, hydralazine, colchicine, sulfadiazine, and adriamycin and control compositions were administered to male Sprague-Dawley rats at various timepoints using administration diluents, protocols and dosing regimes as previously described in the art and previously described in the priority applications discussed above.
- The low and high dose level for each compound are provided in the chart below.

Renal Toxin	Low Dose (mg/kg)	High Dose (mg/kg)	Method of Administration
cephaloridine	100	800	intravenous
cisplatin	1	5	intravenous
PAN	10	150	intravenous
BEA	10	200	intraperitoneal
gentamicin	2	80	intramuscular
ifosfamide	5	100	intraperitoneal
cyclophosphamide	20	2000	intraperitoneal
carboplatin	5	50	intravenous
AY-25329	25	250	oral gavage
indomethacin	1	10	oral gavage
acyclovir	10	100	intraperitoneal
citrinin	1	35	intraperitoneal
mercuric chloride	0.1	1	intravenous
diflunisal	2	400	oral gavage
cidofovir	10	100	intraperitoneal
pamidronate	1	60	intraperitoneal
lithium	0.3 (nmol/kg)	3 (nmol/kg)	intraperitoneal
hydralazine	2.5	25	intraperitoneal
colchicine	0.15	1.5	intraperitoneal
sulfadiazine	100	1000	intravenous
adriamycin	1.3	12.8	intravenous

After administration, the dosed animals were observed and tissues were collected as described below:

### OBSERVATION OF ANIMALS

#### 1. Clinical Observations-

Twice daily: mortality and moribundity check.  
 Cage Side Observations - skin and fur, eyes and mucous membrane, respiratory system, circulatory system, autonomic and central nervous system, somatomotor pattern, and behavior pattern.

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Potential signs of toxicity, including tremors, convulsions, salivation, diarrhea, lethargy, coma or other atypical behavior or appearance, were recorded as they occurred and included a time of onset, degree, and duration.

5

2. **Physical Examinations-** Prior to randomization, prior to initial treatment, and prior to sacrifice.

3. Body Weights- Prior to randomization, prior to initial treatment, and prior to sacrifice.

## 10 CLINICAL PATHOLOGY

1. Frequency Prior to necropsy.

2. Number of animals All surviving animals.

3. **Bleeding Procedure** Blood was obtained by puncture of the orbital sinus while under 70% CO<sub>2</sub>/30% O<sub>2</sub> anesthesia.

4. Collection of Blood Samples

Approximately 0.5 mL of blood was collected into EDTA tubes for evaluation of hematology parameters. Approximately 1 mL of blood was collected into serum separator tubes for clinical chemistry analysis. Approximately 200  $\mu$ L of plasma was obtained and frozen at  $\sim$ 80°C for test compound/metabolite estimation. An additional  $\sim$ 2 mL of blood was collected into a 15 mL conical polypropylene vial to which  $\sim$ 3 mL of Trizol was immediately added. The contents were immediately mixed with a vortex and by repeated inversion. The tubes were frozen in liquid nitrogen and stored at  $\sim$ 80°C.

## TERMINATION PROCEDURES

### Terminal Sacrifice

30 Approximately 3, 6, 24, 48, 72, 120, 144, 168, 336, and/or 360 hours after

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5 the initial dose, rats were weighed, physically examined, sacrificed by decapitation, and exsanguinated. The animals were necropsied within approximately five minutes of sacrifice. Separate sterile, disposable instruments were used for each animal, with the exception of bone cutters, which were used to open the skull cap. The bone cutters were dipped in disinfectant solution between animals.

Necropsies were conducted on each animal following procedures approved by board-certified pathologists.

10 Animals not surviving until terminal sacrifice were discarded without necropsy (following euthanasia by carbon dioxide asphyxiation, if moribund). The approximate time of death for moribund or found dead animals was recorded.

#### Postmortem Procedures

15 Fresh and sterile disposable instruments were used to collect tissues. Gloves were worn at all times when handling tissues or vials. All tissues were collected and frozen within approximately 5 minutes of the animal's death. The liver sections and kidneys were frozen within approximately 3-5 minutes of the animal's death. The time of euthanasia, an interim  
20 time point at freezing of liver sections and kidneys, and time at completion of necropsy were recorded. Tissues were stored at approximately -80°C or preserved in 10% neutral buffered formalin.

#### Tissue Collection and Processing

##### Liver

- 25
1. Right medial lobe – snap frozen in liquid nitrogen and stored at ~-80°C.
  2. Left medial lobe - Preserved in 10% neutral-buffered formalin (NBF) and evaluated for gross and microscopic pathology.
  3. Left lateral lobe – snap frozen in liquid nitrogen and stored at ~-80°C.

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## Heart

A sagittal cross-section containing portions of the two atria and of the two ventricles was preserved in 10% NBF. The remaining heart was frozen in liquid nitrogen and stored at  $\sim -80^{\circ}\text{C}$ .

5

## Kidneys (both)

1. Left – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at  $\sim -80^{\circ}\text{C}$ .
2. Right – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at  $\sim -80^{\circ}\text{C}$ .

10

## Testes (both)

A sagittal cross-section of each testis was preserved in 10% NBF. The remaining testes were frozen together in liquid nitrogen and stored at  $\sim -80^{\circ}\text{C}$ .

## Brain (whole)

15

A cross-section of the cerebral hemispheres and of the diencephalon was preserved in 10% NBF, and the rest of the brain was frozen in liquid nitrogen and stored at  $\sim -80^{\circ}\text{C}$ .

Microarray sample preparation was conducted with minor modifications, following the protocols set forth in the Affymetrix GeneChip Expression Analysis

20

Manual. Frozen tissue was ground to a powder using a Spex Certiprep 6800 Freezer Mill. Total RNA was extracted with Trizol (GibcoBRL) utilizing the manufacturer's protocol. The total RNA yield for each sample was 200-500  $\mu\text{g}$  per 300 mg tissue weight. mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen) followed by ethanol precipitation. Double stranded cDNA was generated from mRNA using the

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SuperScript Choice system (GibcoBRL). First strand cDNA synthesis was primed with a T7-(dT24) oligonucleotide. The cDNA was phenol-chloroform extracted and ethanol precipitated to a final concentration of 1  $\mu\text{g}/\text{ml}$ . From 2  $\mu\text{g}$  of cDNA, cRNA was synthesized using Ambion's T7 MegaScript in vitro Transcription Kit.

To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo

Diagnostics) were added to the reaction. Following a 37°C incubation for six hours, impurities were removed from the labeled cRNA following the RNeasy Mini kit protocol (Qiagen). cRNA was fragmented (fragmentation buffer consisting of 200 mM Tris-acetate, pH 8.1, 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C.

- 5 Following the Affymetrix protocol, 55 µg of fragmented cRNA was hybridized on the Affymetrix rat array set for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step
- 10 in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Data was analyzed using Affymetrix GeneChip® version 2.0 and Expression Data Mining (EDMT) software (version 1.0), GeneExpress2000, and S-Plus.

- Tables 1 and 2 disclose those genes that are differentially expressed upon
- 15 exposure to the named toxins and their corresponding GenBank Accession and Sequence Identification numbers, the identities of the metabolic pathways in which the genes function, the gene names if known, and the unigene cluster titles. The model code represents the various toxicity state that each gene is able to discriminate as well as the individual toxin type associated with each gene. The codes are defined in Table 4. The
- 20 GLGC ID is the internal Gene Logic identification number.

Table 3 discloses those genes that are the human homologues of those genes in Tables 1 and 2 that are differentially expressed upon exposure to the named toxins. The corresponding GenBank Accession and Sequence Identification numbers, the gene names if known, and the unigene cluster titles of the human homologues are listed.

- 25 Table 4 defines the comparison codes used in Tables 1, 2, 3, and 5.

- Tables 5-5CC disclose the summary statistics for each of the comparisons performed. Each of these tables contains a set of predictive genes and creates a model for predicting the renal toxicity of an unknown, *i.e.*, untested compound. Each gene is identified by its Gene Logic identification number and can be cross-referenced to a gene
- 30 name and representative SEQ ID NO. in Tables 1 and 2. For each comparison of gene expression levels between samples in the toxicity group (samples affected by exposure to a specific toxin) and samples in the non-toxicity group (samples not affected by exposure

to that same specific toxin), the tox mean (for toxicity group samples) is the mean signal intensity, as normalized for the various chip parameters that are being assayed. The non-tox mean represents the mean signal intensity, as normalized for the various chip parameters that are being assayed, in samples from animals other than those treated with the high dose of the specific toxin. These animals were treated with a low dose of the specific toxin, or with vehicle alone, or with a different toxin. Samples in the toxicity groups were obtained from animals sacrificed at the timepoint(s) indicated in the Table 5 headings, while samples in the non-toxicity groups were obtained from animals sacrificed at all time points in the experiments. For individual genes, an increase in the tox mean compared to the non-tox mean indicates up-regulation upon exposure to a toxin. Conversely, a decrease in the tox mean compared to the non-tox mean indicates down-regulation.

The mean values are derived from Average Difference (AveDiff) values for a particular gene, averaged across the corresponding samples. Each individual Average Difference value is calculated by integrating the intensity information from multiple probe pairs that are tiled for a particular fragment. The normalization multiplies each expression intensity for a given experiment (chip) by a global scaling factor. The intent of this normalization is to make comparisons of individual genes between chips possible. The scaling factor is calculated as follows:

1. From all the unnormalized expression values in the experiment, delete the largest 2% and smallest 2% of the values. That is, if the experiment yields 10,000 expression values, order the values and delete the smallest 200 and largest 200.
2. Compute the trimmed mean, which is equal to the mean of the remaining values.
3. Compute the scale factor  $SF = 100/(\text{trimmed mean})$

The value of 100 used here is the standard target valued used. Some AveDiff values may be negative due to the general noise involved in nucleic acid hybridization experiments. Although many conclusions can be made corresponding to a negative value on the GeneChip platform, it is difficult to assess the meaning behind the negative value for individual fragments. Our observations show that, although negative values are observed at times within the predictive gene set, these values reflect a real biological

phenomenon that is highly reproducible across all the samples from which the measurement was taken. For this reason, those genes that exhibit a negative value are included in the predictive set. It should be noted that other platforms of gene expression measurement may be able to resolve the negative numbers for the corresponding genes.

- 5 The predictive ability of each of those genes should extend across platforms, however. Each mean value is accompanied by the standard deviation for the mean. The linear discriminant analysis score (discriminant score), as disclosed in the tables, measures the ability of each gene to predict whether or not a sample is toxic. The discriminant score is calculated by the following steps:

10 **Calculation of a discriminant score**

Let  $X_i$  represent the AveDiff values for a given gene across the non-tox samples,  $i=1 \dots n$ .

Let  $Y_i$  represent the AveDiff values for a given gene across the tox samples,  $i=1 \dots t$ .

The calculations proceed as follows:

1. Calculate mean and standard deviation for  $X_i$ 's and  $Y_i$ 's, and denote these by  $m_x, m_y, s_x, s_y$ .
- 15 2. For all  $X_i$ 's and  $Y_i$ 's, evaluate the function  $f(z) = ((1/s_y) * \exp(-.5 * ((z - m_y)/s_y)^2)) / (((1/s_y) * \exp(-.5 * ((z - m_y)/s_y)^2)) + ((1/s_x) * \exp(-.5 * ((z - m_x)/s_x)^2)))$ .
3. The number of correct predictions, say P, is then the number of  $Y_i$ 's such that  $f(Y_i) > .5$  plus the number of  $X_i$ 's such that  $f(X_i) < .5$ .
- 20 4. The discriminant score is then  $P/(n+t)$ .

- Linear discriminant analysis uses both the individual measurements of each gene and the calculated measurements of all combinations of genes to classify samples. For each gene a weight is derived from the mean and standard deviation of the toxic and nontox groups. Every gene is multiplied by a weight and the sum of these values results in a collective discriminate score. This discriminant score is then compared against
- 25 collective centroids of the tox and nontox groups. These centroids are the average of all tox and nontox samples respectively. Therefore, each gene contributes to the overall prediction. This contribution is dependent on weights that are large positive or negative numbers if the relative distances between the tox and nontox samples for that gene are large and small numbers if the relative distances are small. The discriminant score for
- 30 each unknown sample and centroid values can be used to calculate a probability between zero and one as to the group in which the unknown sample belongs.

**Example 2: General Toxicity Modeling**

Samples were selected for grouping into tox-responding and non-tox-responding groups by examining each study individually with Principal Components Analysis (PCA) to determine which treatments had an observable response. Only groups where confidence of their tox-responding and non-tox-responding status was established were included in building a general tox model (Table 5).

Linear discriminant models were generated to describe toxic and non-toxic samples. The top discriminant genes and/or EST's were used to determine toxicity by calculating each gene's contribution with homo and heteroscedastic treatment of variance and inclusion or exclusion of mutual information between genes. Prediction of samples within the database exceeded 80% true positives with a false positive rate of less than 5%. It was determined that combinations of genes and/or EST's generally provided a better predictive ability than individual genes and that the more genes and/or EST used the better predictive ability. Although the preferred embodiment includes fifty or more genes, many pairings or greater combinations of genes and/or EST can work better than individual genes. All combinations of two or more genes from the selected list (Table 5) could be used to predict toxicity. These combinations could be selected by pairing in an agglomerate, divisive, or random approach. Further, as yet undetermined genes and/or EST's could be combined with individual or combination of genes and/or EST's described here to increase predictive ability. However, the genes and/or EST's described here would contribute most of the predictive ability of any such undetermined combinations.

Other variations on the above method can provide adequate predictive ability. These include selective inclusion of components via agglomerate, divisive, or random approaches or extraction of loading and combining them in agglomerate, divisive, or random approaches. Also the use of composite variables in logistic regression to determine classification of samples can also be accomplished with linear discriminate analysis, neural or Bayesian networks, or other forms of regression and classification based on categorical or continual dependent and independent variables.

**Example 3: Modeling Methods**

The above modeling methods provide broad approaches of combining the expression of genes to predict sample toxicity. One could also provide no weight in a

simple voting method or determine weights in a supervised or unsupervised method using agglomerate, divisive, or random approaches. All or selected combinations of genes may be combined in ordered, agglomerate, or divisive, supervised or unsupervised clustering algorithms with unknown samples for classification. Any form of correlation matrix may also be used to classify unknown samples. The spread of the group distribution and discriminate score alone provide enough information to enable a skilled person to generate all of the above types of models with accuracy that can exceed discriminate ability of individual genes. Some examples of methods that could be used individually or in combination after transformation of data types include but are not limited to: Discriminant Analysis, Multiple Discriminant Analysis, logistic regression, multiple regression analysis, linear regression analysis, conjoint analysis, canonical correlation, hierarchical cluster analysis, k-means cluster analysis, self-organizing maps, multidimensional scaling, structural equation modeling, support vector machine determined boundaries, factor analysis, neural networks, bayesian classifications, and resampling methods.

**Example 4: Grouping of Individual compound and Pathology Classes**

Samples were grouped into individual pathology classes based on known toxicological responses and observed clinical chemical and pathology measurements or into early and late phases of observable toxicity within a compound (Tables 5A-5CC). The top 10, 25, 50, 100 genes based on individual discriminate scores were used in a model to ensure that combination of genes provided a better prediction than individual genes. As described above, all combinations of two or more genes from this list could potentially provide better prediction than individual genes when selected in any order or by ordered, agglomerate, divisive, or random approaches. In addition, combining these genes with other genes could provide better predictive ability, but most of this predictive ability would come from the genes listed herein.

Samples may be considered toxic if they score positive in any pathological or individual compound class represented here or in any modeling method mentioned under general toxicology models based on combination of individual time and dose grouping of individual toxic compounds obtainable from the data. The pathological groupings and early and late phase models are preferred examples of all obtainable combinations of sample time and dose points. Most logical groupings with one or more genes and one or

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more sample dose and time points should produce better predictions of general toxicity, pathological specific toxicity, or similarity to known toxicant than individual genes.

- 5        Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, patent applications and publications referred to in this application are herein incorporated by reference in their entirety.

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TABLE 1: SUMMARY						Allyl Pocket No. 44921 subseq
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	ESTs	UniGene Cluster No.
1	6949	AA012785	q			ESTs
2	25098	AA108277	h.v			ESTs, Highly similar to includes exons 3 through 12 [M.musculus]
3	17312	AA108308	r			ESTs, Moderately similar to NADH-ubiquinone oxidoreductase subunit C1-SGDH [H.sapiens]
4	16882	AA684537	o			ESTs, Highly similar to alpha NAC1.9.2. protein [M.musculus]
5	6049	AA685178	y			ESTs
6	4426	AA685974	l.m			ESTs, Weakly similar to T23657 hypothetical protein M01F1.6 - Caenorhabditis elegans [C.elegans]
7	21815	AA686423	g			ESTs, Weakly similar to T23657 hypothetical protein M01F1.6 - Caenorhabditis elegans [C.elegans]
8	1600	AA686470	i	DNA-damage inducible transcript 3		DNA-damage inducible transcript 3
8	1599	AA686470	i	DNA-damage inducible transcript 3		DNA-damage inducible transcript 3
9	21997	AA799325	u			ESTs
10	18396	AA799330	v			ESTs, Highly similar to AF132951 1 CGI-17 protein [H.sapiens]
11	6581	AA799412	f.l			ESTs, Weakly similar to ESR1 RAT ESTROGEN RECEPTOR [R.norvegicus]
12	16538	AA799449	k			ESTs, Weakly similar to nucleosome assembly protein [R.norvegicus]
13	23294	AA799472	u			ESTs, Moderately similar to CGI-116 protein [H.sapiens]
14	18290	AA799497	r			ESTs
15	19981	AA799523	e			ESTs, Moderately similar to hnRNP protein [R.norvegicus]
16	20843	AA799545	h			ESTs, Weakly similar to TCPA RAT 1 COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
17	16993	AA799560	b			ESTs
18	16576	AA799570	d			ESTs
19	18351	AA799591	i			ESTs, Highly similar to TBB1 RAT TUBULIN BETA CHAIN [R.norvegicus]
20	17712	AA799598	z			ESTs
22	18346	AA799718	f			ESTs
23	8768	AA799726	l			ESTs
24	11687	AA799732	w			ESTs, Highly similar to Dgcr6 protein [M.musculus]
25	18348	AA799744	u			ESTs
26	17494	AA799751	n			ESTs
27	18360	AA799771	General			ESTs
28	18880	AA799801	w			ESTs
29	20998	AA799803	z			ESTs, Weakly similar to senne protease [R.norvegicus]
30	21006	AA799861	c			ESTs, Highly similar to IRF7 MOUSE INTERFERON REGULATORY FACTOR 7 [M.musculus]
31	15011	AA799883	General			ESTs, Highly similar to DORT helix-destabilizing protein - rat [R.norvegicus]
32	20811	AA799899	a			ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L18A [R.norvegicus]
33	23202	AA799971	General			ESTs, Weakly similar to S52875 probable membrane protein YDR109c yeast [Saccharomyces cerevisiae] [S.cerevisiae]
34	4832	AA800190	b			ESTs, Highly similar to glycogen phosphorylase [R.norvegicus]
35	21656	AA800202	d			ESTs

TABLE 1: SUMMARY						Atty. Docket No. 44274-5083W
						Doc. No. 17883W.1
Sequence ID No.	Identifier	GenBank Acc# Ref. Seq ID	Model Code	Gene Name	Unigene Cluster Title	
36	18433	AA800218	ly,z		ESTs, Weakly similar to T15476 hypothetical protein C09F5.2 - <i>Caenorhabditis elegans</i> [C.elegans]	
37	6386	AA800235	u		ESTs	
38	18442	AA800256	h,k		ESTs	
39	21092	AA800380	y		ESTs, Weakly similar to CORTICOSTEROID 11-BETA-DEHYDROGENASE, ISOZYME 1 [R.norvegicus]	
40	17325	AA800587	General		ESTs, Weakly similar to glutathione peroxidase [R.norvegicus]	
41	13930	AA800613	cc, General		<i>Rattus norvegicus</i> gene for TIS11, complete cds	
42	21372	AA800693	v		ESTs	
42	21373	AA800693	s		ESTs	
43	18161	AA800701	k		ESTs	
44	6595	AA800753	w		ESTs	
45	13348	AA800928	General		ESTs	
46	23115	AA801165	o,y		ESTs, Highly similar to H2A1 RAT HISTONE H2A.1 [R.norvegicus]	
47	12399	AA801307	General		ESTs	
48	7543	AA801395	General		ESTs	
49	24237	AA817726	t,General		ESTs	
50	11215	AA817921	o		ESTs, Moderately similar to T25763 hypothetical protein F46F11.4 - <i>Caenorhabditis elegans</i> [C.elegans]	
51	5985	AA818005	g		ESTs	
52	11338	AA818016	x		ESTs, Highly similar to rabkinesin-6 [M.musculus]	
53	2845	AA818026	k,General		ESTs, Weakly similar to PRSC MOUSE 26S PROTEASOME REGULATORY SUBUNIT S12 [M.musculus]	
54	16756	AA818089	l,t, General		ESTs, Highly similar to glycyl-tRNA synthetase [H.sapiens]	
55	17771	AA818224	e,g,p, General		ESTs, Highly similar to TBB1 RAT TUBULIN BETA CHAIN [R.norvegicus]	
56	6522	AA818261	g,m		ESTs, Moderately similar to autoantigen p542 [H.sapiens]	
57	5924	AA818359	y		ESTs	
58	7806	AA818421	b,aa		ESTs	
59	8237	AA818512	v		ESTs	
60	17434	AA818574	h		ESTs	
61	8728	AA818615	General		ESTs	
62	6054	AA818658	b,v,cc, General	Diphtheria toxin receptor (heparin binding epidermal growth factor - like growth factor)	Diphtheria toxin receptor (heparin binding epidermal growth factor - like growth factor)	
63	11590	AA818721	d		ESTs, Moderately similar to S65785 mef-13a protein - mouse [M.musculus]	
64	4291	AA818741	g,General		ESTs	
65	4330	AA818747	o,General		ESTs	
66	19723	AA818761	v,General		ESTs	
67	13684	AA818770	h,j,j,m		<i>Rattus norvegicus</i> serine protease gene, complete cds	
68	6322	AA818801	k		ESTs	
69	7690	AA818875	General	uroguanylin	uroguanylin	
70	4952	AA818907	q,General		ESTs	
71	6094	AA818911	t		ESTs	
72	10985	AA818998	o,General		ESTs, Weakly similar to HP33 [R.norvegicus]	
73	6120	AA819008	t		ESTs	

TABLE 1: SUMMARY						Atty. Docket No. 44291-5083WG
						Doc. No. 1798837.1
Sequence ID No.	Identifier	GenBank Accn Ref. Seq ID	Model Code	Gene Name	Sequence Cluster Title	
74	2586	AA819081	c		ESTs, Weakly similar to testis specific protein [R.norvegicus]	
76	6438	AA819269	o		ESTs	
77	24721	AA819306	d,w		ESTs	
78	6250	AA819376	o,y		Rattus norvegicus mRNA for inositol hexakisphosphate kinase, complete cds	
80	6281	AA819517	j		ESTs, Weakly similar to JC5707 HYA22 protein [H.sapiens]	
81	10141	AA819526	j		ESTs	
82	6551	AA819558	t		ESTs	
83	6723	AA819653	r		ESTs, Moderately similar to dJ30M3.1 [H.sapiens]	
84	14958	AA819744	aa		ESTs	
85	19433	AA819776	v		ESTs, Weakly similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]	
86	6204	AA819889	aa		ESTs	
87	22820	AA848315	General	HmM:inosine 5'-phosphate dehydrogenase 2	ESTs, Weakly similar to guanosine monophosphate reductase [R.norvegicus]	
88	6614	AA848389	bb		ESTs, Weakly similar to T26686 hypothetical protein Y38F1A.6 - Caenorhabditis elegans [C.elegans]	
89	21125	AA848437	General		ESTs	
90	23504	AA848496	q		ESTs, Moderately similar to IF4B_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 4B [H.sapiens]	
91	18532	AA848675	g		ESTs, Weakly similar to FMO1 RAT DIMETHYLANILINE MONOOXYGENASE [R.norvegicus]	
92	21140	AA848738	c		ESTs	
93	16128	AA848807	o		ESTs, Moderately similar to AF132946.1 CG1-12 protein [H.sapiens]	
94	22923	AA848929	g		ESTs	
95	17339	AA849497	General		ESTs	
96	11727	AA849518	l		ESTs	
97	21275	AA849796	(J,m, General)		ESTs	
98	16678	AA849827	aa		ESTs	
99	8515	AA849917	e		ESTs	
100	18447	AA849939	General		ESTs	
101	12130	AA850037	p		ESTs	
102	23881	AA850040	x,aa	cyclase-associated protein homologue	cyclase-associated protein homologue	
103	13615	AA850364	l		ESTs, Moderately similar to RB17 MOUSE RAS-RELATED PROTEIN RAB-17 [M.musculus]	
105	2637	AA850893	x		ESTs, Highly similar to hypothetical protein [H.sapiens]	
106	22093	AA850909	d		ESTs	
107	21766	AA850916	c		ESTs	
108	2847	AA850919	w		ESTs, Weakly similar to dithiolethione-inducible gene-1 [R.norvegicus]	
109	12162	AA850975	h		Rattus norvegicus mRNA for ras-GTPase-activating protein SH3-domain binding protein, partial cds	
110	9514	AA850978	General		ESTs	
111	3924	AA851017	e,q		ESTs, Highly similar to molybdopterinsynthase large subunit [M.musculus]	
111	3925	AA851017	o,General		ESTs, Highly similar to molybdopterinsynthase large subunit [M.musculus]	
112	4490	AA851184	a,k		Rattus norvegicus mRNA for cathepsin Y, partial cds	

TABLE 1: SUMMARY					
Atty. Pocket No. 4422-3023WC					
Doc. No. 1792237.1					
Sequence ID No.	Identifier	GenBank/ Acc. Ref. Seq. ID	Model Code	Gene Name	Uniprot Cluster Title
113	19187	AA851230	General		ESTs, Weakly similar to T28050 hypothetical protein ZK856.11 - <i>Caenorhabditis elegans</i> [C.elegans]
114	19189	AA851237	c		ESTs, Highly similar to ubiquitin specific protease UBPA3 [M.musculus]
115	15386	AA851241	m		ESTs, Highly similar to hypothetical protein [H.sapiens]
116	21462	AA851261	g.l. General		ESTs, Weakly similar to A61362 phosphorylation regulatory protein HP-10 [H.sapiens]
117	21471	AA851343	General		ESTs
118	16902	AA851379	p	HHs:NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	ESTs, Moderately similar to NUIM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR [H.sapiens]
119	23376	AA851392	l.x		ESTs, Moderately similar to kinesin-like DNA binding protein [H.sapiens]
119	23377	AA851392	x		ESTs, Moderately similar to kinesin-like DNA binding protein [H.sapiens]
120	13349	AA851417	General		ESTs
121	21527	AA851733	r.u.		ESTs
122	4048	AA851814	l.o.u. General		Rattus norvegicus osteocalcin mRNA, complete cds
123	10561	AA851871	bb		ESTs, Highly similar to SSRA HUMAN TRANSLOCAN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR [H.sapiens]
124	17411	AA858621	j.y		Rattus norvegicus CaM-kinase II inhibitor alpha mRNA, complete cds
125	1801	AA858636	k.s.x.bb		ESTs, Weakly similar to MCM6 RAT DNA REPLICATION LICENSING FACTOR MCM6 [R.norvegicus]
126	16350	AA858674	p		ESTs
127	19484	AA858653	e		ESTs
128	6360	AA858636	d		ESTs
129	17334	AA858704	p		ESTs, Weakly similar to Reg receptor [R.norvegicus]
130	6380	AA858758	q		ESTs, Weakly similar to dJ413H6.1.1 [H.sapiens]
131	13219	AA858759	a		ESTs
132	6384	AA858788	l.m.General		ESTs
134	13412	AA858830	p		ESTs, Highly similar to p40 seven-transmembrane-domain protein [M.musculus]
135	7279	AA858892	f		ESTs
136	18217	AA858930	t		ESTs
137	5867	AA858953	v.General	HHs:asparaginyl-tRNA synthetase	ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]
138	14479	AA858969	r		ESTs, Moderately similar to I56526 interleukin 1 receptor type 1 - rat [R.norvegicus]
139	6431	AA859085	t		ESTs
140	17361	AA859114	o.General		ESTs
141	21025	AA859241	General	outer membrane protein	outer membrane protein
142	10076	AA859271	c		ESTs
143	21791	AA859333	k		ESTs, Weakly similar to CYSR RAT CYSTEINE-RICH PROTEIN 1 [R.norvegicus]
144	16314	AA859348	cc.General		ESTs
145	18862	AA859520	f		ESTs
146	15059	AA859545	r		ESTs

TABLE SUMMARY						Atty. Docket No. 44924-008WO
						Doc. No. 1788397.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title	
147	19894	AA855581	s		Rattus norvegicus late gestation lung protein 1 (Lg1) mRNA, complete cds	
148	14353	AA855585	h		ESTs	
149	16318	AA859648	h		ESTs, Weakly similar to DnaJ homolog 2 (R.norvegicus)	
150	17316	AA859652	General		ESTs	
151	19067	AA859663	n,q		ESTs	
152	22406	AA859680	n		ESTs	
153	20599	AA859690	x		ESTs	
154	14261	AA859693	u		ESTs, Weakly similar to YNH2_CAEAL HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III (C.elegans)	
155	14138	AA859700	v	Hh:protoporphyrinogen oxidase	ESTs, Highly similar to PPOX MOUSE PROTOPORPHYRIN OXIDASE [M.musculus]	
155	14139	AA859700	v	Hh:protoporphyrinogen oxidase	ESTs, Highly similar to PPOX MOUSE PROTOPORPHYRIN OXIDASE [M.musculus]	
157	22374	AA859804	l		ESTs, Weakly similar to IF4E MOUSE EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (R.norvegicus)	
158	22385	AA859805	b,k		ESTs, Moderately similar to LYOX RAT PROTEIN-LYSINE 6-OXIDASE PRECURSOR (R.norvegicus)	
159	22773	AA859885	n		ESTs	
160	22816	AA859898	k,x,z		ESTs	
161	11891	AA859926	x		ESTs	
162	23070	AA859942	k		ESTs, Highly similar to N-myristoyltransferase 1 [M.musculus]	
163	23121	AA859948	k		ESTs	
164	23166	AA859954	cc, General		ESTs	
165	18468	AA859966	aa		ESTs, Weakly similar to Edp1 protein [M.musculus]	
166	23336	AA859981	q	Hh:inositol(myo)-1(or 4)-monophosphatase 2	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE [R.norvegicus]	
167	4222	AA860024	a,bb		ESTs, Highly similar to EF1G_HUMAN ELONGATION FACTOR 1-3AMMA [H.sapiens]	
168	13974	AA860030	u,x, General		Rattus norvegicus mRNA for class I beta-tubulin, complete cds	
169	7090	AA860039	x	Hyaluronan mediated motility receptor (RHAMM)	EST, Hyaluronan mediated motility receptor (RHAMM)	
170	23769	AA860055	k,x		ESTs, Moderately similar to T08681 anti-silencing protein ASF1 homolog DKFZp547E2110.1 [H.sapiens]	
171	16323	AA866240	w		EST	
172	4482	AA866264	General		ESTs, Weakly similar to PE2R RAT 20 ALPHA-HYDROXYSTEROID DEHYDROGENASE [R.norvegicus]	
173	15884	AA866276	k		ESTs, Weakly similar to A60543 protein kinase [R.norvegicus]	
174	17742	AA866302	c,y	4-hydroxyphenylpyruvic acid dioxygenase	4-hydroxyphenylpyruvic acid dioxygenase	
175	16333	AA866414	a,h	Solute carrier family 4, member 1, anion exchange protein 1 (kidney band 3)	Solute carrier family 4, member 1, anion exchange protein 1 (kidney band 3)	
176	18918	AA866444	p,q		ESTs, Moderately similar to AF141884 1 oligophrenin-1 like protein [H.sapiens]	
177	16853	AA866454	jj,m,y,z		ESTs	
178	18995	AA866459	h,m		ESTs	

TABLE 1: SUMMARY					Atty. Docket No. 44324-3068WG
					Doc. No. 4798397.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title
179	18013	AA866482	s		ESTs, Highly similar to FGD1 MOUSE PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [M.musculus]
180	26036	AA874849	r		
181	16059	AA874857	h		ESTs
182	16069	AA874873	r		ESTs
183	21633	AA874951	f		ESTs, Weakly similar to RNA binding protein [H.sapiens]
184	16192	AA874995	w		ESTs
185	16254	AA875025	j		ESTs, Highly similar to RET3 BOVIN RETINOIC ACID-BINDING PROTEIN I, CELLULAR [R.norvegicus]
186	16312	AA875032	cc, General		ESTs
187	20701	AA875097	b		Rat alpha-fibrinogen mRNA, 3' end
188	16416	AA875098	bb		ESTs, Highly similar to ARF3_HUMAN ADP-RIBOSYLATION FACTOR [R.norvegicus]
189	16419	AA875102	bb		ESTs, Highly similar to RUXE_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN E [M.musculus]
190	15313	AA875126	lm, General		ESTs
191	10936	AA875146	w		ESTs, Weakly similar to AF151834.1 COI-78 protein [H.sapiens]
192	18084	AA875186	n		ESTs
193	15371	AA875205	u		ESTs, Highly similar to IF39_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 [H.sapiens]
194	15401	AA875257	z,z		ESTs
195	15410	AA875268	p,s	Hh:NADH dehydrogenase (ubiquinone) Fe-S protein 7 (20kD) (NADH-coenzyme Q reductase)	ESTs, Highly similar to NUKM HUMAN, partial CDS [H.sapiens]
196	15420	AA875286	f		ESTs
197	15446	AA875327	s,w		ESTs
198	7936	AA875495	b, General		ESTs
199	17314	AA875509	il,m		ESTs, Highly similar to includes exons 3 through 12 [M.musculus]
200	24472	AA875523	k		ESTs, Highly similar to MLES RAT MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM [R.norvegicus]
201	15587	AA875577	j		ESTs
202	15617	AA875620	General		ESTs
202	15618	AA875620	General		ESTs
203	5384	AA891041	f,cc, Gene	jun B proto-oncogene	jun B proto-oncogene
204	24814	AA891209	f,p		ESTs, Moderately similar to R33729.1, partial CDS [H.sapiens]
205	21930	AA891322	d		ESTs, Weakly similar to AF151373.1 nucleolin-related protein NRP [R.norvegicus]
206	17225	AA891553	h		ESTs, Highly similar to eIF3 p66 [M.musculus]
207	7522	AA891571	j,m		ESTs, Weakly similar to S67314 regulatory protein RMS1 - yeast (Saccharomyces cerevisiae) [S.cerevisiae]
208	9071	AA891578	b		ESTs
209	19321	AA891666	u	melanoma antigen, family D, 1	melanoma antigen, family D, 1

TABLE 1: SUMMARY					
Ally, Pocket No. 43921-50870					
Doc. No. 179389					
Sequence ID/No.	Identifier	GenBank Acc#	Model Code	Gene Name	Uniprot Cluster Title
210	17693	AA891737	JLM,n,y,z		ESTs
211	17256	AA891739	General		ESTs, Weakly similar to T2521 hypothetical protein F52H3.5 - <i>Caenorhabditis elegans</i> [C.elegans]
213	18269	AA891769	General		ESTs, Moderately similar to FINC RAT FIBRONECTIN PRECURSOR [R.norvegicus]
214	9905	AA891774	s,bb,D239General		ESTs
215	17061	AA891812	d		ESTs, Highly similar to alpha-adducin, hypertensive phenotype [R.norvegicus]
216	7050	AA891824	h		Rattus norvegicus clone ZG52 mRNA sequence
217	4463	AA891831	General		ESTs, Weakly similar to PE2R RAT 20 ALPHA-HYDROXYSTEROID DEHYDROGENASE [R.norvegicus]
218	14289	AA891838	i		ESTs, Highly similar to muscle protein 864 [M.musculus]
219	20523	AA891842	r,cc		ESTs
220	17779	AA891914	g,s,z		ESTs, Moderately similar to ACY1_HUMAN AMINOACYLASE-1 [H.sapiens]
221	17438	AA891943	General		ESTs
222	22862	AA891944	p		ESTs
223	1159	AA891949	e,z		ESTs
224	4473	AA891965	General		ESTs, Weakly similar to T31496 hypothetical protein Y116A8C.25 - <i>Caenorhabditis elegans</i> [C.elegans]
225	6362	AA892053	f,j,l,m		ESTs, Highly similar to chromatin structural protein homolog Supt5hp [M.musculus]
226	9037	AA892066	y		ESTs
227	19469	AA892112	General		ESTs, Weakly similar to proline dehydrogenase [M.musculus]
228	14595	AA892128	o,l,v		ESTs
229	16527	AA892154	cc		ESTs
230	4482	AA892173	bb		EST
231	20917	AA892238	h		ESTs
232	2357	AA892268	d		ESTs, Weakly similar to PC4221 protein-tyrosine kinase [R.norvegicus]
233	18183	AA892271	h		ESTs
234	6523	AA892299	d		ESTs
236	13647	AA892367	a		ESTs, Highly similar to RL3 RAT 60S RIBOSOMAL PROTEIN L3 [R.norvegicus]
237	3473	AA892378	v		ESTs, Highly similar to AF151853 1 CGI-135 protein [H.sapiens]
238	17682	AA892382	j,p,s,x,General		ESTs, Moderately similar to AF185570 putative N-acetyltransferase Camello 4 [R.norvegicus]
239	820	AA892395	g,s	Aldolase B, fructose-biphosphate	
240	14754	AA892414	u		ESTs
241	17439	AA892446	f		ESTs
242	16469	AA892462	p		ESTs, Moderately similar to UCYR_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 5.4 KD PROTEIN [H.sapiens]
243	13609	AA892468	i,General		Rattus norvegicus mRNA for prostatic precursor, complete cds
243	13610	AA892468	n,v,General		Rattus norvegicus mRNA for prostatic precursor, complete cds

TABLE 1: SUMMARY						Atty. Docket No. 43929-5083WG
						Doc. No. 1798997
Sequence ID No.	Identifying	GenBank Acc/ Ref. Seq ID	Model Code	Gene Name	Accession Title	
244	9254	AA892470	n,u		ESTs, Highly similar to HISTONE H2A Z [R.norvegicus]	
245	11991	AA892483	s		ESTs	
246	1522	AA892486	f		ESTs, Moderately similar to LYAG MOUSE LYOSOMAL ALPHA-GLUCOSIDASE PRECURSOR [M.musculus]	
247	11994	AA892507	aa		ESTs, Moderately similar to S63540 protein DS 1, 24K [H.sapiens]	
248	23888	AA892520	w		ESTs	
248	23889	AA892520	h		ESTs	
249	8589	AA892522	p		ESTs	
250	15154	AA892532	p		R.norvegicus (Wistar) CaBP1 mRNA	
251	17468	AA892545	r		ESTs, Highly similar to multi-membrane spanning polyspecific transporter [M.musculus]	
252	11203	AA892554	f,h		ESTs, Highly similar to ras-GTPase-activating protein SH3-domain binding protein [M.musculus]	
253	18906	AA892561	a,bb, General		ESTs, Moderately similar to PTDO12 [H.sapiens]	
254	19327	AA892562	f,l,y,z		R.norvegicus mRNA for nucleolar protein NAP57	
255	18274	AA892572	p		ESTs	
256	4512	AA892576	cc		ESTs	
257	15676	AA892582	w		ESTs, Highly similar to RLB_HUMAN 60S RIBOSOMAL PROTEIN L [R.norvegicus]	
258	19085	AA892588	General		ESTs	
258	19086	AA892588	General		ESTs	
259	20065	AA892647	l		ESTs, Highly similar to H4_HUMAN HISTONE H4 [R.norvegicus]	
260	20088	AA892666	a,n		ESTs	
261	23763	AA892773	n		ESTs	
262	17549	AA892776	f,z		Rat mitochondrial proton/phosphate symporter mRNA, complete cds	
263	13542	AA892798	b		ESTs	
264	22537	AA892799	General	HHs:glyoxylate reductase/hydroxypyruvate reductase	ESTs, Weakly similar to SERA RAT D-3-PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus]	
264	22539	AA892799	v	HHs:glyoxylate reductase/hydroxypyruvate reductase	ESTs, Weakly similar to SERA RAT D-3-PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus]	
264	22538	AA892799	General	HHs:glyoxylate reductase/hydroxypyruvate reductase	ESTs, Weakly similar to SERA RAT D-3-PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus]	
265	6951	AA892820	h		ESTs, Weakly similar to S70642 ubiquitin ligase Nedd4 - rat [R.norvegicus]	
266	23322	AA892821	j,z		Rattus norvegicus air mRNA for androgen-inducible aldehyde reductase, complete cds	
267	17923	AA892843	f		ESTs, Weakly similar to T29904 hypothetical protein F59A3.3 - Caenorhabditis elegans [C.elegans]	
268	22871	AA892859	m		ESTs, Weakly similar to procollagen-lysine 5-dioxygenase [R.norvegicus]	
269	9053	AA892861	p,v, General		ESTs	
270	16482	AA892940	w		ESTs, Weakly similar to EF2 RAT ELONGATION FACTOR 2 [R.norvegicus]	
271	12020	AA893035	j,y		Rattus norvegicus HP33 mRNA, complete cds	
272	3863	AA893060	General		ESTs	
273	13332	AA893080	i,General		ESTs	

TABLE 1a. SUMMARY					Atty. Docket No. 44924-5039WG Doc. No. 192849-1	
Sequence ID No.	Identifier	SanBank Accel Ref. Seq. ID	Model Code	Seq. Name	Juliano Cluster Title	
274	21305	AA893062	General		ESTs	
275	16591	AA893191	j,z		ESTs	
276	17447	AA893192	General		ESTs	
277	3876	AA893205	n		ESTs	
278	3878	AA893230	General		ESTs, Weakly similar to CALM_HUMAN CALMODULIN [R.norvegicus]	
279	20986	AA893242	q	Acyl CoA synthetase, long chain	Acyl CoA synthetase, long chain	
280	16168	AA893280	i,z, General		ESTs, Moderately similar to adipophelin [H.sapiens]	
281	3886	AA893289	m,y		ESTs	
282	15209	AA893327	y		ESTs	
283	17800	AA893436	cc		ESTs	
284	17836	AA893626	h		ESTs, Weakly similar to LIS1 MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE B ALPHA SUBUNIT [R.norvegicus]	
285	9084	AA893717	x		ESTs	
286	22731	AA893743	d		ESTs	
287	12031	AA893860	v	HHs:threonyl-tRNA synthetase	ESTs, Moderately similar to SYTC_HUMAN THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]	
288	17897	AA893905	k		ESTs	
289	3447	AA893962	d		ESTs	
290	22583	AA894009	n		ESTs	
291	10540	AA894027	i		EST	
292	4569	AA894059	x		ESTs, Highly similar to A55746 protein kinase [M.musculus]	
293	18419	AA894130	d		ESTs, Weakly similar to APP2 RAT AMYLOID-LIKE PROTEIN 2 PRECURSOR [R.norvegicus]	
294	17338	AA894297	j		ESTs	
295	19120	AA894318	j		ESTs	
296	19762	AA899113	i		ESTs	
297	18286	AA899219	u		Rat mRNA for beta-tubulin T beta15	
298	22051	AA899498	w		ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans [C.elegans]	
299	22052	AA899498	q		ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans [C.elegans]	
299	21628	AA899563	aa		ESTs	
300	4262	AA899590	i		ESTs	
301	4661	AA899709	t,General	receptor activity modifying protein 3	receptor activity modifying protein 3	
302	21354	AA899721	q		ESTs	
303	17905	AA899762	General		Rattus norvegicus epidermal growth factor receptor related protein (Erp) mRNA, complete cds	
304	15231	AA899840	r		ESTs	
305	23778	AA899854	c,k,x	topoisomerase (DNA) II alpha	topoisomerase (DNA) II alpha	
306	22060	AA899898	b		ESTs	
307	9114	AA899951	v,General		ESTs	
308	8988	AA900148	f		ESTs	
309	11841	AA900247	v		Rattus norvegicus mRNA for Hsp70/Hsp90 organizing protein	
310	4725	AA900290	cc		ESTs, Highly similar to ALPHA-2-MACROGLOBULIN PRECURSOR [R.norvegicus]	
311	4747	AA900465	General		ESTs	
312	20988	AA900562	o		ESTs	
313	3822	AA900863	b,g, General		ESTs, Weakly similar to nuclear RNA helicase [R.norvegicus]	

TABLE 1: SUMMARY						Atty. Docket No. 44392-5083WG
						Doc. No. 1798397.1
Sequence ID No.	Identifier	GenBank/ACGI Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title	
315	12420	AA901017	b		ESTs, Weakly similar to T20702 hypothetical protein F10C2.6 - Caenorhabditis elegans [C.elegans]	
316	4849	AA901155	s		Rattus norvegicus CDK105 mRNA	
317	3959	AA901336	General		ESTs, Highly similar to IF2B_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT [H.sapiens]	
318	22846	AA923982	a,d		ESTs, Highly similar to ATP-specific succinyl-CoA synthetase beta subunit [M.musculus]	
319	4895	AA923999	k		ESTs	
320	21546	AA924188	cc, General		ESTs	
321	24192	AA924210	n,General		ESTs	
322	4933	AA924301	g,i,Gener al		EST	
323	4944	AA924405	l,General		ESTs, Moderately similar to NOS6_HUMAN NUCLEOLAR PROTEIN NOP56 [H.sapiens]	
324	4948	AA924426	r		ESTs	
325	4949	AA924432	General		ESTs, Weakly similar to NPT2 RAT RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [R.norvegicus]	
326	18891	AA924588	e		ESTs	
327	22540	AA924630	v,General	HHs:glyoxylate reductase/hydroxypyruvate reductase	ESTs, Weakly similar to SERA RAT D- 3-PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus]	
327	22541	AA924630	General	HHs:glyoxylate reductase/hydroxypyruvate reductase	ESTs, Weakly similar to SERA RAT D- 3-PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus]	
328	14759	AA924766	k		ESTs	
329	23123	AA924794	x		ESTs	
330	4067	AA924813	g,p		ESTs	
331	2688	AA924902	r,General		ESTs	
332	18130	AA924964	d		ESTs, Highly similar to sec7 domain family member [H.sapiens]	
333	23141	AA925019	r		ESTs	
334	23195	AA925026	General		ESTs, Weakly similar to MCT17 RAT MAST CELL PROTEASE 7 PRECURSOR [R.norvegicus]	
335	21458	AA925049	f,a, General		ESTs	
336	5073	AA925061	m		ESTs, Moderately similar to S20710 hypothetical protein, 16K - mouse [M.musculus]	
337	14790	AA925087	o,General		ESTs	
338	5069	AA925126	g		EST, Highly similar to T50621 hypothetical protein DKFZp762O076.1 [H.sapiens]	
339	23261	AA925145	k,General		ESTs, Moderately similar to BHMT RAT BETAINE-HOMOCYSTEINE S- METHYLTRANSFERASE [R.norvegicus]	
340	17363	AA925150	a		ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]	
341	23448	AA925167	l		ESTs	
342	23159	AA925318	e	l-kappa-B-beta	l-kappa-B-beta	
343	21500	AA925353	k		ESTs	
344	22479	AA925418	l		ESTs	
345	21151	AA925539	b		ESTs	

TABLE 1: SUMMARY					
Atty. Docket No. 44221-388WC					
Doc. No. 1798397.1					
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq ID	Model Code	Gene Name	Unigene Cluster Title
346	16944	AA925541	f	heterogeneous nuclear ribonucleoprotein L	heterogeneous nuclear ribonucleoprotein L
346	16945	AA925541	t	heterogeneous nuclear ribonucleoprotein L	heterogeneous nuclear ribonucleoprotein L
347	17514	AA925554	bb	Hh:succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	ESTs, Highly similar to DHSA_HUMAN SUCCINATE DEHYDROGENASE [H.sapiens]
348	5183	AA925662	i,General		ESTs
349	23189	AA925844	r		ESTs
350	23190	AA925863	aa		ESTs, Highly similar to IMB3_HUMAN IMPORTIN BETA-3 SUBUNIT [H.sapiens]
351	5252	AA926051	General		EST
352	22967	AA926080	h,cc		ESTs
353	17157	AA926129	b		ESTs
354	13411	AA926196	u,General		ESTs
355	5295	AA926247	General	putative potassium channel TWIK	putative potassium channel TWIK
356	22928	AA926262	General		ESTs, Moderately similar to NEURONAL PROTEIN 3.1 [M.musculus]
357	8948	AA926316	r		ESTs, Moderately similar to T13963 formin related protein, lymphocyte specific - mouse [M.musculus]
358	21798	AA926365	aa		ESTs, Moderately similar to AF151827.1 CGI-69 protein [H.sapiens]
359	9942	AA942697	s		ESTs
360	6039	AA942716	x,General		ESTs, Highly similar to HN1 [M.musculus]
361	11174	AA942745	g,o,w		ESTs
362	23005	AA942770	g		ESTs
363	21318	AA942774	General		ESTs
364	6615	AA942889	v		ESTs, Weakly similar to Y26686 hypothetical protein Y38F1A.6 - Caenorhabditis elegans [C.elegans]
365	6691	AA943028	c		ESTs, Highly similar to KFMS RAT MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR PRECURSOR [R.norvegicus]
366	22142	AA943066	p		ESTs, Weakly similar to p68 RNA helicase [R.norvegicus]
367	21993	AA943149	v,General		ESTs, Weakly similar to T00084 hypothetical protein KIAA0512 [H.sapiens]
368	9061	AA943508	General		ESTs, Highly similar to T08666 hypothetical protein DKFZp547N0510.1 [H.sapiens]
369	24390	AA943531	b,i,n,y		ESTs, Weakly similar to VILT1 MOUSE VILLIN [M.musculus]
370	13676	AA943532	f,s,x		Rattus norvegicus mRNA for class I beta-tubulin, complete cds
371	22248	AA943537	cc, General		Rattus norvegicus zyxin mRNA, partial cds
372	22257	AA943558	m		ESTs, Highly similar to T2DA_HUMAN TRANSCRIPTION INITIATION FACTOR TFIIID 2015 KDA SUBUNITS [H.sapiens]
373	12673	AA943773	u,cc, General		ESTs
374	13641	AA944154	u		ESTs
375	2658	AA944155	f		ESTs
376	12770	AA944161	d		ESTs

TABLE 1: SUMMARY						Atty. Docket No. 44921-508WG
						Doc. No. 179899.1
Sequence ID No.	Identifier	GenBank Acc/Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title	
377	20903	AA9441180	lx		ESTs, Highly similar to CKS2 MOUSE CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 [M.musculus]	
378	13507	AA944244	v		ESTs	
379	15596	AA944353	General		ESTs	
380	22681	AA944413	l.v.cc, General		ESTs	
381	6711	AA944439	General		ESTs, Highly similar to hypothetical protein [M.musculus]	
382	14763	AA944481	l.a, General		ESTs, Weakly similar to FIBA RAT FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR [R.norvegicus]	
383	22466	AA944605	h		ESTs	
384	12301	AA944727	b		ESTs, Weakly similar to A44437 regenerating liver inhibitory factor RL/IF-1 - rat [R.norvegicus]	
385	7023	AA944792	d.m,aa		ESTs, Highly similar to RNA polymerase II 23kD subunit [H.sapiens]	
386	22636	AA944803	bb		ESTs, Highly similar to RNA polymerase II 23kD subunit [H.sapiens]	
387	22501	AA944811	qj		ESTs	
388	23967	AA944831	s		ESTs	
389	26084	AA944922	i		ESTs	
390	11974	AA944958	General		ESTs	
391	22547	AA944970	aa		ESTs	
392	22554	AA945076	z, General		ESTs	
393	14352	AA945181	General		ESTs	
395	1798	AA945589	General		R.norvegicus alpha-1-macroglobulin mRNA, complete cds	
396	22050	AA945604	l,aa		ESTs	
397	19731	AA945615	d,o		ESTs	
398	22612	AA945624	a, General		ESTs, Weakly similar to DHQW RAT NAD(P)H DEHYDROGENASE [R.norvegicus]	
399	22818	AA945656	aa		ESTs	
400	11871	AA945679	v		ESTs	
401	22658	AA945818	General		ESTs	
402	6720	AA945828	p		ESTs	
403	22351	AA945867	m		ESTs	
404	22665	AA945877	f		ESTs	
405	24243	AA945950	b		ESTs	
406	22689	AA945962	General		ESTs	
407	22692	AA945986	d		ESTs	
408	22696	AA945996	c, General		ESTs	
409	22697	AA945996	c,o		ESTs	
409	22658	AA945998	w		ESTs	
410	20832	AA946040	s		ESTs, Highly similar to COXG MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE VIB [M.musculus]	
411	16337	AA946046	General		ESTs	
412	825	AA946108	General		Rattus norvegicus laminin-5 alpha 3 chain mRNA, complete cds	
413	8639	AA946221	e,cc, General		ESTs	
414	23237	AA946224	f		ESTs	
415	15600	AA946250	o,aa		ESTs	
416	19387	AA946275	i		ESTs, Highly similar to AR21_HUMAN ARP23 COMPLEX 21 KD SUBUNIT [H.sapiens]	
417	6351	AA946344	d	PCTAIRE-1 protein kinase, alternatively spliced	PCTAIRE-1 protein kinase, alternatively spliced	
418	22057	AA946348	e		ESTs, Highly similar to autoantigen [H.sapiens]	
419	22069	AA946349	aa		ESTs	

TABLE 1: SUMMARY						Atty. Docket No. 44921-5089WO
						Doc. No. 172837.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title	
420	13962	AA946351	General		ESTs	
421	18280	AA946361	g		ESTs, Highly similar to Ring3 [M.musculus]	
422	18944	AA946391	v		ESTs	
424	21410	AA946408	l		ESTs, Moderately similar to p18 component of aminoacyl-tRNA synthetase complex [H.sapiens]	
425	643	AA946439	o,y		Rat H4 gene for somatic histone H4	
426	20736	AA946443	x		ESTs, Highly similar to NP01 MOUSE NEURAL PROLIFERATION DIFFERENTIATION AND CONTROL PROTEIN-1 PRECURSOR [M.musculus]	
427	21878	AA946448	r		ESTs	
428	21947	AA946451	bb		ESTs, Highly similar to AF151863.1 CGI-105 protein [H.sapiens]	
429	17499	AA946457	General		ESTs	
430	1809	AA946503	x,General		Rat mRNA for alpha-2u globulin-related protein	
431	23360	AA955104	f		ESTs	
432	23471	AA955162	General		ESTs	
433	9452	AA955206	b,General		ESTs	
434	23512	AA955262	General		ESTs	
435	22598	AA955298	General		ESTs	
436	23283	AA955391	h	lipoprotein-binding protein	lipoprotein-binding protein	
437	23546	AA955393	General		ESTs	
438	12404	AA955408	b		ESTs, Weakly similar to SX10 RAT TRANSCRIPTION FACTOR SOX-10 [R.norvegicus]	
439	23626	AA955540	aa		ESTs	
441	17540	AA955914	bb		EST, EST, Moderately similar to FBRL MOUSE FIBRILLARIN [M.musculus], ESTs, Highly similar to FBRL MOUSE FIBRILLARIN [M.musculus]	
442	24277	AA955952	General		ESTs	
443	19939	AA955980	General		ESTs, Moderately similar to pescadillo [H.sapiens]	
444	24000	AA956005	i		ESTs, Weakly similar to AF139894.1 RNA-binding protein alpha-CP1 [M.musculus]	
445	11050	AA956164	s,v		ESTs, Weakly similar to TCPA RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]	
446	498	AA956278	a,General		ESTs	
447	23409	AA956294	g		ESTs	
449	23773	AA956476	f,x		ESTs	
450	23799	AA956530	d		ESTs, Highly similar to ET putative translation product [M.musculus]	
451	23800	AA956534	aa		ESTs, Weakly similar to RNG1_HUMAN RING1 PROTEIN [H.sapiens]	
452	23834	AA956659	cc, General		EST	
453	16425	AA956688	f,x		ESTs, Moderately similar to C8 [M.musculus]	
454	23847	AA956723	s		EST	
455	23852	AA956746	j,l,m,z		ESTs, Highly similar to Mi-2 protein [H.sapiens]	
456	5989	AA956907	g,s		ESTs, Highly similar to p162 protein [M.musculus]	
456	5990	AA956907	General		ESTs, Highly similar to p162 protein [M.musculus]	

TABLE 1: SUMMARY						Atty. Docket No. 443Ph-5068WG
						Doc. No. 17928347.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title	
457	23957	AA957123	u, General		ESTs, Weakly similar to AF187065.1 p75NTR-associated cell death executor [R.norvegicus]	
458	22357	AA957264	General		ESTs, Highly similar to hypothetical protein [H.sapiens]	
459	23314	AA957270	g,l,m,p,v, cc, General		ESTs	
460	23995	AA957292	a,b		ESTs	
461	2702	AA957307	General	Hts: seryl-tRNA synthetase	ESTs, Moderately similar to SYS. HUMAN SERYL-TRNA SYNTHETASE [H.sapiens]	
462	24040	AA957422	c		ESTs, Highly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR GAMMA-SUBUNIT PRECURSOR [R.norvegicus]	
463	12478	AA957554	m		ESTs, Highly similar to P3 MOUSE P3 PROTEIN [M.musculus]	
464	21306	AA957811	v		ESTs	
465	24183	AA957889	t		ESTs	
466	24178	AA957905	d		ESTs	
467	17034	AA963071	e		ESTs, Highly similar to epsilon-COP [M.musculus]	
468	24053	AA963092	General		ESTs, Weakly similar to AF187065.1 p75NTR-associated cell death executor [R.norvegicus]	
469	2767	AA963201	o		ESTs	
470	2022	AA963259	g		ESTs	
471	2126	AA963488	d		ESTs	
472	24246	AA963703	b		ESTs, Highly similar to cell cycle protein p38-2G4 homolog [H.sapiens]	
473	2195	AA963746	General		ESTs	
474	19370	AA963767	i		ESTs	
475	2282	AA964147	e		ESTs	
476	2284	AA964152	x		ESTs	
478	2350	AA964368	g, General		ESTs, Highly similar to TGT_HUMAN QUEUEINE TRNA-RIBOSYLTRANSFERASE [H.sapiens]	
479	18830	AA964496	aa		ESTs, Highly similar to ATRTC actin beta - rat [R.norvegicus]	
480	2392	AA964541	b		EST	
481	2395	AA964554	General		ESTs, Highly similar to U3 snRNP associated 55 kDa protein [H.sapiens]	
482	2410	AA964589	i, aa		EST	
483	19145	AA964613	t		ESTs	
484	2424	AA964617	g		ESTs	
485	3107	AA964687	General		ESTs	
486	2457	AA964752	q,t		EST	
487	6778	AA964763	b		ESTs, Highly similar to DRIM protein [H.sapiens]	
489	2468	AA964807	l		ESTs, Weakly similar to 123337 hypothetical protein K05C4.2 - Caenorhabditis elegans [C.elegans]	
490	2469	AA964814	w	Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory	Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory	
491	12561	AA964815	General		ESTs	
492	2326	AA964892	aa		ESTs, Highly similar to PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR [M.musculus]	
493	21339	AA964962	General		ESTs, Highly similar to ABC1 MOUSE ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 1 [M.musculus]	
494	21390	AA964986	General		ESTs	
495	12569	AA965023	g		ESTs	

TABLE 1: SUMMARY					
Atty.CKET No. 44924-008W0					
Doc. No. 179837.1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title
496	2583	AA965166	bb		ESTs, Moderately similar to inorganic pyrophosphatase [H.sapiens]
497	15885	AA965207	r		ESTs, Highly similar to KIAA0958 protein [H.sapiens]
499	2905	AA996727	bj,mu, General		ESTs
500	2915	AA996782	u.bb		ESTs, Moderately similar to S27267 lamin A - rat [R.norvegicus]
501	2920	AA996813	d		ESTs
502	19525	AA996856	aa, General		EST
503	2984	AA997015	c		ESTs
504	2966	AA997028	General		ESTs
505	3145	AA997237	General		ESTs
506	19249	AA997342	m		ESTs
507	16883	AA997345	General		ESTs, Weakly similar to nitrilase homolog 1 [M.musculus]
508	12598	AA997362	s		ESTs, Moderately similar to LONN HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
509	3470	AA997374	p		ESTs, Weakly similar to LIS1 MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus]
510	3180	AA997425	t		ESTs
511	3245	AA997608	General		ESTs, Weakly similar to PAI2 RAT PLASMINOGEN ACTIVATOR INHIBITOR-2, TYPE A [R.norvegicus]
512	3020	AA997656	t		ESTs, Moderately similar to T09071 SH3 domains-containing protein POSH - mouse [M.musculus]
513	3269	AA997600	x,aa		ESTs, Moderately similar to T30249 cell proliferation antigen Ki-67 - mouse [M.musculus]
514	3288	AA997677	f		ESTs
515	23992	AA998164	k,x	Cyclin B1	Cyclin B1
516	17470	AA998264	b		ESTs, Moderately similar to FLRE_HUMAN FLAVIN REDUCTASE [H.sapiens]
517	3773	AA998356	General		ESTs, Weakly similar to BCL3_HUMAN B-CELL LYMPHOMA 3-ENCODED PROTEIN [H.sapiens]
518	19623	AA998422	General		EST
519	3572	AA998516	x		ESTs, Highly similar to CGA2 MOUSE CYCLIN A2 [M.musculus]
520	2782	AA998565	c		ESTs, Moderately similar to CYCLIN-DEPENDENT KINASE INHIBITOR 1C [M.musculus]
521	26119	AA998576	u,f,w, General		
522	22737	AA998660	aa		ESTs
523	3696	AA999030	e		ESTs, Moderately similar to AF132966 1 CGI-32 protein [H.sapiens]
524	3079	AA999169	k,x, General		ESTs
525	3081	AA999171	e,p,f	Signal transducer and activator of transcription 1	Signal transducer and activator of transcription 1
526	3082	AA999172	General	H-Hs:guanine monophosphate synthetase	ESTs, Highly similar to GUAA_HUMAN GMP SYNTHASE [H.sapiens]
527	17337	AB000717	k		ESTs
528	1535	AB000778	a	Phospholipase D gene 1	Phospholipase D gene 1
529	1382	AB002406	k	RuvB-like protein 1	RuvB-like protein 1
530	20184	AB003753	d		

TABLE 1: SUMMARY					
Atty. Docket No. 44924-5083WG					
Doc. No. 1792397.1					
Sequence ID No.	Identifier	Start/End Ref. Seq ID	Model Code	Gene Name	Unique Identifier
531	4312	AB010635	c,j,k,y,z		Rattus norvegicus mRNA for carboxylesterase precursor, complete cds
532	21666	AB012214	k	Hm/DNA methyltransferase (cytosine-5) 1	ESTs, Highly similar to JE0376 DNA [R.norvegicus]
533	15772	AB015645	g		Rattus norvegicus mRNA for G protein coupled receptor, complete cds
534	1183	AF013144	h		Rattus norvegicus MAP-kinase phosphatase (cp21) mRNA, complete cds
535	1582	AF015911	h,z		Rattus norvegicus NAC-1 protein (NAC-1) mRNA, complete cds
536	11483	AF020618	u,cc, General		ESTs, Moderately similar to MY16 MOUSE MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116 [M.musculus], Rattus norvegicus progression elevated gene 3 protein mRNA, complete cds
537	20295	AF024712	aa		Rattus norvegicus MHC class Ib M4 (RT1.M4) pseudogene, complete sequence
538	19077	AF030358	y,z		Rattus norvegicus chemokine CX3C mRNA, complete cds
539	23044	AF034218	General	hyaluronidase 2	hyaluronidase 2
540	25178	AF035955	d		
541	1564	AF035963	x,bb, General		Rattus norvegicus kidney injury molecule-1 (KIM-1) mRNA, complete cds
542	8426	AF036335	f		Rattus norvegicus NonOp54nr homolog mRNA, partial cds
543	21817	AF036537	k		Rattus norvegicus homocysteine respondent protein HCYP2 mRNA, complete cds
544	21145	AF038571	General	Solute carrier family 1 A1 (brain glutamate transporter)	Solute carrier family 1 A1 (brain glutamate transporter)
545	22602	AF044574	General	putative peroxisomal 2,4-dienoyl-CoA reductase	putative peroxisomal 2,4-dienoyl-CoA reductase
546	13464	AF047707	h	UDP-glucose:ceramide glycosyltransferase	UDP-glucose:ceramide glycosyltransferase
547	24024	AF052695	x	cell cycle protein p55CDC	cell cycle protein p55CDC
548	12259	AF061266	h	transient receptor protein 1	Rattus norvegicus tpr1 beta variant mRNA, complete cds
549	4589	AF062389	y,z		Rattus norvegicus kidney-specific protein (KS) mRNA, complete cds
550	16007	AF062594	t	nucleosome assembly protein 1-like 1	Rattus norvegicus nucleosome assembly protein mRNA, complete cds
551	15761	AF062741	u		Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 2 mRNA, complete cds
552	17426	AF073839	p		Rattus norvegicus bithorax-like protein mRNA, complete cds
553	18615	AF074608	s	RT1 class Ib gene	RT1 class Ib gene
554	15797	AF084205	f		Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds
555	12932	AF102552	s	ankyrin 3 (G)	Rattus norvegicus 190 kDa ankyrin isoform mRNA, complete cds
556	18603	AI007649	x		ESTs, Highly similar to A49013 tumor cell suppression protein HTS1 [H.sapiens]
557	22733	AI007668	r		ESTs
558	22746	AI007672	r		ESTs
559	24109	AI007725	General		ESTs

TABLE 1 SUMMARY						Atty. Docket No. 44924-5083W
						Doc. No. 172897.1
Sequence ID No.	Identifier	GenBank Acc# Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title	
560	15848	AI007820	n.v		ESTs, ESTs, Highly similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]	
561	10108	AI007857	f	Hrs	Hrs	
562	6804	AI007877	General		ESTs	
563	20099	AI007893	f,u		ESTs	
564	11368	AI007948	d		ESTs, Weakly similar to T18778 hypothetical protein B0513.2b - Caenorhabditis elegans [C.elegans]	
565	15849	AI008074	h		ESTs, ESTs, Highly similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]	
566	3121	AI008160	General		ESTs, Moderately similar to AF151841 1 CGI-83 protein [H.sapiens]	
567	16646	AI008190	t		ESTs, Highly similar to Chain G, G Protein Heterotrimer G $\alpha$ 1 Beta 1 Gamma 2 With Gdp Bound [R.norvegicus]	
568	12683	AI008203	x		ESTs, Weakly similar to G2/MITOTIC-SPECIFIC CYCLIN B1 [R.norvegicus]	
569	22018	AI008309	b		ESTs, Moderately similar to PIM1 RAT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE PIM-1 [R.norvegicus]	
570	23917	AI008441	n		ESTs, Highly similar to 6PGD_HUMAN 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATIN [H.sapiens]	
571	22599	AI008458	General		ESTs	
572	22698	AI008578	p, General		ESTs	
573	14405	AI008579	r,x		ESTs	
574	4086	AI008629	x		ESTs, Moderately similar to JH0446 75K autoantigen [H.sapiens]	
575	3808	AI008643	i,v, General		ESTs, Weakly similar to heat shock protein hsp40-3 [M.musculus]	
576	3931	AI008697	l		ESTs, Weakly similar to T29897 hypothetical protein F38A5.1 - Caenorhabditis elegans [C.elegans]	
577	7785	AI008758	aa	Dipeptidyl peptidase 4	Dipeptidyl peptidase 4	
578	16701	AI008838	q		ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]	
579	21789	AI008930	ik		ESTs, Weakly similar to CYSR RAT CYSTEINE-RICH PROTEIN 1 [R.norvegicus]	
580	21895	AI008971	General		ESTs	
581	410	AI008974	l,aa, General		R.norvegicus mRNA encoding 45kDa protein which binds to heymann nephritis antigen gp330	
582	21632	AI009167	General		ESTs, Highly similar to BAG-family molecular chaperone regulator-2 [H.sapiens]	
583	21596	AI009168	General		ESTs	
584	22801	AI009197	General		ESTs	
585	11876	AI009321	cc, General		ESTs, Highly similar to similar to human DNA-binding protein 5 [H.sapiens]	
586	2506	AI009341	General		ESTs	
587	6382	AI009362	General		ESTs	
588	14370	AI009427	k		ESTs, Highly similar to Lmp10 proteasome subunit [M.musculus]	

TABLE 1: SUMMARY						Atty. Docket No. 43924-5689WG
						Doc. No. 125597.4
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Gene	Gene Name	Unigene Cluster Title	
589	19275	AI009460	x		ESTs, Highly similar to flamin [H.sapiens]	
590	4154	AI009467	g		ESTs	
591	3464	AI009589	cc		ESTs	
592	3926	AI009592	e		ESTs, Highly similar to molybdopterinsynthase large subunit [M.musculus]	
593	19358	AI009675	c		EST	
594	22545	AI009747	g		ESTs	
595	15089	AI009752	cc, General		ESTs	
596	5458	AI009756	n	ALG-2 interacting protein 1	ALG-2 interacting protein 1	
597	6844	AI009770	e,r,cc		ESTs	
598	15627	AI009810	aa		ESTs, Highly similar to RS16_HUMAN 40S RIBOSOMAL PROTEIN S1 [R.norvegicus]	
599	22619	AI009825	d		ESTs	
600	7857	AI009898	j,l,m,z		ESTs	
601	13269	AI009946	r		ESTs	
602	21105	AI010067	General		ESTs	
603	24627	AI010102	aa	Testis enhanced gene transcript	Testis enhanced gene transcript	
604	12716	AI010178	General		ESTs, Moderately similar to YAO0_HUMAN HYPOTHETICAL PROTEIN CGI-100 PRECURSOR [H.sapiens]	
605	18757	AI010216	aa		ESTs	
606	2912	AI010220	aa, General		ESTs, Weakly similar to claudin-7 [R.norvegicus]	
607	3316	AI010237	t		ESTs	
608	15644	AI010256	General		R.norvegicus mRNA for histone H3.3	
609	657	AI010262	b		Rattus norvegicus mRNA for interleukin-4 receptor (membrane-bound form), complete cds	
610	3271	AI010303	b		ESTs	
611	11081	AI010407	bb		ESTs, Moderately similar to erythroblast macrophage protein EMP [H.sapiens]	
612	18521	AI010470	c,s,t, General	Cenuloplasmin (ferroxidase)	Cenuloplasmin (ferroxidase)	
613	6927	AI010542	General		ESTs	
614	17524	AI010568	a,j,y, General	Growth hormone receptor	Growth hormone receptor	
615	6946	AI010642	n		ESTs	
616	23509	AI010962	aa		ESTs, Highly similar to SDP3 [M.musculus]	
617	6044	AI011285	t		ESTs	
618	13855	AI011361	o		ESTs	
619	21779	AI011380	cc		ESTs	
621	12534	AI011460	cc		ESTs	
622	12629	AI011492	e,f		ESTs, Moderately similar to HYA22 [H.sapiens]	
623	735	AI011560	f		ESTs, Weakly similar to B Chain B, Solution Structure Of The C-Terminal Negative Regulatory Domain Of P53 In A Complex With Ca2+-Bound S100b(Bb) [R.norvegicus]	
624	3941	AI011598	General		ESTs, Moderately similar to LMA5 MOUSE LAMININ ALPHA-5 CHAIN [M.musculus]	
625	17550	AI011607	j,General		ESTs, Weakly similar to JE0360 gamma-Butyrobetaine hydroxylase [H.sapiens]	
626	10636	AI011634	e		ESTs, Weakly similar to I(3)S12 protein [D.melanogaster]	
627	3995	AI011678	General		ESTs	

TABLE 1. SUMMARY					
Atty. Docket No. 44971-5689WG					
Doc. No. 1798357.1					
Sequencing ID No.	Identifier	GenBank Acc/ Ref. Seq ID	Model Code	Gene Name	Original Cluster Title
626	16112	AI011706	h		ESTs, Weakly similar to SFR5 RAT SPLICING FACTOR, ARGININE/SERINE-RICH 5 [R.norvegicus]
629	13354	AI011757	c		ESTs, Weakly similar to A35902 Fc gamma [R.norvegicus]
630	12745	AI011799	cc		ESTs
631	18684	AI011812	t		ESTs, Highly similar to AF151842 1 CGI-84 protein [H.sapiens]
632	4205	AI011982	b		ESTs
633	6518	AI012114	General		ESTs, Moderately similar to R29425 1 [H.sapiens]
634	17407	AI012145	General		ESTs
635	13093	AI012177	r		ESTs, Weakly similar to PPP5 RAT SERINE/THREONINE PROTEIN PHOSPHATASE 5 [R.norvegicus]
636	15395	AI012216	f		ESTs, Moderately similar to Y33K_HUMAN HYPOTHETICAL 33.4 KDA PROTEIN [H.sapiens]
637	21796	AI012221	d,General		ESTs, Weakly similar to S70484 RS43 protein - rat (fragment) [R.norvegicus]
638	3981	AI012235	i,General		ESTs
639	6606	AI012308	i,r		ESTs
640	3417	AI012337	w		ESTs, Highly similar to NHPX RAT NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG [R.norvegicus]
641	24200	AI012356	b,i,General		ESTs
642	7471	AI012379	cc		ESTs
643	7247	AI012438	g		ESTs
644	7127	AI012464	p,General		ESTs
645	3304	AI012471	b		ESTs, Weakly similar to T26998 hypothetical protein Y48B6A.6 - Caenorhabditis elegans [C.elegans]
646	2311	AI012485	aa	glutathione S-transferase, pi 2	ESTs
647	20817	AI012589	g,n,q		glutathione S-transferase, pi 2
648	3493	AI012590	v,General		ESTs
649	8975	AI012613	General		ESTs
650	11335	AI012619	j		ESTs, Highly similar to unknown [H.sapiens]
651	21409	AI012637	General		ESTs
652	8015	AI012638	aa		ESTs, Moderately similar to AF151834 1 CGI-76 protein [H.sapiens]
653	8476	AI012647	w		ESTs, Highly similar to RS20_HUMAN 40S RIBOSOMAL PROTEIN S2 [R.norvegicus]
654	4232	AI012958	p,p,General		ESTs
655	23128	AI013011	General		ESTs
656	20086	AI013260	General	lamin	lamin
657	11969	AI013273	k		ESTs, Highly similar to GLIA DERIVED NEXIN PRECURSOR [R.norvegicus]
658	26147	AI013387	aa		ESTs
659	8815	AI013437	p		ESTs
660	19722	AI013508	k		Rattus norvegicus Hsp70 binding protein HspBP mRNA, complete cds
661	6674	AI013568	General		ESTs
662	23145	AI013647	o,i		ESTs
663	15130	AI013676	w		ESTs

TABLE 1: SUMMARY					Atty. Docket No. 44921-5089WG
					Doc. No. 179893V.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Grade	Gene Name	RefSeq Cluster Title
664	7274	AI013715	aa		ESTs, Moderately similar to BMP6 RAT BONE MORPHOGENETIC PROTEIN 6 PRECURSOR [R.norvegicus]
665	7276	AI013730	e		ESTs, Highly similar to KIAA1102 protein [H.sapiens]
666	7278	AI013738	y,z,aa		ESTs
667	22592	AI013740	s,x,bb, General		ESTs, Highly similar to proteolipid protein 2 [M.musculus]
668	16584	AI013765	w	Arrestin, beta 2	Arrestin, beta 2
669	24143	AI013804	ij		ESTs, Highly similar to 127225 ADP-ribosylation factor Y57G11C.13 (similarity) - Caenorhabditis elegans [C.elegans]
670	15928	AI013829	a,General		ESTs
671	21950	AI013861	j	3-hydroxyisobutyrate dehydrogenase	3-hydroxyisobutyrate dehydrogenase
672	3260	AI013875	t		ESTs
673	2708	AI013882	d,g		ESTs, Moderately similar to MSSP [M.musculus]
674	8585	AI013886	i		ESTs
675	7299	AI013911	p,i,i, General		ESTs, Weakly similar to CIRP [R.norvegicus]
676	15904	AI013971	General		Rat ankyrin binding glycoprotein-1 related mRNA sequence
677	12781	AI014023	w		ESTs, Moderately similar to R32184.1 [H.sapiens]
678	19372	AI014135	aa		Rattus norvegicus mRNA for beta-carotene 15,15'-dioxygenase, complete cds
679	4241	AI014140	w		ESTs, Highly similar to hypothetical protein [H.sapiens]
680	15247	AI014169	c,u		Rattus norvegicus clone N27 mRNA
681	7315	AI028831	n		ESTs, Moderately similar to mitogen-activated protein kinase kinase kinase 6 [H.sapiens]
682	16631	AI028856	General		ESTs
683	23297	AI028953	x		ESTs, Highly similar to S55054 Sm protein G [H.sapiens]
684	11326	AI029015	b		ESTs
685	2896	AI029058	n,y		ESTs
686	12812	AI029126	General		ESTs
687	17602	AI029156	p		ESTs
688	7392	AI029185	aa		EST
689	6517	AI029264	d,k,x		ESTs
690	7639	AI029292	b		ESTs
691	3874	AI029428	i,General		ESTs, Highly similar to CB80_HUMAN 80 KDA NUCLEAR CAP BINDING PROTEIN [H.sapiens]
692	12619	AI029437	f		ESTs
693	7482	AI029466	r		ESTs
694	7493	AI029608	b		ESTs
696	7537	AI029829	o,General		ESTs
697	2310	AI029969	v		ESTs
698	7585	AI030023	x		ESTs
699	7586	AI030024	b,n		ESTs
700	14492	AI030091	cc		ESTs
701	10673	AI030134	f		ESTs, Weakly similar to ankyrin [R.norvegicus]
702	7615	AI030163	o,r		ESTs
703	2370	AI030179	General		ESTs
704	7681	AI030449	n		ESTs, Moderately similar to methyltransferase related protein [M.musculus]

TABLE 1: SUMMARY						Atiy. Becket No. 44921-508390
						Doc. No. 1788897.1
Sequence ID No.	Identifier	SanPark Accl. Ref. Seq ID	Model Code	Gene Name	Unigene Cluster Title	
705	11559	AI030472	General		ESTs	
706	7665	AI030668	l.bb		Rattus norvegicus nucleosome assembly protein mRNA, complete cds	
707	24222	AI030704	k		ESTs	
708	10740	AI030743	h		EST	
709	10742	AI030773	e		EST	
711	16169	AI030932	General		ESTs, Moderately similar to adipophilin [H.sapiens]	
712	19527	AI030991	f		EST	
713	22614	AI031004	r		ESTs, Highly similar to SX17 MOUSE TRANSCRIPTION FACTOR SOX-17 [M.musculus]	
714	3167	AI031012	e		ESTs, Highly similar to CLPP MOUSE PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT, MITOCHONDRIAL PRECURSOR [M.musculus]	
715	5350	AI043611	a		ESTs	
716	7858	AI043654	t		EST	
717	10764	AI043678	d		EST	
718	9180	AI043694	aa	HHs:phosphoribosyl pyrophosphate amidotransferase	ESTs, Weakly similar to T27134 hypothetical protein Y53C12B.2 - Caenorhabditis elegans [C.elegans]	
719	7867	AI043695	aa		Rattus norvegicus mRNA for amidophosphoribosyltransferase	
720	7584	AI043724	General		ESTs	
721	7895	AI043768	e		ESTs, Highly similar to AF151810.1 CGI-52 protein [H.sapiens]	
722	7903	AI043805	General		ESTs	
723	7913	AI043849	cc		ESTs, Weakly similar to ELL MOUSE RNA POLYMERASE II ELONGATION FACTOR ELL [M.musculus]	
724	3899	AI043904	i		ESTs	
725	5766	AI043914	f		ESTs	
726	10818	AI043990	g,l,m, General		ESTs	
727	7956	AI044018	f		EST	
728	5393	AI044170	p		EST	
729	5398	AI044177	q		EST	
730	5425	AI044237	a,d		ESTs, Weakly similar to AF121693.1 sequence-specific single-stranded-DNA-binding protein [R.norvegicus]	
731	8692	AI044247	r		ESTs, Weakly similar to putative peroxisomal 2,4-dienoyl-CoA reductase [R.norvegicus]	
732	5430	AI044253	i		EST	
733	5461	AI044338	g,p, General		ESTs	
734	5464	AI044345	i		ESTs	
735	3359	AI044347	aa		ESTs	
737	2695	AI044396	b		Rat (clones rLQ[08,14,25]) interleukin 6 signal transducer mRNA sequence	
738	5494	AI044425	General		ESTs	
740	9682	AI044588	j,m		ESTs	
741	5575	AI044688	g		ESTs	
742	2348	AI044794	General		ESTs	
743	18205	AI044836	n		ESTs, Weakly similar to AF165892.1 RNA-binding protein SiahBP [R.norvegicus]	
744	5626	AI044864	u		ESTs	
745	5630	AI044869	f		ESTs	
746	5634	AI044883	General		ESTs, Moderately similar to AF151873.1 CGI-115 protein [H.sapiens]	

TABLE 1: SUMMARY						Atty. Docket No. 44924-5689 WO
						Doc. No. 176839-1
Sequence ID No.	Identifier	GenBank Acc# Ref. Seq. ID	Model Grade	Gene Name	UniGene Cluster Title	
747	4047	AI044947	l,m		ESTs, Moderately similar to dJ116312.1 [H.sapiens]	
748	5684	AI044976	w		EST	
749	5684	AI045056	r		ESTs	
750	19235	AI045074	General		ESTs, Highly similar to B3AL MOUSE BETA-GALACTOSIDASE PRECURSOR [M.musculus]	
751	5689	AI045075	l,aa, General		ESTs, Moderately similar to HEM45 [H.sapiens]	
752	5711	AI045151	General		ESTs, Moderately similar to AF118838 1 citrin [H.sapiens]	
753	19237	AI045153	c		ESTs, Weakly similar to TVRTK6 ribosomal protein S6 kinase [R.norvegicus]	
754	9964	AI045161	f		EST	
755	5735	AI045223	f		ESTs	
756	5474	AI045477	a,General		ESTs	
757	5811	AI045502	d,e		ESTs	
758	5819	AI045537	General		ESTs	
759	5839	AI045594	i		ESTs	
760	6808	AI045600	s		ESTs, Highly similar to S30034 translocating chain-associating membrane protein [H.sapiens]	
761	11755	AI045608	y		ESTs	
763	10020	AI045632	a		ESTs	
764	5855	AI045669	General		ESTs	
765	5881	AI045789	i		ESTs, Weakly similar to T12540 hypothetical protein DKFZp434J214.1 [H.sapiens]	
766	5897	AI045862	General		ESTs, Moderately similar to S64732 scaffold attachment factor B [H.sapiens]	
767	5900	AI045866	y,z		ESTs	
768	7540	AI045882	o,l, General		ESTs, Weakly similar to B48013 proline-rich proteoglycan 2 precursor, parotid - rat [R.norvegicus]	
769	5329	AI045970	p		ESTs	
770	15093	AI058265	d		ESTs	
771	8002	AI058304	i		ESTs	
772	8017	AI058341	c		EST	
773	6826	AI058359	General		ESTs, Weakly similar to T46465 hypothetical protein DKFZp434A0530.1 [H.sapiens]	
774	8177	AI058603	aa		ESTs	
775	3090	AI058730	aa		ESTs	
776	10093	AI058746	g		ESTs	
777	8143	AI058759	General		ESTs	
778	18659	AI058762	f		ESTs	
779	8163	AI058837	aa		ESTs	
780	4789	AI058889	General		ESTs	
781	8221	AI059061	General		ESTs	
782	10159	AI059147	d		EST	
783	8245	AI059154	b		ESTs, Weakly similar to unnamed protein product [H.sapiens]	
784	8283	AI059290	n		ESTs	
785	8314	AI059306	g,General		ESTs	
786	10200	AI059444	i		ESTs	
787	8347	AI059519	s		ESTs, Weakly similar to EGF RAT PRO-EPIDERMAL GROWTH FACTOR PRECURSOR [R.norvegicus]	
788	18359	AI059675	n		Rattus norvegicus transitional endoplasmic reticulum ATPase mRNA, complete cds	

TABLE 1: SUMMARY					Atty. Docket No. 44924-5683VC Doc. No. 128837.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title
789	10281	AI059947	b.i		EST
790	8494	AI059968	aa		ESTs
					ESTs, Weakly similar to TNRC MOUSE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR [M.musculus]
791	8495	AI059971	General		ESTs, Moderately similar to KIAA0978 protein [H.sapiens]
792	8496	AI059974	General		ESTs, Weakly similar to CGI-142 hypothetical protein [H.sapiens]
793	10289	AI060053	i		ESTs
794	8548	AI060176	k		ESTs
795	8565	AI060236	l		EST
796	18322	AI060279	l.y.z		ESTs
797	8745	AI069939	r		ESTs
					ESTs, Highly similar to rer [M.musculus]
798	8785	AI070067	o		ESTs, Weakly similar to 2104282A Gadd45 gene [R.norvegicus]
799	17506	AI070068	cc		ESTs, Weakly similar to NUCLEOLIN [R.norvegicus]
800	9067	AI070087	General		ESTs, Moderately similar to CGI-97 protein [H.sapiens]
801	3551	AI070122	e		ESTs, Moderately similar to GLMB RAT GLIA MATURATION FACTOR BETA [R.norvegicus]
802	4967	AI070179	k		ESTs, Moderately similar to AF132954 1 CGI-20 protein [H.sapiens]
803	18	AI070195	General		ESTs, Moderately similar to ARVC_HUMAN ARMADILLO REPEAT PROTEIN DELETED IN VELO-CARDIO-FACIAL SYNDROME [H.sapiens]
804	24197	AI070314	General		ESTs
805	8869	AI070330	r		ESTs
806	8874	AI070336	b.cc		ESTs
807	10417	AI070410	m		ESTs
					ESTs, Moderately similar to T08664 Toll protein-like receptor [DKFZp54710610.1] [H.sapiens]
808	8901	AI070419	aa		ESTs
809	14424	AI070421	l.p.		ESTs
810	10434	AI070467	General		ESTs
811	8927	AI070523	v		ESTs
812	8946	AI070611	q		ESTs
813	8950	AI070621	w		ESTs
814	8972	AI070673	General		ESTs
815	8981	AI070715	bb		EST
816	26184	AI070784	l.j		ESTs, Weakly similar to hypothetical protein [H.sapiens]
817	3007	AI070824	w		ESTs
818	8999	AI070839	p		ESTs
819	10477	AI070668	e.f	bone morphogenetic protein 1 (procollagen C-proteinase)	bone morphogenetic protein 1 (procollagen C-proteinase)
820	24301	AI070911	k		ESTs
821	8721	AI071024	General		EST
822	9212	AI071098	x		ESTs
823	1831	AI071137	c		Rat mRNA for cdc25B, complete cds
824	11005	AI071139	r		EST
					ESTs, Highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G [M.musculus]
825	9104	AI071173	i.m		ESTs
826	9583	AI071185	General		ESTs
827	9644	AI071410	c		ESTs

TABLE 1: SUMMARY					
Atty. Docket No. 41921-0089WC					
Doc. No. 1929097.1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title
828	16058	Ai071490	General	Hh:s:serine palmitoyltransferase, long chain base subunit 2	ESTs, Highly similar to JC5180 serine C-palmitoyltransferase [M.musculus]
829	11057	Ai071509	f,o		ESTs
831	5695	Ai071566	bb		ESTs, Weakly similar to SYBSR threonine synthase (EC 4.2.99.2) - yeast (Saccharomyces cerevisiae) [S.cerevisiae]
832	9671	Ai071568	w		EST
833	22929	Ai071578	General		ESTs, Moderately similar to NEURONAL PROTEIN 3.1 [M.musculus]
834	9673	Ai071581	General		ESTs
835	9699	Ai071646	General		ESTs
837	9799	Ai072008	q,y,z		ESTs
838	9808	Ai072050	d		ESTs
839	22796	Ai072213	General		ESTs
840	9271	Ai072405	v		ESTs
841	10869	Ai072425	w		ESTs
842	21797	Ai072439	General		ESTs, Weakly similar to S70484 RS43 protein - rat (fragment) [R.norvegicus]
843	9306	Ai072521	r		ESTs
844	9312	Ai072550	j		ESTs
845	10893	Ai072559	x		EST
846	1501	Ai072634	cc,General		Rattus norvegicus cytokeratin-18 mRNA, partial cds
847	6548	Ai072658	General		ESTs
848	9363	Ai072695	d		ESTs, Highly similar to JE0170 dnaJ heat shock protein MCG18 - mouse [M.musculus]
850	9409	Ai072841	n		ESTs, Moderately similar to LMG2 MOUSE LAMININ GAMMA-2 CHAIN PRECURSOR [M.musculus]
851	9410	Ai072842	w		ESTs
852	9468	Ai073021	General		ESTs
853	9518	Ai073223	f		EST
854	11183	Ai100768	t	Hh:s:carbonic anhydrase VIII	ESTs, Weakly similar to CAH2 RAT CARBONIC ANHYDRASE II [R.norvegicus]
855	9190	Ai100835	e		ESTs
856	2029	Ai100842	p		ESTs
857	5687	Ai101006	e		ESTs
858	15192	Ai101099	g,cc		Rat metallothionein-2 and metallothionein-1 genes, complete cds
859	17399	Ai101157	o		ESTs, Highly similar to ATPK MOUSE ATP SYNTHASE F CHAIN, MITOCHONDRIAL [M.musculus]
860	9339	Ai101160	l,m,o		ESTs, Weakly similar to S46930 teg292 protein - mouse [M.musculus]
861	6321	Ai101256	General		ESTs, Weakly similar to AIF-C1 [R.norvegicus]
862	5421	Ai101270	c		ESTs, Highly similar to GDIS MOUSE RHO GDP-DISSOCIATION INHIBITOR 2 [M.musculus]
863	11910	Ai101323	General		ESTs, Highly similar to ERM_HUMAN ETS-RELATED PROTEIN ERM [H.sapiens]
864	23140	Ai101608	e		ESTs
865	4119	Ai101901	General		ESTs
866	16324	Ai102009	b		ESTs, Weakly similar to TRBP MOUSE PROTAMINE-1 RNA BINDING PROTEIN [M.musculus]
867	18642	Ai102023	o		ESTs, Moderately similar to unknown [H.sapiens]

TABLE 1: SUMMARY						Atly. Pocket No. 4-921-3083WG
						Doc. No. 173097.1
Sequence Identifier ID No.	Identifier	GenBank Accession Ref. Seq ID	Model Code	Gene Name	Unigene Cluster Title	
868	19373	AI102044	a	Drosophila polarity gene (frizzled) homologue	Rattus norvegicus mRNA for beta-carotene 15,15'-dioxygenase, complete cds	
869	7051	AI102055	h		Rattus norvegicus clone ZG52 mRNA sequence	
870	6544	AI102064	c		ESTs, Weakly similar to AF147718.1 glycine decarboxylase [R.norvegicus]	
871	10227	AI102248	w		ESTs	
872	23649	AI102318	e,q		ESTs	
873	11954	AI102505	g,j,s	HmM:cytochrome c oxidase, subunit VIIIa	Rattus norvegicus liver cytochrome c oxidase subunit VIII (COX-VIII) mRNA, 3' end of cds	
874	2125	AI102519	c,k		ESTs, Moderately similar to DAP12 [M.musculus]	
875	5967	AI102520	y		ESTs, Moderately similar to AF161588.1 GABA-A receptor-associated protein [R.norvegicus]	
875	5969	AI102520	p,w		ESTs, Moderately similar to AF161588.1 GABA-A receptor-associated protein [R.norvegicus]	
876	11563	AI102560	General		ESTs	
877	15190	AI102562	b,g,n,p,v		Rat metallothionein-I (mt-1) mRNA	
878	19769	AI102570	bb		EST, Weakly similar to A60716 somatotropin intron-related protein RDE.25 - rat [R.norvegicus]	
879	22487	AI102578	General		ESTs, Highly similar to 149523 Mouse primary response gene B94 mRNA, 3' end - mouse [M.musculus]	
880	19011	AI102618	General		ESTs	
881	23837	AI102620	q,l		ESTs	
882	23538	AI102727	g,General	solute carrier family 20 (phosphate transporter), member 1	solute carrier family 20 (phosphate transporter), member 1	
883	17234	AI102741	c	Tissue inhibitor of metalloproteinase 3	Tissue inhibitor of metalloproteinase 3	
884	5891	AI102745	k		ESTs	
885	6796	AI102753	General		ESTs	
886	8837	AI102849	o,p		ESTs	
887	15861	AI102868	i		ESTs, Weakly similar to phosphoserine aminotransferase [H.sapiens]	
888	3533	AI102877	g		ESTs	
889	13222	AI102977	General		ESTs, Highly similar to PCAF associated factor 85 beta [H.sapiens]	
890	6806	AI103018	o,x		ESTs	
891	10659	AI103059	w,cc,General		ESTs	
892	17400	AI103097	e		ESTs, Highly similar to ATPK MOUSE ATP SYNTHASE F CHAIN, MITOCHONDRIAL [M.musculus]	
893	3584	AI103106	x,aa		ESTs	
894	13298	AI103143	r		ESTs	
895	15981	AI103150	i,x		ESTs, Weakly similar to UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD [R.norvegicus]	
896	3475	AI103245	w		ESTs, Highly similar to AF151893.1 CGI-135 protein [H.sapiens]	
898	23619	AI103314	p		ESTs	
899	24181	AI103320	e		ESTs, Moderately similar to T26785 hypothetical protein Y40B12.7 - Caenorhabditis elegans [C.elegans]	
901	4355	AI103410	General		ESTs	
902	7622	AI103472	General		ESTs	
903	20918	AI103552	n		ESTs	
904	21579	AI103572	General		ESTs	

TABLE 1. SUMMARY					
Atty. Docket No. 43924-008W0					
Doc. No. 178894.1					
Sequence ID No.	Identifier	GenBank Acc#	Model Code	Gene Name	UniGene Cluster Title
905	2222	AI103631	o		ESTs, Highly similar to RIE2 [M.musculus]
906	2752	AI103641	e		ESTs, Highly similar to sarcosine dehydrogenase [R.norvegicus]
907	4856	AI103708	i		ESTs
908	8690	AI103719	l,m,y,z		ESTs
909	15942	AI103738	r		ESTs
910	22885	AI103828	e,General		ESTs
911	15853	AI103841	x	Complement component 4	Complement component 4
				HHs:ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Rat Rieske iron-sulfur protein mRNA, complete cds
912	15050	AI103911	l,y		ESTs
913	12376	AI103939	u		ESTs
914	22271	AI103947	o,y		ESTs, Weakly similar to AF151109.1 putative BRCA1-interacting protein [H.sapiens]
915	20833	AI104035	f,g	Hm:RIKEN cDNA 201000G05 gene	ESTs, Highly similar to COXG MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE VIB [M.musculus]
916	7010	AI104059	w		ESTs
917	22101	AI104251	General		ESTs
918	22833	AI104258	General		ESTs
919	22211	AI104279	g,m		ESTs, Highly similar to translation initiation factor eIF6 [M.musculus]
920	10720	AI104296	i		ESTs
921	15416	AI104340	i		ESTs
922	10991	AI104342	a		ESTs
923	18831	AI104357	p		ESTs, Highly similar to ATRTC actin beta -rat [R.norvegicus]
924	7223	AI104373	e		ESTs
925	23574	AI104520	e,g,s	Cytochrome c oxidase subunit Via (liver)	Cytochrome c oxidase subunit Via (liver)
926	18509	AI104528	q		ESTs, Weakly similar to NADH:ubiquinone oxidoreductase B17 subunit [H.sapiens]
927	11680	AI104605	v		ESTs
928	12342	AI104658	w		ESTs, Weakly similar to RENAL TRANSCRIPTION FACTOR KID-1 [R.norvegicus]
929	23689	AI104685	r		Rat mitochondrial succinyl-CoA synthetase alpha subunit (cytoplasmic precursor) mRNA, complete cds
930	15377	AI104821	o,cc		ESTs, Moderately similar to T50611 DKFZp434H2035.1 [H.sapiens]
931	22957	AI104897	General		ESTs, Moderately similar to meningioma-expressed antigen 11 [H.sapiens]
932	18451	AI104953	o,s	HHs:ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	Rattus norvegicus delta subunit of F1F0 ATPase gene, complete cds
933	24375	AI104979	n,General		ESTs, Moderately similar to nucleolar protein p40 [H.sapiens]
					ESTs, Moderately similar to SCOT_HUMAN SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR [H.sapiens]
934	18278	AI105080	bb		ESTs
935	2196	AI105243	g		ESTs
936	5199	AI105272	bb, General		ESTs, Weakly similar to T21641 hypothetical protein F3286.2 - Caenorhabditis elegans [C.elegans]
937	12901	AI105301	o,s		ESTs

TABLE 1: SUMMARY						Atty. Pocket No. 44921-888WO
						Doc. No. 1798892.1
Sequence ID No.	Identifier	SeqBank/Accession Ref. Seq ID	Model Code	Gene Name	Unique Cluster Title	
938	7700	AI105383	cc, General		ESTs, Weakly similar to T19707 hypothetical protein C34C6.5 - <i>Caenorhabditis elegans</i> [C.elegans]	
939	13343	AI105398	u		ESTs	
940	22931	AI105417	s, General		ESTs, Moderately similar to NEURONAL PROTEIN 3.1 [M.musculus]	
941	23596	AI105435	bb	HMM:glutaryl-Coenzyme A dehydrogenase	ESTs, Highly similar to GCDH MOUSE GLUTARYL-COA DEHYDROGENASE PRECURSOR [M.musculus]	
942	15893	AI105465	o		ESTs, Moderately similar to DHSD_HUMAN SUCCINATE DEHYDROGENASE [H.sapiens]	
943	12660	AI111492	c		ESTs	
944	4479	AI111599	General		ESTs	
945	24211	AI111853	k		ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [R.norvegicus]	
946	2539	AI111960	r		ESTs, Weakly similar to FKBP5 MOUSE 81 KDA FKBP-BINDING PROTEIN [M.musculus]	
947	5729	AI111990	k		EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (FIBULIN-3) (FIBL-3) (T16 PROTEIN) [R.norvegicus]	
948	4049	AI112012	i, q, u, General		Rattus norvegicus osteocalcin mRNA, complete cds	
949	12908	AI112043	t		ESTs	
950	20041	AI112161	t		ESTs	
951	12937	AI112462	General		ESTs	
952	3713	AI112571	b		ESTs	
953	12921	AI112636	General		ESTs, Moderately similar to UDP_HUMAN URIDINE PHOSPHORYLASE [H.sapiens]	
954	12965	AI112928	General		ESTs	
955	7499	AI112986	General		ESTs	
956	4969	AI113008	r		ESTs, Moderately similar to megakaryocyte stimulating factor [H.sapiens]	
957	11817	AI136295	f		ESTs, Highly similar to BC-2 protein [H.sapiens]	
959	11165	AI136372	c		ESTs, Weakly similar to JC4975 plexin 2 precursor - mouse [M.musculus]	
960	4045	AI136460	cc		ESTs	
961	12782	AI136493	k		ESTs	
962	6850	AI136665	h	ecto-aprase	ecto-aprase	
963	20920	AI136891	p, v	butyrate response factor 1	butyrate response factor 1	
964	8552	AI137062	o		ESTs, Highly similar to 6.2 kd protein [H.sapiens]	
965	22722	AI137211	i		ESTs	
966	13111	AI137224	o, General		ESTs, Highly similar to oxysterol-binding protein [M.musculus]	
967	15969	AI137302	e		ESTs	
968	14349	AI137303	d		ESTs	
969	9166	AI137406	General		ESTs	
970	9525	AI137516	r		ESTs, Weakly similar to ZF37_RAT ZINC FINGER PROTEIN 37 (ZFP-37) [R.norvegicus]	
971	6638	AI137579	General		ESTs	
972	7414	AI137586	General		ESTs, Highly similar to IMB3_HUMAN IMPORTIN BETA-3 SUBUNIT [H.sapiens]	
973	11321	AI137752	z		ESTs	
974	23473	AI137932	i		ESTs	

TABLE 1: SUMMARY						Atty. Docket No. 44021-5083WG
						Doc. No. 1728a97.1
Sequence ID No.	Identifier	GenBank Accel Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title	
975	13158	AI138024	i		ESTs	
976	13467	AI138034	cc	UDP-glucose:ceramide glycosyltransferase	UDP-glucose:ceramide glycosyltransferase	
977	11337	AI138105	v		ESTs	
978	6790	AI144801	d,h		ESTs	
979	6506	AI144919	j,l,y		ESTs	
980	8027	AI144958	i		ESTs	
982	14458	AI145095	General		ESTs	
983	7476	AI145202	g		ESTs	
984	17545	AI145384	e		ESTs, ESTs, Weakly similar to GTP-binding protein [H.sapiens]	
985	17479	AI145385	r		ESTs	
986	4194	AI145387	r		ESTs	
987	8634	AI145722	g		ESTs, Weakly similar to T31511 hypothetical protein Y116A8C.9 - Caenorhabditis elegans [C.elegans]	
988	8339	AI145761	y, General		ESTs, Weakly similar to T21659 hypothetical protein F3ZD8.4 - Caenorhabditis elegans [C.elegans]	
989	2059	AI146005	h, General		ESTs, Highly similar to pseudouridine synthase 1 [M.musculus]	
990	23224	AI146033	o		Rattus norvegicus small zinc finger-like protein (TIM9a) mRNA, partial cds	
991	5232	AI168942	bb	branched chain keto acid dehydrogenase E1, beta polypeptide	branched chain keto acid dehydrogenase E1, beta polypeptide	
992	18472	AI168975	u		ESTs	
992	18473	AI168975	u		ESTs	
993	13235	AI169020	r		ESTs	
994	11618	AI169115	o,y, General		ESTs	
995	17386	AI169144	o		ESTs, Weakly similar to T23206 hypothetical protein K01H12.1 - Caenorhabditis elegans [C.elegans]	
996	10984	AI169156	o,u		ESTs, Weakly similar to HP33 [R.norvegicus]	
997	8205	AI169176	e		ESTs	
998	12979	AI169177	e		ESTs, Highly similar to RADIATION-INDUCIBLE IMMEDIATE-EARLY GENE IEX-1 [M.musculus]	
999	2607	AI169211	c		ESTs, Highly similar to A47318 RNA-binding protein Raly - mouse [M.musculus]	
1000	22661	AI169265	s,z	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	
1001	13239	AI169278	g,j,l,y,z		ESTs	
1002	24162	AI169279	m		ESTs	
1003	16879	AI169284	o		ESTs, Highly similar to Y069_HUMAN HYPOTHETICAL PROTEIN KIAA0069 [H.sapiens]	
1004	24213	AI169289	p		ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [R.norvegicus]	
1005	13240	AI169311	cc		ESTs	
1006	5931	AI169324	b		ESTs	
1007	20891	AI169337	d		ESTs, Highly similar to CGI-117 protein [H.sapiens]	
1008	11979	AI169365	cc		ESTs	
1009	10947	AI169372	s	arachidonic acid epoxidase	arachidonic acid epoxidase	
1010	20697	AI169494	o,u		ESTs	
1011	8234	AI169517	z		ESTs	
1012	18343	AI169648	o		ESTs	
1013	10839	AI169655	l,m		ESTs	
1014	24146	AI169668	j,l		ESTs, Weakly similar to hypothetical protein [H.sapiens]	

TABLE 1: SUMMARY					
Affy. Docket No. 44921-3085WG					
Doc. No. 1793937.1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1015	22575	AI169728	r		ESTs, Moderately similar to T47184 hypothetical protein [H.sapiens]
1016	804	AI169756	cc		ESTs, Highly similar to GENIE 33 POLYPEPTIDE [R.norvegicus]
1017	8213	AI169883	p	ferritin light chain 1	ferritin light chain 1
1018	3916	AI169947	l,bb		ESTs
1019	3733	AI170053	u,General		ESTs
1020	14179	AI170224	cc		ESTs
1021	11406	AI170263	r		ESTs, Moderately similar to class II cytokine receptor 4 (M.musculus)
1022	3547	AI170279	General		ESTs, Weakly similar to ZNT1 RAT ZINC TRANSPORTER 1 [R.norvegicus]
1023	11524	AI170340	j,y,z		ESTs, Weakly similar to CL36 RAT LIM DOMAIN PROTEIN CLP-36 [R.norvegicus]
1024	2729	AI170383	e,j		ESTs
1025	18811	AI170525	i		ESTs
1026	22524	AI170542	h		ESTs
1027	24048	AI170570	e,g		ESTs, Highly similar to CGI-10 protein [H.sapiens]
1028	5968	AI170692	y,aa		ESTs, Moderately similar to AF161588 1 GABA-A receptor-associated protein [R.norvegicus]
1029	9757	AI170693	b		ESTs
1030	18905	AI170770	e,s		ESTs, Highly similar to NADH-ubiquinone oxidoreductase NDUF52 subunit [H.sapiens]
1031	18170	AI170894	i		ESTs, Moderately similar to adipophilin [H.sapiens]
1032	7089	AI171185	c	Hyaluronan mediated motility receptor (RHAMM)	Hyaluronan mediated motility receptor (RHAMM)
1033	17591	AI171354	b		ESTs
1034	13285	AI171361	h		ESTs, Weakly similar to AIF-C1 [R.norvegicus]
1035	4428	AI171362	a	HHs:NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)	ESTs, Moderately similar to NUAM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR [H.sapiens]
1036	18126	AI171369	w		ESTs, Highly similar to S16788 probable reverse transcriptase - rat [R.norvegicus]
1037	23253	AI171448	o		ESTs, Moderately similar to 68MP MOUSE 6.8 KD MITOCHONDRIAL PROTEOLIPID [M.musculus]
1038	4584	AI171492	m, General		ESTs
1039	11158	AI171542	r,s		ESTs, Moderately similar to NADH:ubiquinone oxidoreductase B22 subunit [H.sapiens]
1040	15345	AI171587	i		ESTs
1041	21183	AI171676	x		ESTs
1042	8215	AI171692	i	ferritin light chain 1	Rattus norvegicus kynurenine aminotransferase/glutamine transaminase K (Kat) gene, complete cds, ferritin light chain 1
1043	11437	AI171794	i		ESTs
1044	2625	AI171800	cc		ESTs
1045	23579	AI171802	v		ESTs
1046	11708	AI171807	l,l		ESTs
1047	17204	AI171844	s,y,z	HMm:RIKEN cDNA 2410043G19 gene	Rattus norvegicus F1-ATPase epsilon subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds

TABLE 1: SUMMARY						Atty. Docket No. 44921-508WG
						Doc. No. 1798897.1
Sequence ID No.	Identifier	GenBank Acc'd Ref. Seq ID	Model Code	Gene Name	Unigene Cluster Title	
1048	4420	AI171916	m		ESTs	
1049	3266	AI171948	l,m		ESTs, Highly similar to T08675 hypothetical protein	
1050	19012	AI172056	t		DKFZp564F0522.1 [H.sapiens]	
1051	11205	AI172057	a,q,bb		ESTs	
1052	6057	AI172102	b		ESTs, Weakly similar to T33236 hypothetical protein T10H9.3 -	
1053	19128	AI172103	m		Caenorhabditis elegans [C.elegans]	
1054	15673	AI172107	z		ESTs	
1055	6630	AI172184	n		Rat mRNA for 5E5 antigen, complete cds	
1056	11968	AI172206	bb		ESTs, Weakly similar to FETA RAT ALPHA-FETOPROTEIN	
1057	6974	AI172263	l,m		PRECURSOR [R.norvegicus]	
1058	23313	AI172271	d		ESTs	
1059	2140	AI172272	General		ESTs, Moderately similar to A53004 transcription elongation factor S-II - rat [R.norvegicus]	
1060	15382	AI172302	l,p, General		ESTs, Weakly similar to S43056 hypothetical protein - mouse [M.musculus]	
1061	18689	AI172329	l		ESTs	
1062	17887	AI172414	o		Rattus norvegicus apoptosis-regulating basic protein mRNA, complete cds	
1063	3042	AI172447	General		ESTs, Highly similar to A44437 regenerating liver inhibitory factor RL/IF-1 - rat [R.norvegicus]	
1064	17291	AI172491	bb	HMm:isocitrate dehydrogenase 2 (NADP+), mitochondrial	ESTs, Weakly similar to IDHC RAT ISOCITRATE DEHYDROGENASE [R.norvegicus]	
1065	26222	AI172506	p		ESTs	
1066	13095	AI172595	r		ESTs	
1067	8795	AI172618	General		ESTs	
1068	6454	AI175342	l,l,m,y		ESTs, Weakly similar to T31067 BIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse [M.musculus]	
1070	4445	AI175466	x		ESTs, Highly similar to RRAS MOUSE RAS-RELATED PROTEIN R-RAS [M.musculus]	
1071	3418	AI175475	m		ESTs, Highly similar to NHPX RAT NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG [R.norvegicus]	
1072	18507	AI175551	bb		ESTs, Moderately similar to AF145050 t translation elongation factor 1-delta subunit [R.norvegicus]	
1073	10217	AI175628	w		ESTs	
1074	7262	AI175833	l,m,x		ESTs	
1075	19004	AI175875	p		ESTs	
1076	22352	AI175959	l,General		ESTs	
1077	7022	AI176041	h,n		ESTs, Highly similar to pirin [H.sapiens]	
1078	21467	AI176061	t		ESTs, Weakly similar to tazarotene-induced gene 2 [H.sapiens]	
1079	18581	AI176160	General		ESTs	
1080	14159	AI176169	p		ESTs	
1081	21742	AI176172	w		ESTs	
1082	10182	AI176185	v		ESTs, Highly similar to P55-C-FOS PROTO-ONCOGENE PROTEIN [R.norvegicus]	
1083	22765	AI176265	General		ESTs	

TABLE 1: SUMMARY						Atty. Docket No. 44921-6889WO
						Doc. No. 179397.1
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq ID	Modif Code	Gene Name	UniGene Cluster Title	
1084	6905	AI176275	a		ESTs, Weakly similar to GSHH RAT PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE PEROXIDASE [R.norvegicus]	
1085	12999	AI176276	cc		UAPT_HUMAN UDP-N-ACETYLHEXOSAMINE PYROPHOSPHORYLASE [H.sapiens]	
1086	16438	AI176284	e		ESTs, Highly similar to SMD2_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2 [H.sapiens]	
1087	21130	AI176288	y		ESTs	
1088	3014	AI176362	e		ESTs	
1089	15015	AI176363	r		ESTs	
1090	19006	AI176393	x		ESTs	
1091	20001	AI176396	o		ESTs, Moderately similar to QPS1 [H.sapiens]	
1092	12174	AI176435	l,m		ESTs	
1093	15191	AI176456	b,o,l,v,cc		Rat metallothionein-2 and metallothionein-1 genes, complete cds	
1094	24236	AI176473	d,General		ESTs	
1095	16518	AI176546	v		ESTs, Moderately similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]	
1096	2161	AI176592	General		ESTs	
1097	12436	AI176610	General		ESTs, Weakly similar to S63220 probable membrane protein YNL247w - yeast (Saccharomyces cerevisiae) [S.cerevisiae]	
1098	2538	AI176616	l,v, General		ESTs	
1099	18525	AI176792	u		ESTs	
1100	23449	AI176828	g		ESTs	
1101	23299	AI176839	General		ESTs	
1102	3580	AI176848	e		ESTs	
1103	22103	AI176849	d,General		ESTs	
1104	16036	AI176855	f		ESTs	
1105	15588	AI176916	General		ESTs, Highly similar to phosphomannomutase Sec53p homolog [M.musculus]	
1106	16917	AI176951	l		ESTs	
1107	16124	AI176963	cc		Rattus norvegicus transcription factor MRG1 mRNA, complete cds	
1108	15146	AI176969	b,General		ESTs	
1109	5786	AI177058	f		ESTs, Weakly similar to PSE-binding factor PTF delta subunit [H.sapiens]	
1110	2852	AI177059	c		ESTs	
1112	3156	AI177092	g		ESTs, Highly similar to AF139894 1 RNA-binding protein alpha-CP1 [M.musculus]	
1113	14384	AI177096	a	HMM:adenine phosphoribosyl transferase	Rat adenine phosphoribosyltransferase (APRT) gene, complete cds	
1114	13310	AI177119	General		ESTs, Weakly similar to C1QB RAT COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR [R.norvegicus]	
1115	24049	AI177341	g,p,s,u		ESTs, Highly similar to CGI-10 protein [H.sapiens]	
1116	15964	AI177360	o,General		ESTs	
1117	14989	AI177366	u	Integrin, beta 1	Integrin, beta 1	
1118	7975	AI177374	aa		ESTs	

TABLE 1: SUMMARY					
Atty. Docket No. 44924-6089WG					
Doc. No. 79189-1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1119	3006	AI177395	k		Rattus norvegicus substrate binding subunit of type II 5'-deiodinase D2p29 mRNA, complete cds
1120	17570	AI177683	r		Rattus norvegicus mRNA for hnRNP protein, partial
1121	9521	AI177706	b		ESTs
1122	14425	AI177755	g.General		ESTs
1123	10611	AI177790	j,m		ESTs
1124	5356	AI177813	cc		ESTs, Moderately similar to S27962 modulator recognition factor 1 [H.sapiens]
1125	11791	AI177843	General		ESTs, Highly similar to SAS_HUMAN SARCOMA AMPLIFIED SEQUENCE [H.sapiens]
1126	14484	AI177867	General		ESTs, Weakly similar to putative eps protein [R.norvegicus]
1127	5780	AI177869	General		ESTs, Weakly similar to DRAL [R.norvegicus]
1128	19184	AI178025	General		ESTs, Highly similar to TGIF MOUSE 5'-TG-3' INTERACTING FACTOR [M.musculus]
1129	6059	AI178245	c.General		ESTs, Moderately similar to C17orf1 protein [H.sapiens]
1130	23248	AI178267	y		ESTs, Weakly similar to hypothetical protein [H.sapiens]
1131	4073	AI178272	c		ESTs, Weakly similar to YAE6_YEAST HYPOTHETICAL 13.4 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION [S.cerevisiae]
1132	7836	AI178291	e		ESTs
1133	18996	AI178326	y		ESTs
1134	22488	AI178392	b		ESTs, Highly similar to 149523 Mouse primary response gene 894 mRNA, 3'end - mouse [M.musculus]
1135	16800	AI178504	n.p,aa		ESTs
1136	22197	AI178527	g.General		ESTs
1137	3401	AI178684	bb		ESTs, Highly similar to MCM3 MOUSE DNA REPLICATION LICENSING FACTOR MCM3 [M.musculus]
1138	17713	AI178700	m		ESTs
1139	14874	AI178735	e		ESTs
1140	23567	AI178746	v.General		ESTs
1141	18907	AI178971	c		Rattus norvegicus alpha-globin (GloA) gene, complete cds
1142	20991	AI178979	i		ESTs
1143	5887	AI179099	q,t		ESTs, Moderately similar to Varin-1 [M.musculus]
1144	8477	AI179167	b,a General		ESTs
1145	3348	AI179288	u,v		ESTs
1146	13608	AI179314	e		ESTs
1147	8849	AI179315	g,p		ESTs
1148	13611	AI179378	v.General		Rattus norvegicus mRNA for prostatic precursor, complete cds
1149	15438	AI179399	m,x	collagen type V, alpha 2	collagen type V, alpha 2
1150	13614	AI179407	e,t General		ESTs, Moderately similar to RB17 MOUSE RAS-RELATED PROTEIN RAB-17 [M.musculus]
1151	15042	AI179422	b.General		ESTs
1152	2768	AI179481	i.General		ESTs
1153	24041	AI179580	b,j		ESTs

TABLE 1: SUMMARY						Atty. Docket No. 44121-688WG
						Box No. 179-47-1
Sequence ID No.	Identifier	GenBank Acc# Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title	
1154	19822	AI179599	o,General		R norvegicus mRNA for ras-related GTPase Rab29	
1155	23270	AI179601	q,General		ESTs	
1156	5901	AI179605	e		ESTs	
1157	16081	AI179610	g,j,p	Heme oxygenase	Heme oxygenase	
1158	14564	AI179717	k		ESTs	
1159	7918	AI179750	General		ESTs	
1160	6647	AI179795	g		ESTs	
1161	9097	AI179875	o,General	hypothetical protein LOC56728	hypothetical protein LOC56728	
1162	23989	AI179953	a		ESTs, Highly similar to GAP JUNCTION BETA-2 PROTEIN [R.norvegicus]	
1163	12899	AI179967	b		ESTs	
1164	1687	AI179971	c	Hemoglobin, alpha 1	Hemoglobin, alpha 1	
1165	22569	AI179979	General		ESTs	
1166	23514	AI179986	o,General	Hts:phosphoserine phosphatase	ESTs, Highly similar to L-3-phosphoserine phosphatase [H.sapiens]	
1167	15892	AI179988	c,General		ESTs	
1168	12402	AI180004	g		ESTs, Highly similar to Unknown [H.sapiens]	
1169	5443	AI180165	General		ESTs, Moderately similar to testis specific DNA-homolog [M.musculus]	
1170	5481	AI180170	General		ESTs, Highly similar to A Chain A, The Crystal Structure Of Human Eukaryotic Release Factor ERF1-Mechanism Of Stop Codon Recognition And Peptidyl-Tma Hydrolysis [H.sapiens]	
1171	24028	AI180239	l		ESTs	
1172	17089	AI180281	g		ESTs, Moderately similar to JC4978 oxidative stress protein A170 - mouse [M.musculus]	
1173	3701	AI180306	aa		ESTs, Moderately similar to Y273_HUMAN HYPOTHETICAL PROTEIN KIAA0273 [H.sapiens]	
1174	3352	AI180334	m		ESTs	
1175	24368	AI180392	l,m		ESTs, Highly similar to AF114169 1 nucleotide-binding protein short form [M.musculus]	
1176	14337	AI180414	c		ESTs, Moderately similar to SPA1 MOUSE GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]	
1177	19080	AI227647	j,y,z		Rattus norvegicus chemokine CX3C mRNA, complete cds	
1178	22838	AI227667	aa		ESTs	
1179	6765	AI227761	l,General		ESTs, Highly similar to T00367 hypothetical protein KIAA0665 [H.sapiens]	
1180	24054	AI227867	General		ESTs, Weakly similar to AF187065 1 p75NTR-associated cell death executor [R.norvegicus]	
1181	7324	AI227885	i		ESTs	
1182	23898	AI227987	d		ESTs	
1183	1651	AI228068	n,w	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase	
1184	14237	AI228128	e		EST	
1185	14242	AI228197	General		ESTs, Weakly similar to C21I1_HUMAN PUTATIVE PROTEIN C21ORF18 [H.sapiens]	
1186	16913	AI228236	o		ESTs	
1187	22915	AI228299	r		ESTs, Highly similar to p97 homologous protein (H.sapiens)	

TABLE 1: SUMMARY					Atty. Docket No. 44924-506W9
					Doc. No. 44924-506W9
Sequence ID No.	Id. #	GenBank Acc./ Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1188	8917	A1228301	General		ESTs
1189	15879	A1228313	r.General		ESTs
1190	13727	A1228326	o.General		ESTs, Weakly similar to AFG1_YEAST AFG1 PROTEIN [S.cerevisiae]
1191	6102	A1228335	General		ESTs
1192	13730	A1228356	a		ESTs, Weakly similar to S70642 ubiquitin ligase Nedda4 - rat [R.norvegicus]
1193	13745	A1228494	b,cc		EST
1194	4217	A1228587	s		ESTs, Weakly similar to M172_HUMAN MEMBRANE COMPONENT, CHROMOSOME 17, SURFACE MARKER 2 [H.sapiens]
1195	16053	A1228596	cc		ESTs, Weakly similar to T16757 hypothetical protein R144.3 - Caenorhabditis elegans [C.elegans]
1196	3557	A1228672	e		ESTs
1197	11805	A1228682	e		ESTs
1198	13203	A1228728	r		ESTs
1199	13771	A1228848	g		ESTs, Highly similar to protein inhibitor of activated STAT protein PIAS1 [H.sapiens]
1200	5918	A1229036	r		ESTs
1201	8235	A1229154	k		ESTs
1202	16203	A1229196	r	Vesicle-associated membrane protein (synaptobrevin 2)	Vesicle-associated membrane protein (synaptobrevin 2)
1203	13826	A1229304	a		ESTs
1204	13144	A1229320	g		ESTs
1205	4640	A1229404	x,aa		ESTs
1206	23583	A1229421	l		ESTs, Moderately similar to MKK2 MOUSE MAP KINASE-ACTIVATED PROTEIN KINASE 2 [M.musculus]
1207	15426	A1229497	s		ESTs, Moderately similar to NADH-ubiquinone oxidoreductase PDSW subunit [H.sapiens]
1208	15193	A1229508	bb		ESTs
1209	19243	A1229638	x		ESTs, Highly similar to KITH RAT THYMIDINE KINASE, CYTOSOLIC [R.norvegicus]
1210	23078	A1229647	p		ESTs
1211	3099	A1229680	o	HHs:NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	ESTs, Highly similar to NADH:ubiquinone oxidoreductase NDUF33 subunit [H.sapiens]
1212	19508	A1229698	bb		Sprague-Dawley D-beta-hydroxybutyrate dehydrogenase mRNA, complete cds
1213	13977	A1229707	x		Rattus norvegicus mRNA for class I beta-tubulin, complete cds
1214	23983	A1229708	v		ESTs, Moderately similar to NADC_HUMAN NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE [H.sapiens]
1215	2688	A1229793	e		ESTs
1216	13874	A1229832	g		ESTs, Weakly similar to KIA0859 protein [H.sapiens]
1217	12587	A1229879	General		ESTs, Weakly similar to MOT2 RAT MONOCARBOXYLATE TRANSPORTER 2 [R.norvegicus]
1218	20591	A1229993	lm		ESTs
1219	24042	A1230002	a,b,d, General		ESTs
1220	13880	A1230042	u		Rattus norvegicus mRNA for voltage-gated ca channel, complete cds

TABLE 1: SUMMARY						Atty. Becket No. 4394-5893W6
						Doc. No. 178937.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title	
1221	17672	AI230074	d	Hfm:NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	ESTs, Highly similar to NIMM MOUSE NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT [M.musculus]	
1222	3652	AI230113	General		Rattus norvegicus hb2 mRNA, complete cds	
1223	18650	AI230121	aa		ESTs, Weakly similar to HS98 RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]	
1224	13025	AI230173	c		ESTs, Moderately similar to CHD3_HUMAN CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 3 [H.sapiens]	
1225	4280	AI230247	z	selenoprotein P, plasma, 1	selenoprotein P, plasma, 1	
1226	18528	AI230284	General		ESTs	
1227	7094	AI230362	p		ESTs, Moderately similar to T46458 hypothetical protein DKFZp434M102.1 [H.sapiens]	
1228	20895	AI230549	b,p		ESTs	
1229	12961	AI230554	General		ESTs	
1230	15636	AI230616	r		Rattus norvegicus mRNA for galectin-2 related protein, complete cds	
1231	4121	AI230647	j,m		ESTs	
1232	14368	AI230702	General		ESTs, Highly similar to HN1 [M.musculus]	
1233	18529	AI230716	x,General		ESTs	
1234	13618	AI230724	General		Rattus norvegicus phosphoinositide phosphatase SAC1 mRNA, complete cds	
1235	8304	AI230746	cc		ESTs	
1236	4731	AI230773	e		ESTs	
1237	14430	AI230798	c,k,x		ESTs, Moderately similar to CDN3_HUMAN CYCLIN-DEPENDENT KINASE INHIBITOR 3 [H.sapiens]	
1238	16627	AI230822	bb	HHs:Alg5, S. cerevisiae, homolog of	ESTs, Highly similar to AF102850 1 dolichyl-phosphate beta-glucosyltransferase [H.sapiens]	
1239	3125	AI231028	General		Rattus norvegicus mRNA for brain 4.1(S), complete cds	
1240	633	AI231127	k		ESTs	
1241	20846	AI231140	p		ESTs, Highly similar to RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [R.norvegicus]	
1242	6743	AI231219	d		ESTs	
1244	26292	AI231391	k		ESTs	
1245	12343	AI231433	w		ESTs	
1246	7337	AI231465	aa		ESTs	
1247	16321	AI231506	General		ESTs	
1248	8004	AI231532	j,j		ESTs, Highly similar to Z183_HUMAN ZINC FINGER PROTEIN 183 [H.sapiens]	
1249	15171	AI231792	g		ESTs, Moderately similar to BAG-family molecular chaperone regulator-3 [H.sapiens]	
1250	6193	AI231797	i		ESTs	
1252	14227	AI231999	u		ESTs, Moderately similar to tumor protein D53 [M.musculus]	
1253	24501	AI232006	w,y,bb		Rattus norvegicus translation elongation factor 1-delta subunit mRNA, partial cds	
1254	3434	AI232014	g,q,z,cc,General		ESTs	
1255	19094	AI232021	n,General		ESTs, Highly similar to Human Translation Initiation Factor Eif1, Nmr, 29 Structures [H.sapiens]	

TABLE 1: SUMMARY						Atty. Docket No. 44321-5083WG
						Doc. No. 1798897.1
Sequence ID No.	Ion Size	GenBank Acc/ Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title	
1256	14020	A1232076	u		ESTs	
1257	6726	A1232157	d		ESTs	
1258	11549	A1232174	l,m		ESTs	
1259	23125	A1232266	j,s		ESTs	
1260	2085	A1232270	bb		ESTs, Moderately similar to JC4914 anti-sigma cross-reacting protein homolog 1 beta precursor [H.sapiens]	
1261	2913	A1232272	o		ESTs, Weakly similar to T25417 hypothetical protein T26D6.9 - Caenorhabditis elegans [C.elegans]	
1262	14304	A1232281	g		ESTs, Weakly similar to KIAA0971 protein [H.sapiens]	
1263	15955	A1232294	u,bb, General		ESTs	
1264	15122	A1232303	y		ESTs, Weakly similar to Sid1669p [M.musculus]	
1265	4716	A1232313	y	purinergic receptor P2X, ligand-gated ion channel 4	purinergic receptor P2X, ligand-gated ion channel 4	
1266	15246	A1232332	l,u		ESTs	
1267	24321	A1232340	o	Stromal cell-derived factor 1	Stromal cell-derived factor 1	
1268	16172	A1232341	d		ESTs, Weakly similar to YQ42_CAEEL HYPOTHETICAL 40.0 KD PROTEIN C1389.2 IN CHROMOSOME III [C.elegans]	
1269	11411	A1232346	h		ESTs	
1270	19287	A1232379	f	Platelet-derived growth factor receptor alpha	Platelet-derived growth factor receptor alpha	
1271	5601	A1232461	n, General		ESTs, Weakly similar to FMO1 RAT DIMETHYLANILINE MONOOXYGENASE [R.norvegicus]	
1272	14051	A1232489	l,m		ESTs, Weakly similar to PIR1 [H.sapiens]	
1273	5572	A1232490	l,i		ESTs, Moderately similar to A27340 complement C7 precursor [H.sapiens]	
1274	11157	A1232494	cc		ESTs	
1275	8709	A1232534	o		ESTs, Weakly similar to DnaJ homolog 2 [R.norvegicus]	
1276	20350	A1232552	j,v,y		EST	
1277	14069	A1232631	e		ESTs	
1278	4440	A1232643	w		ESTs	
1279	17895	A1232784	e		ESTs, Weakly similar to putative peroxisomal 2,4-dienoyl-CoA reductase [R.norvegicus]	
1280	15796	A1232874	v		ESTs	
1281	12467	A1232924	General		ESTs	
1282	12873	A1232964	i		ESTs	
1283	5355	A1233031	r		ESTs	
1284	18794	A1233121	c		ESTs, Moderately similar to MHC class I [M.musculus]	
1285	3823	A1233147	b,g, General		ESTs, Weakly similar to nuclear RNA helicase [R.norvegicus]	
1286	11967	A1233155	c,k General		ESTs	
1287	11561	A1233182	d		ESTs	
1288	3471	A1233183	g		ESTs, Highly similar to PM1_HUMAN PROTEIN PM [H.sapiens]	
1289	21948	A1233191	j		ESTs, Weakly similar to T15919 hypothetical protein EEED8.9 - Caenorhabditis elegans [C.elegans]	
1290	13598	A1233194	g,p,y		ESTs	
1291	15552	A1233195	y		ESTs, Highly similar to Bodenin [M.musculus]	
1292	17907	A1233224	bb		Rattus norvegicus epidermal growth factor receptor related protein (Erp) mRNA, complete cds	
1293	14111	A1233269	cc		ESTs	

TABLE 1: SUMMARY						Atty. Doct. No. 44924-5083W
						Doc. No. 1798397.1
Sequence ID/No.	Identifier	GenBank Acc./Ref. Seq. ID	Modal Code	Gene Name	Unigene Cluster Title	
1294	12894	A1233365	d		ESTs, Weakly similar to T24956 hypothetical protein T116G1.10 - <i>Caenorhabditis elegans</i> [C.elegans]	
1295	7161	A1233407	General		ESTs, Weakly similar to S44853 K12H4.3 protein - <i>Caenorhabditis elegans</i> [C.elegans]	
1296	15906	A1233425	q		ESTs	
1297	14120	A1233433	d		ESTs	
1298	14095	A1233468	a,d		ESTs	
1299	3075	A1233494	u,aa		ESTs, Weakly similar to I38079 OXA1 homolog [H.sapiens]	
1300	6046	A1233530	General		ESTs	
1301	18900	A1233570	General		PSD8, HUMAN 26S PROTEASOME REGULATORY SUBUNIT S14 [H.sapiens]	
1302	7888	A1233583	General	HHs:arginyl-tRNA synthetase	ESTs, Moderately similar to SYR_HUMAN ARGINYL-tRNA SYNTHETASE [H.sapiens]	
1303	16709	A1233602	General	Adenosin kinase	Adenosin kinase	
1304	5163	A1233712	y		ESTs, Highly similar to P2CD_MOUSE PROTEIN PHOSPHATASE 2C DELTA ISOFORM (PP2C-DELTA) (P53-INDUCED PROTEIN PHOSPHATASE 1) (PROTEIN PHOSPHATASE MAGNESIUM-DEPENDENT 1 DELTA) [M.musculus]	
1305	7243	A1233717	General		ESTs, Moderately similar to ERHUAH coatomer complex alpha chain homolog [H.sapiens]	
1306	3816	A1233729	g		ESTs, Highly similar to PSD5_HUMAN 26S PROTEASOME SUBUNIT S5B [H.sapiens]	
1307	13023	A1233740	d,h, General		ESTs, Weakly similar to ALDR RAT ALDOSE REDUCTASE [R.norvegicus]	
1308	14871	A1233743	g		ESTs	
1309	7469	A1233767	cc		ESTs, Highly similar to Gene product with similarity to KIAA0154 [H.sapiens]	
1310	7804	A1233771	b		ESTs	
1311	13563	A1233773	e		ESTs, Weakly similar to T24413 hypothetical protein T04A11.2 - <i>Caenorhabditis elegans</i> [C.elegans]	
1312	2154	A1233818	k,cc		ESTs	
1313	16616	A1234079	h		ESTs	
1314	13393	A1234100	a,d, General	cysteine rich protein	cysteine rich protein	
1315	7071	A1234162	r		ESTs	
1316	14677	A1234620	General		EST	
1317	4443	A1234629	m		ESTs, Weakly similar to transcription factor C1 [M.musculus]	
1318	22453	A1234678	b		ESTs	
1319	23964	A1234748	t,General		ESTs	
1320	19581	A1234753	f		EST	
1321	22152	A1234822	o,General	DEXRAS1 (Dextrast)	DEXRAS1 (Dextrast)	
1322	18942	A1234865	d		ESTs, Weakly similar to S12207 hypothetical protein [M.musculus]	
1323	22662	A1234939	aa	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	
1324	3875	A1235047	o,General		ESTs, Highly similar to CB80_HUMAN 80 KDA NUCLEAR CAP BINDING PROTEIN [H.sapiens]	
1325	19478	A1235135	o		EST	

TABLE 1: SUMMARY						Atty. Docket No. 43921-5889WC
						Doc. No. 1798397.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title	
1326	14906	AI235192	g		ESTs, Highly similar to ABF2_HUMAN ATP-BINDING CASSETTE, SUB-FAMILY F, MEMBER 2 (IRON INHIBITED ABC TRANSPORTER 2) [H.sapiens]	
1327	14718	AI235210	e		ESTs	
1328	15004	AI235224	b,General		Rattus norvegicus tissue inhibitor of metalloproteinase-1 (TIMP1), mRNA, complete cds	
1329	6632	AI235277	v		ESTs	
1330	14722	AI235284	x,z		ESTs, Weakly similar to single-pass transmembrane protein [R.norvegicus]	
1331	1462	AI235585	u,General		Rat mRNA for preprocathepsin D (EC 3.4.23.5)	
1332	21061	AI235631	l,m		ESTs	
1333	14665	AI235646	m	MAD homolog 4 (Drosophila)	MAD homolog 4 (Drosophila)	
1334	19940	AI235689	General		ESTs, Moderately similar to pescadillo [H.sapiens]	
1335	5698	AI235692	u		ESTs	
1336	23745	AI235732	k		ESTs, Highly similar to NID2 MOUSE NIDOGEN-2 PRECURSOR [M.musculus]	
1337	11164	AI235739	General		ESTs, Moderately similar to A56716 aromatic ester hydrolase [H.sapiens]	
1338	5212	AI235745	d		ESTs	
1339	14768	AI235912	h		ESTs, Weakly similar to hypothetical protein [H.sapiens]	
1340	14776	AI235950	m		ESTs	
1341	3091	AI236027	n,General		ESTs	
1342	14861	AI236045	r		ESTs	
1343	14862	AI236048	e		EST	
1344	16943	AI236097	p		ESTs, Highly similar to E25B protein [M.musculus]	
1345	8336	AI236101	i		ESTs, Highly similar to JC7107 development related unidentified 27K protein - mouse [M.musculus]	
1346	23230	AI236146	v		ESTs	
1347	22855	AI236150	ie		ESTs, Highly similar to JC7301 Down syndrome critical region protein 5 alpha [H.sapiens]	
1348	14594	AI236152	l		ESTs	
1349	18406	AI236168	r		ESTs	
1350	15051	AI236332	General		ESTs, Highly similar to ATDA MOUSE DIAMINE ACETYLTRANSFERASE [M.musculus]	
1351	19298	AI236338	bb		ESTs, Weakly similar to NHPX RAT NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG [R.norvegicus]	
1352	10667	AI236366	b	siah binding protein 1; FBP interacting repressor, pyrimidine tr	siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1	
1353	10774	AI236397	l		ESTs	
1354	9407	AI236402	aa		ESTs	
1355	26335	AI236460	General		Rattus norvegicus retinol dehydrogenase type II mRNA, complete cds	
1356	17950	AI236550	l,General		ESTs	
1357	18259	AI236601	h,v		ESTs	
1358	11445	AI236613	ly		ESTs	
1359	17248	AI236635	o,aa		ESTs, Highly similar to SCF complex protein Skp1 [M.musculus]	
1360	16859	AI236753	l,General		ESTs	

TABLE 1: SUMMARY					Atty. Docket No. 4492-3083WG Doc. No. 172897.1
Sequence ID No.	Identifier	GenBank Acc# Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title
1361	5208	AI236754	g		ESTs, Weakly similar to hT41 [H.sapiens]
1362	24388	AI236772	e,General		ESTs
1363	15850	AI236795	n,v,w		ESTs, ESTs, Highly similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]
1364	14800	AI236856	w		ESTs
1365	11404	AI237002	m	spermidine synthase	spermidine synthase
1367	18151	AI237212	o,General		ESTs, Highly similar to hepatitis B virus X interacting protein [H.sapiens]
1368	21653	AI237535	l,General	estrogen-responsive uterine transcript	estrogen-responsive uterine transcript
1369	11208	AI237586	z		ESTs, Moderately similar to INB RAT INTERFERON-INDUCIBLE PROTEIN [R.norvegicus]
1370	21893	AI237713	l,k,aa		ESTs, Moderately similar to Y101_HUMAN HYPOTHETICAL PROTEIN KIAA0101 [H.sapiens]
1371	14842	AI237724	r		ESTs
1372	3467	AI237835	General		ESTs, Moderately similar to MK11 RAT MAX INTERACTING PROTEIN 1 [R.norvegicus]
1373	25840	AI638972	u		
1374	17108	AI639017	n		ESTs, Highly similar to G9A [M.musculus]
1375	16676	AI639062	c,k,x	mini chromosome maintenance deficient 6 (S. cerevisiae)	mini chromosome maintenance deficient 6 (S. cerevisiae)
1376	12400	AI639107	k		ESTs
1377	19652	AI639108	d,v		ESTs
1379	25907	AI639167	o,w		ESTs
1381	18533	AI639231	n		ESTs, Highly similar to T46480 hypothetical protein DKFZp434L1850.1 [H.sapiens]
1382	18353	AI639233	l,aa	decorin	decorin
1384	15330	AI639285	General		ESTs
1385	20026	AI639354	g		EST
1386	25971	AI639365	r		
1388	19152	AI639387	u,General		ESTs
1390	18338	AI639422	y		ESTs, Moderately similar to CAQC RAT CALSEQUESTRIN, CARDIAC MUSCLE ISOFORM PRECURSOR [R.norvegicus]
1392	20082	AI639488	i,m		EST, Highly similar to A42772 mdm2 protein - rat [R.norvegicus]
1394	20056	AI639504	a,bb, General		ESTs, Weakly similar to T13607 hypothetical protein EG:87B1.3 - fruit fly [D.melanogaster]
1395	4713	AI639518	q		ESTs, Highly similar to RPB8_HUMAN DNA-DIRECTED RNA POLYMERASES I, II, AND III 17.1 KD POLYPEPTIDE [H.sapiens]
1396	14332	AJ001044	bb	protein phosphatase 1, regulatory (inhibitor) subunit 5	protein phosphatase 1, regulatory (inhibitor) subunit 5
1397	7602	AJ001929	k	reticulocalbin	reticulocalbin
1398	9857	AJ005424	u		Rattus norvegicus mRNA for BMK1/ERK5 protein, partial
1400	16351	AJ011811	General	claudin 7	claudin 7
1401	20116	AJ011969	l,General	growth differentiation factor 15	growth differentiation factor 15
1402	17635	AJ223355	v,w		Rattus norvegicus mRNA for mitochondrial dicarboxylate carrier

TABLE 1: SUMMARY						Atty. Docket No. 44924-5883WG
						Doc. No. 178837.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title	
1403	18686	D00729	q	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A	Rat mRNA for delta3, delta2-enoyl-CoA isomerase, dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	
1404	5049	D10655	n,w	dihydrolipoamide acetyltransferase	dihydrolipoamide acetyltransferase	
1405	25257	D13623	j			
1405	15281	D13623	h		ESTs	
1406	11434	D14014	cc		ESTs	
1407	1613	D14076	x		Rat mRNA for testicular dynamin, complete cds	
1408	1728	D16479	q	HHs:hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	Rat mRNA for mitochondrial long-chain 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, complete cds	
1409	3015	D16554	c,s,v,z		Rat mRNA for polyubiquitin (four repetitive ubiquitins in tandem), complete cds	
1410	472	D26111	d,s,bb		R. norvegicus mRNA for chloride channel (putative) 2313bp	
1412	16233	D29960	j,l		Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds	
1413	9029	D30804	n		ESTs, Highly similar to PR6C RAT PROTEASOME SUBUNIT RC6-1 [R. norvegicus]	
1414	1485	D38222	y,z		Rattus norvegicus tyrosine phosphatase-like protein IA-2a mRNA, partial cds	
1415	9135	D45247	s	proteasome beta type subunit 5	ESTs, Highly similar to PRCE RAT PROTEASOME EPSILON CHAIN PRECURSOR [R. norvegicus]	
1416	16354	D50564	u	HHs:mercaptopyruvate sulfurtransferase	Rattus norvegicus mRNA for mercaptopyruvate sulfurtransferase, complete cds	
1417	1884	D50695	i,m,bb		Rattus norvegicus mRNA for proteasomal ATPase (Tat-binding protein?), complete cds	
1418	21147	D63772	General	Solute carrier family 1 A1 (brain glutamate transporter)	Solute carrier family 1 A1 (brain glutamate transporter)	
1419	826	D82928	f	HHs:CDP-diacylglycerol-inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	Rat mRNA for phosphatidylinositol synthase, complete cds	
1420	25306	D84485	u			
1421	16867	D88250	t		Rattus norvegicus mRNA for serine protease, complete cds	
1423	22543	H31117	f,v, General			
1424	12360	H31456	w		ESTs	
1425	20514	H31489	h,j		ESTs	
1426	11358	H31610	h		ESTs, Highly similar to mtrpd [M. musculus]	
1427	4360	H31813	bb, General		ESTs, Moderately similar to T14781 hypothetical protein DKFZp586B1621.1 [H. sapiens]	
1428	9343	H32169	i		ESTs, Moderately similar to CDF1 RAT COFILIN, NON-MUSCLE ISOFORM [R. norvegicus]	
1429	4386	H33093	h,w		EST	
1430	4415	H33636	h		ESTs	

TABLE 1: SUMMARY						Atty. Docket No. 44924-5083WG
						Doc. No. 179337.1
Sequence ID No.	Identifier	GenBank Acc/Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title	
1431	15374	H34186	l		ESTs, highly similar to IF39_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 [H.sapiens]	
1432	17159	J00797	u.General	alpha-tubulin	alpha-tubulin	
1433	16260	J01878	f		Rat brain-specific identifier sequence RNA, clone p1b224	
1434	17284	J02827	bb	Branched chain alpha-ketoacid dehydrogenase subunit E1 alpha	Branched chain alpha-ketoacid dehydrogenase subunit E1 alpha	
1435	15017	J03752	n		Rat glutathione S-transferase mRNA, complete cds	
1436	44	J03819	p.s	Thyroid hormone receptor, beta (avian erythroblastic leukemia viral (v-erb-a) oncogene homolog 2)	Thyroid hormone receptor, beta (avian erythroblastic leukemia viral (v-erb-a) oncogene homolog 2)	
1437	21014	J03914	e.f. General	Glutathione-S-transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)	
1438	20429	J05035	f	Steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	Steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	
1439	1247	J05181	j.m.s.y.z	Glutamylcysteine gamma synthetase light chain	Glutamylcysteine gamma synthetase light chain	
1440	10464	J05510	n.u.	Inositol 1,4,5-triphosphate receptor type 1	Rat inositol-1,4,5-triphosphate receptor mRNA, complete cds	
1441	20149	K03243	q		Rat peroxisomal enoyl-CoA hydratase-3-hydroxyacyl-CoA bifunctional enzyme mRNA, complete cds	
1442	17758	K03249	q		Elastase 2, pancreatic	
1443	381	L00124	w	Elastase 2, pancreatic	Elastase 2, pancreatic	
1444	2048	L00382	k.x			
1445	10500	L04619	s			
1447	108	L14002	p		Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats	
1448	25366	L14003	l		Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats	
1449	109	L14004	c.p		Phospholipase C-beta1	
1450	20414	L14323	General	Phospholipase C-beta1	Phospholipase C-beta1	
1451	25369	L14937	y		2,3'-Cyclic nucleotide 3'-phosphodiesterase	
1452	16119	L16532	k		2,3'-Cyclic nucleotide 3'-phosphodiesterase	
1453	25377	L25387	h		ESTs, highly similar to A53047 6-phosphofructokinase [R.norvegicus]	
1453	12058	L25387	h		Solute carrier family 1 A1 (brain glutamate transporter)	
1455	21146	L35558	General	Solute carrier family 1 A1 (brain glutamate transporter)	Rattus norvegicus guanylyl cyclase (GC-D) mRNA, complete cds	
1456	106	L37203	w		Rattus norvegicus serine protease gene, complete cds	
1458	13682	L38482	f.j.k.m.z		Glutathione synthetase gene	
1459	6405	L38615	p	Glutathione synthetase gene	Glutathione synthetase gene	
1461	15189	M11794	n.v		Rat c-ras-H-1 gene, complete cds	
1462	17086	M13011	j		Rat insulin-like growth factor-1 mRNA, 3' end	
1464	21053	M15481	o			
1465	25405	M18330	j.l			
1466	25415	M19648	a			
1488	14967	M22366	w		Propionyl Coenzyme A carboxylase, alpha polypeptide	
1469	20481	M22631	bb	Propionyl Coenzyme A carboxylase, alpha polypeptide		

TABLE 1: SUMMARY					Atty. Docket No. 44921-5689WG Doc. No. 174337.1
Sequence ID	Accession	GenBank Acc# Ref. Seq ID	Model Code	Gene Name	Unique Cluster Title
1471	15048	M24542	g	HHS:ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Rat Rieske iron-sulfur protein mRNA, complete cds
1472	20921	M29853	m		Rat cytochrome P-450 isozyme 5 (P450 1B2) mRNA, complete cds
1473	1224	M31931	u	Cytochrome P450, an olfactory-specific steroid hydroxylase	Cytochrome P450, an olfactory- specific steroid hydroxylase
1474	15579	M33648	g		Rat mitochondrial 3-hydroxy-3- methylglutaryl-CoA synthase mRNA, complete cds
1474	15580	M33648	g		Rat mitochondrial 3-hydroxy-3- methylglutaryl-CoA synthase mRNA, complete cds
1475	17211	M34331	g,h,q,v		ESTs, Weakly similar to KRAB-zinc finger protein KZF-1 [R norvegicus]
1476	20699	M35601	b,x,bb		Rat alpha-fibrinogen mRNA, 3' end
1476	20700	M35601	b,1,bb		Rat alpha-fibrinogen mRNA, 3' end
1477	9223	M36151	o		Rat mRNA for MHC class II antigen RT1.B-1 beta-chain, Rattus norvegicus MHC class II antigen RT1.B beta chain mRNA, partial cds
1479	1585	M57728	j,m,y		Rat general mitochondrial matrix processing protease (MPP) mRNA, 3' end
1480	24844	M58040	c	transferrin receptor	transferrin receptor
1481	25057	M58495	h		
1482	457	M60666	d,General	Tropomyosin 1 (alpha)	Tropomyosin 1 (alpha)
1483	1223	M75281	f		Rat cystatin S (CysS) gene, complete cds
1484	5733	M81855	l,k,aa	P-glycoprotein/multidrug resistance 1	P-glycoprotein/multidrug resistance 1
1485	4198	M83143	m		Rat beta-galactoside-alpha 2,6- sialyltransferase mRNA
1485	4199	M83143	m		Rat beta-galactoside-alpha 2,6- sialyltransferase mRNA
1486	24651	M83678	k,x,z	RAB13	RAB13
1487	1430	M84648	General	Dopa decarboxylase (aromatic L-amino acid decarboxylase)	Dopa decarboxylase (aromatic L- amino acid decarboxylase)
1488	25467	M93297	c	ornithine aminotransferase	ornithine aminotransferase
1489	729	M95762	a,y		Rattus norvegicus GABA transporter GAT-2 mRNA, complete cds
1490	23698	NM_012489	q	Rattus norvegicus Acetyl- CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal (Acaa), mRNA. Length = 1619	Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal
1490	23699	NM_012489	q	Rattus norvegicus Acetyl- CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal (Acaa), mRNA. Length = 1619	Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal
1491	7062	NM_012495	q	Rattus norvegicus Aldolase A, fructose-bisphosphate (Aldoa), mRNA. Length = 1442	Aldolase A, fructose-bisphosphate
1492	15511	NM_012498	u	Rattus norvegicus Aldehyde reductase 1 (low Km aldose reductase) (5.8 kb PstI fragment, probably the functional gene) (Akr1b1), mRNA. Length = 1339	Aldehyde reductase 1 (low Km aldose reductase) (5.8 kb PstI fragment, probably the functional gene)

TABLE 1: SUMMARY					Atty. Docket No. 43921-5638WG Doc. No. 1798957.1
Sequence ID No.	Identifier	GenBank Accession No.	Model Code	Gene Name	Original Cluster Title
1494	7427	NM_012515	General	Rattus norvegicus Benzodiazepin receptor (peripheral) (Bzpr), mRNA. Length = 781	Benzodiazepin receptor (peripherel)
1495	24433	NM_012527	l	Rattus norvegicus Cholinergic receptor, muscarinic 3 (Chrm3), mRNA. Length = 3578	Cholinergic receptor, muscarinic 3
1496	4467	NM_012529	d	Rattus norvegicus Creatine kinase, brain (Ckb), mRNA. Length = 1146	Creatine kinase, brain
1497	18520	NM_012532	General	Rattus norvegicus Ceruloplasmin (ferroxidase) (Cp), mRNA. Length = 3700	Ceruloplasmin (ferroxidase)
1498	225	NM_012544	x,z	Rattus norvegicus Angiotensin I-converting enzyme (Dipeptidyl carboxypeptidase 1) (Ace), mRNA. Length = 4142	Dipeptidyl carboxypeptidase 1 (Angiotensin I-converting enzyme)
1499	1431	NM_012545	General	Rattus norvegicus Dopa decarboxylase (aromatic L-amino acid decarboxylase) (Ddc), mRNA. Length = 1954	Dopa decarboxylase (aromatic L-amino acid decarboxylase)
1500	23868	NM_012551	l,m,v, General	Rattus norvegicus Early growth response 1 (Egr1), mRNA. Length = 3112	Early growth response 1
1500	23872	NM_012551	l,v,cc, General	Rattus norvegicus Early growth response 1 (Egr1), mRNA. Length = 3112	Early growth response 1
1500	23869	NM_012551	v,General	Rattus norvegicus Early growth response 1 (Egr1), mRNA. Length = 3112	Early growth response 1
1501	19407	NM_012554	z	Rattus norvegicus Enolase 1, alpha (Eno1), mRNA. Length = 1725	Enolase 1, alpha
1501	19408	NM_012554	n,s,y,z	Rattus norvegicus Enolase 1, alpha (Eno1), mRNA. Length = 1725	Enolase 1, alpha
1502	21836	NM_012555	k	Rattus norvegicus Ets avian erythroblastosis virus E2 oncogene homolog 1 (tumor progression locus 1) (Ets1), mRNA. Length = 4991	Ets avian erythroblastosis virus E2 oncogene homolog 1 (tumor progression locus 1)
1503	16895	NM_012558	q,s	Rattus norvegicus Fructose-1,6- biphosphatase (Fbp1), mRNA. Length = 1357	Fructose-1,6- biphosphatase
1504	25317	NM_012559	bb	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA. Length = 1358	Fibrinogen, gamma polypeptide
1504	5477	NM_012559	b,bb	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA. Length = 1358	Fibrinogen, gamma polypeptide
1504	5478	NM_012559	bb	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA. Length = 1358	Fibrinogen, gamma polypeptide
1505	11731	NM_012561	k	Rattus norvegicus Follistatin (Fst), mRNA. Length = 1035	Follistatin
1507	4254	NM_012564	a	Rattus norvegicus Group-specific component (vitamin D-binding protein) (Gc), mRNA. Length = 1676	Group-specific component (vitamin D-binding protein)

TABLE 1: SUMMARY					Atty. Docket No. 44824-5183WG Doc. No. 170247.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq ID	Model Code	Gene Name	Uniform Cluster Title
1508	16026	NM_012578	r	Rattus norvegicus Histone H1-0 (H1f0), mRNA. Length = 1779	Histone H1-0
1508	16024	NM_012578	r	Rattus norvegicus Histone H1-0 (H1f0), mRNA. Length = 1779	Histone H1-0
1508	16025	NM_012578	r	Rattus norvegicus Histone H1-0 (H1f0), mRNA. Length = 1779	Histone H1-0
1509	16080	NM_012580	g,m	Rattus norvegicus Heme oxygenase (Hmox1), mRNA. Length = 870	Heme oxygenase
1510	15098	NM_012588	bb	Rattus norvegicus insulin-like growth factor-binding protein (IGF-BP3) (igfbp3), mRNA. Length = 2352	Insulin-like growth factor-binding protein (IGF-BP3)
1511	4450	NM_012592	bb	Rattus norvegicus Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. Length = 2104	Isovaleryl Coenzyme A dehydrogenase
1511	4451	NM_012592	i.bb	Rattus norvegicus Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. Length = 2104	Isovaleryl Coenzyme A dehydrogenase
1511	4452	NM_012592	bb	Rattus norvegicus Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. Length = 2104	Isovaleryl Coenzyme A dehydrogenase
1512	17198	NM_012593	a,x	Rattus norvegicus Kallikrein 1, renal/pancreas/salivary (Kik1), mRNA. Length = 786	Kallikrein 1, renal/pancreas/salivary
1512	17197	NM_012593	x	Rattus norvegicus Kallikrein 1, renal/pancreas/salivary (Kik1), mRNA. Length = 786	Kallikrein 1, renal/pancreas/salivary
1513	18749	NM_012600	a,h	Rattus norvegicus Malic enzyme 1, soluble (Me1), mRNA. Length = 1761	Malic enzyme 1, soluble
1514	2628	NM_012603	General	Rattus norvegicus Avian myelocytomatosis viral (v-myc) oncogene homolog (Myc), mRNA. Length = 2168	Avian myelocytomatosis viral (v-myc) oncogene homolog
1514	2629	NM_012603	x,General	Rattus norvegicus Avian myelocytomatosis viral (v-myc) oncogene homolog (Myc), mRNA. Length = 2168	Avian myelocytomatosis viral (v-myc) oncogene homolog
1515	16849	NM_012608	n,o,q	Rattus norvegicus Membrane metallo-endopeptidase (neutral endopeptidase/enkephalinase) (Mme), mRNA. Length = 3243	Membrane metallo-endopeptidase (neutral endopeptidase/enkephalinase)
1517	15540	NM_012620	General	Rattus norvegicus serine (or cysteine) proteinase inhibitor, clade E (nexin), plasminogen activator inhibitor type 1, member 1 (Serpin1), mRNA. Length = 3053	Plasminogen activator inhibitor
1518	24568	NM_012630	General	Rattus norvegicus Prolactin receptor (Prlr), mRNA. Length = 1635	Prolactin receptor
1518	24566	NM_012630	General	Rattus norvegicus Prolactin receptor (Prlr), mRNA. Length = 1635	Prolactin receptor

TABLE 1. SUMMARY					
Rattus norvegicus (Rn) GenBank Accession Numbers (RefSeq IDs) and UniGene Cluster Titles					
Sequence ID No.	Identifier	GenBank Accession Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1519	18553	NM_012631	k	Rattus norvegicus Prion protein, structural (Pmp), mRNA. Length = 765	Prion protein, structural
1520	1844	NM_012637	General	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 1 (Ptpn1), mRNA. Length = 4127	ESTs, Protein-tyrosine phosphatase
1521	24668	NM_012642	f	Rattus norvegicus Renin (Ren), mRNA. Length = 1059	Renin
1522	18632	NM_012645	a	Rattus norvegicus RT1 class Ib gene (RT1Aw2), mRNA. Length = 1540	RT1 class Ib gene
1523	25435	NM_012647	g	Rattus norvegicus Sodium channel, voltage-gated, type II, alpha polypeptide (Scn2a1), mRNA. Length = 8553	
1524	9423	NM_012649	b,cc	Rattus norvegicus Ryudocan/syndecan 4 (Sdc4), mRNA. Length = 2462	Ryudocan/syndecan 4
1525	24496	NM_012654	n	Rattus norvegicus Solute carrier family 9 (sodium/hydrogen exchanger 3), antiporter 3, Na <sup>+</sup> /H <sup>+</sup> (amiloride insensitive) (Slc3a3), mRNA. Length = 5153	Solute carrier family 9 (sodium/hydrogen exchanger 3), antiporter 3, Na <sup>+</sup> /H <sup>+</sup> (amiloride insensitive)
1526	7101	NM_012679	x,bb, General	Rattus norvegicus Clusterin (Clu), mRNA. Length = 1636	Testosterone-repressed prostate message 2
1527	24707	NM_012693	i	Rattus norvegicus Cytochrome P450 IIA2 (Cyp2a2), mRNA. Length = 2259	Cytochrome P450 IIA2
1528	1850	NM_012696	t	Rattus norvegicus T-kininogen, see also D11Eh1 and D11Mi8 (Kng), mRNA. Length = 1417	T-kininogen
1528	1854	NM_012696	t	Rattus norvegicus T-kininogen, see also D11Eh1 and D11Mi8 (Kng), mRNA. Length = 1417	K-kininogen, differential splicing leads to HMW Kngk, T-kininogen
1529	1603	NM_012697	General	Rattus norvegicus Organic cation transporter (Slc22a1), mRNA. Length = 1882	Organic cation transporter
1530	1372	NM_012734	u	Rattus norvegicus Hexokinase 1 (Hk1), mRNA. Length = 3653	Hexokinase 1
1531	1478	NM_012744	bb, General	Rattus norvegicus Pyruvate carboxylase (Pc), mRNA. Length = 3945	Pyruvate carboxylase
1532	343	NM_012747	h,t	Rattus norvegicus Signal transducer and activator of transcription 3 (Stat3), mRNA. Length = 2924	Signal transducer and activator of transcription 3
1533	8829	NM_012749	General	Rattus norvegicus Nucleolin (Ncl), mRNA. Length = 2142	Nucleolin
1534	20828	NM_012752	General	Rattus norvegicus CD24 antigen (Cd24), mRNA. Length = 1703	CD24 antigen
1534	20829	NM_012752	i, General	Rattus norvegicus CD24 antigen (Cd24), mRNA. Length = 1703	CD24 antigen

TABLE 1: SUMMARY					Atty. Docket No. 4492-3083WC Rev. No. 4788997.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Unique Accession
1534	20830	NM_012752	i.General	Rattus norvegicus CD24 antigen (Cd24), mRNA. Length = 1703	CD24 antigen
1535	15174	NM_012756	b	Rattus norvegicus Insulin-like growth factor 2 receptor (Igf2r), mRNA. Length = 8810	Insulin-like growth factor 2 receptor
1536	21685	NM_012760	j,m,n	Rattus norvegicus Lost on transformation 1 (Lot1), mRNA. Length = 5028	Lost on transformation 1
1537	18068	NM_012762	t	Rattus norvegicus Interleukin 1beta converting enzyme (Casp1), mRNA. Length = 1209	Interleukin 1beta converting enzyme
1538	1246	NM_012770	a.General	Rattus norvegicus Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase) (Gucy1b2), mRNA. Length = 2335	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)
1539	1348	NM_012776	f	Rattus norvegicus adrenergic receptor kinase, beta 1 (Adrbk1), mRNA. Length = 2683	G-protein-linked receptor kinase (beta adrenergic receptor kinase 1)
1540	18135	NM_012791	w	Rattus norvegicus dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a (Dyrk1a), mRNA. Length = 2640	Dual Specificity Yak1-related Kinase, ESTs
1541	16947	NM_012793	p.bb	Rattus norvegicus Guanidinoacetate methyltransferase (Gamt), mRNA. Length = 924	Guanidinoacetate methyltransferase
1542	960	NM_012796	u	Rattus norvegicus glutathione S-transferase, theta 2 (Gstt2), mRNA. Length = 1258	glutathione S-transferase, theta 2
1543	260	NM_012798	f,u	Rattus norvegicus MAL protein gene (Mal), mRNA. Length = 2265	MAL protein gene
1544	556	NM_012803	d	Rattus norvegicus Protein C (Proc), mRNA. Length = 1543	Protein C
1545	21729	NM_012804	q	Rattus norvegicus ATP-binding cassette, sub-family D (ALD), member 3 (Abcd3), mRNA. Length = 3324	ATP-binding cassette, sub-family D (ALD), member 3
1546	15032	NM_012816	General	Rattus norvegicus alpha-methylacyl-CoA racemase (Amacr), mRNA. Length = 1504	Methylacyl-CoA racemase alpha
1547	24895	NM_012817	General	Rattus norvegicus Insulin-like growth factor-binding protein 5 (Igfbp5), mRNA. Length = 1630	Insulin-like growth factor-binding protein 5
1548	18109	NM_012823	u.General	Rattus norvegicus Annexin A3 (Anx3), mRNA. Length = 1454	ESTs, Weakly similar to LURT3 annexin III - rat [R.norvegicus]
1549	373	NM_012833	h,i,g, General	Rattus norvegicus ATP-binding cassette, sub-family C (CFTR/MRP), member 2 (Abcc2), mRNA. Length = 4918	Canalicular multispecific organic anion transporter
1550	2855	NM_012838	e	Rattus norvegicus Cystatin beta (Cstb), mRNA. Length = 590	Cystatin beta

TABLE 1: SUMMARY						Atly. Doclet No. 44921-5039WG
						Doc. No. 1798927.4
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title	
1551	11136	NM_012839	s	Rattus norvegicus Cytochrome C, expressed in somatic tissues (Cycs), mRNA. Length = 318	Cytochrome C, expressed in somatic tissues	
1552	20885	NM_012842	a	Rattus norvegicus Epidermal growth factor (Egf), mRNA. Length = 4801	Epidermal growth factor	
1552	20884	NM_012842	a.bb	Rattus norvegicus Epidermal growth factor (Egf), mRNA. Length = 4801	Epidermal growth factor	
1553	18770	NM_012857	e	Rattus norvegicus Lysosomal associated membrane protein 1 (120 kDa) (Lamp1), mRNA. Length = 2006	Lysosomal associated membrane protein 1 (120 kDa)	
1554	20674	NM_012861	i	Rattus norvegicus O6-methylguanine-DNA methyltransferase (Mgmt), mRNA. Length = 812	ESTs, Weakly similar to S21348 probable polyprotein-related protein 4 - rat [R.norvegicus], O6-methylguanine-DNA methyltransferase	
1555	13151	NM_012862	a,r, General	Rattus norvegicus Matrix Gla protein (Mgp), mRNA. Length = 521	Matrix Gla protein	
1556	24617	NM_012870	General	Rattus norvegicus tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (Tnfrsf11b), mRNA. Length = 2432	Osteoprotegerin	
1557	20945	NM_012875	a,v	Ribosomal protein L39 (Rpl39), mRNA. Length = 324	Ribosomal protein L39	
1558	15872	NM_012879	a,r	Rattus norvegicus Solute carrier family 2 A2 (glucose transporter, type 2) (Slc2a2), mRNA. Length = 2573	Solute carrier family 2 A2 (glucose transporter, type 2)	
1559	495	NM_012880	z	Rattus norvegicus Superoxide dismutase 3 (Sod3), mRNA. Length = 1729	Superoxide dismutase 3	
1559	494	NM_012880	c	Rattus norvegicus Superoxide dismutase 3 (Sod3), mRNA. Length = 1729	Superoxide dismutase 3	
1560	23651	NM_012881	d,u, General	Rattus norvegicus Sialoprotein (osteopontin) (Spp1), mRNA. Length = 1457	Sialoprotein (osteopontin)	
1562	19477	NM_012891	q	Rattus norvegicus Acyl-CoA dehydrogenase, Very long chain (Acadv), mRNA. Length = 2117	EST, Moderately similar to ACADV RAT ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR [R.norvegicus]	
1563	18564	NM_012899	v, General	Rattus norvegicus aminolevulinic acid, delta-, dehydratase (Alad), mRNA. Length = 1116	Delta - aminolevulinic acid dehydratase	
1564	7197	NM_012904	f,r,cc, General	Rattus norvegicus Annexin 1 (p35) (Lipocortin 1) (Anxa1), mRNA. Length = 1402	Annexin 1 (p35) (Lipocortin 1)	
1564	7196	NM_012904	v,cc, General	Rattus norvegicus Annexin 1 (p35) (Lipocortin 1) (Anxa1), mRNA. Length = 1402	Annexin 1 (p35) (Lipocortin 1)	
1565	20202	NM_012909	b,r	Rattus norvegicus Aquaporin 2 (Aqp2), mRNA. Length = 939	Aquaporin 2	

TABLE 1: SUMMARY					Atty. Docket No. 44921-0039WG Doc. No. 1793397.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1566	18581	NM_012911	c,j	Rattus norvegicus Arrestin, beta 2 (Arb2), mRNA. Length = 1758	Arrestin, beta 2
1566	16582	NM_012911	c	Rattus norvegicus Arrestin, beta 2 (Arb2), mRNA. Length = 1758	Arrestin, beta 2
1587	24431	NM_012912	General	Rattus norvegicus Activating transcription factor 3 (Atf3), mRNA. Length = 1893	Activating transcription factor 3
1568	18118	NM_012913	p	Rattus norvegicus ATPase, Na+K+ transporting, beta polypeptide 3 (Alpb3), mRNA. Length = 1818	ATPase, Na+K+ transporting, beta polypeptide 3
1569	6108	NM_012915	n	Rattus norvegicus ATPase inhibitor (rat mitochondrial IF1 protein) (Atpi), mRNA. Length = 833	ATPase inhibitor (rat mitochondrial IF1 protein)
1570	20757	NM_012923	c,l,aa	Rattus norvegicus Cyclin G1 (Cng1), mRNA. Length = 3169	Cyclin G1
1570	20755	NM_012923	i	Rattus norvegicus Cyclin G1 (Cng1), mRNA. Length = 3169	Cyclin G1
1571	2830	NM_012925	f	Rattus norvegicus CD59 antigen (C459), mRNA. Length = 1523	CD59 antigen
1571	2831	NM_012925	f	Rattus norvegicus CD59 antigen (C459), mRNA. Length = 1523	CD59 antigen
1572	1977	NM_012930	q	Rattus norvegicus Carnitine palmitoyltransferase 2 (Cpt2), mRNA. Length = 2296	Carnitine palmitoyltransferase 2
1573	18694	NM_012931	j,l,m,z	Rattus norvegicus v-crk-associated tyrosine kinase substrate (Ctkas), mRNA. Length = 3335	v-crk-associated tyrosine kinase substrate
1574	13723	NM_012935	n	Rattus norvegicus Crystallin, alpha polypeptide 2 (Cryab), mRNA. Length = 528	Crystallin, alpha polypeptide 2, ESTs
1575	9109	NM_012939	j,y,z	Rattus norvegicus Cathepsin H (Ctsh), mRNA. Length = 1362	Cathepsin H
1575	19398	NM_012939	aa	Rattus norvegicus Cathepsin H (Ctsh), mRNA. Length = 1362	EST
1576	223	NM_012945	b,cc	Rattus norvegicus Diphtheria toxin receptor (heparin binding epidermal growth factor - like growth factor) (Dtr), mRNA. Length = 1550	Diphtheria toxin receptor (heparin binding epidermal growth factor - like growth factor)
1577	15058	NM_012950	cc	Rattus norvegicus Thrombin receptor (F2r), mRNA. Length = 3418	Thrombin receptor
1579	19111	NM_012963	g	Rattus norvegicus High mobility group 1 (Hmg1), mRNA. Length = 1225	High mobility group 1
1580	19374	NM_012964	x	Rattus norvegicus Hyaluronan mediated motility receptor (RHAMM) (Hmrm), mRNA. Length = 2049	Hyaluronan mediated motility receptor (RHAMM)
1581	2554	NM_012967	it	Rattus norvegicus Intercellular adhesion molecule 1 (Icam1), mRNA. Length = 2602	Intercellular adhesion molecule 1

TABLE 1: SUMMARY					Atty. Oenhot No. 44924-386WVG
					Box No. 173897.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1581	2555	NM_012967	t.c.c. General	Rattus norvegicus Interleukin-1 (il1cam1), mRNA. Length = 2602	Interleukin-1 (il1cam1)
1582	24528	NM_012973	c	Rattus norvegicus Potassium (K+) channel protein, slowly activating (isk) (Kcne1), mRNA. Length = 585	Potassium (K+) channel protein, slowly activating (isk)
1583	956	NM_012976	c	Rattus norvegicus Lectin, galactose binding, soluble 5 (Galecln-5) (Lgals5), mRNA. Length = 872	Lectin, galactose binding, soluble 5 (Galecln-5)
1584	16417	NM_012991	g	Rattus norvegicus Nucleoprotein 50kD (Nup50), mRNA. Length = 3027	Nuclear pore associated protein
1585	17393	NM_012992	d	Rattus norvegicus Nucleoplasmin-related protein (Nuclear protein B23 (Npm1), mRNA. Length = 1232	Nucleoplasmin-related protein (Nuclear protein B23)
1586	23544	NM_013013	s	Rattus norvegicus Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator) (Pspap), mRNA. Length = 2175	Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator)
1587	1588	NM_013026	k	Rattus norvegicus Syndecan 1 (Sdc1), mRNA. Length = 2410	Syndecan 1
1588	17894	NM_013027	m	Rattus norvegicus Selenoprotein W muscle 1 (Sepw1), mRNA. Length = 664	Selenoprotein W muscle 1
1589	18300	NM_013030	s.v. General	Rattus norvegicus Solute carrier family 17 (sodium/hydrogen exchanger), member 2 (Slc34a1), mRNA. Length = 2440	Rattus norvegicus mRNA for NaPi-2 alpha, complete cds
1589	18076	NM_013030	g.s.z	Rattus norvegicus Solute carrier family 17 (sodium/hydrogen exchanger), member 2 (Slc34a1), mRNA. Length = 2440	Solute carrier family 17 (sodium/hydrogen exchanger), member 2
1589	18078	NM_013030	s	Rattus norvegicus Solute carrier family 17 (sodium/hydrogen exchanger), member 2 (Slc34a1), mRNA. Length = 2440	Rattus norvegicus mRNA for NaPi-2 alpha, complete cds, Solute carrier family 17 (sodium/hydrogen exchanger), member 2
1589	18077	NM_013030	e.s.z	Rattus norvegicus Solute carrier family 17 (sodium/hydrogen exchanger), member 2 (Slc34a1), mRNA. Length = 2440	Solute carrier family 17 (sodium/hydrogen exchanger), member 2
1591	730	NM_013040	w	Rattus norvegicus ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (Abcc9), mRNA. Length = 5000	Sulfonurea receptor 2

TABLE 1: SUMMARY					
ATM, Pocket No. 44924-6083WG					
Doc. No. 1798897.1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Unique Cluster Title
1592	17401	NM 013043	i.o. General	Rattus norvegicus Transforming growth factor beta stimulated clone 22 (Tgfb14), mRNA. Length = 1666	Transforming growth factor beta stimulated clone 22
1593	16684	NM 013052	General	Rattus norvegicus Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (Ywhah), mRNA. Length = 1689	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
1594	14421	NM 013053	u	Rattus norvegicus Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (Ywhah), mRNA. Length = 2099	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
1595	15254	NM 013058	k	Rattus norvegicus Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (Id3), mRNA. Length = 568	Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
1596	14997	NM 013059	s,z	Rattus norvegicus Tissue-nonspecific ALP alkaline phosphatase (Alpi), mRNA. Length = 2415	Tissue-nonspecific ALP alkaline phosphatase
1596	14996	NM 013059	General	Rattus norvegicus Tissue-nonspecific ALP alkaline phosphatase (Alpi), mRNA. Length = 2415	Tissue-nonspecific ALP alkaline phosphatase
1597	25676	NM 013069	aa	Rattus norvegicus CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated) (Cd74), mRNA. Length = 1150	
1597	16924	NM 013069	o	Rattus norvegicus CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated) (Cd74), mRNA. Length = 1150	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated)
1598	24748	NM 013070	h,q	Rattus norvegicus Utrophin (Utrn), mRNA. Length = 10,705	Utrophin
1599	1529	NM 013082	d,General	Rattus norvegicus Ryudocan/syndecan 2 (Sdc2), mRNA. Length = 2153	Ryudocan/syndecan 2
1600	1521	NM 013091	j,l,z, General	Rattus norvegicus Tumor necrosis factor receptor superfamily, member 1a (Tnfr1), mRNA. Length = 2130	Tumor necrosis factor receptor
1601	1685	NM 013096	c,aa	Rattus norvegicus Hemoglobin, alpha 1 (Hba1), mRNA. Length = 556	Hemoglobin, alpha 1
1601	26150	NM 013096	c,j	Rattus norvegicus Hemoglobin, alpha 1 (Hba1), mRNA. Length = 556	
1601	1688	NM 013096	p	Rattus norvegicus Hemoglobin, alpha 1 (Hba1), mRNA. Length = 556	Hemoglobin, alpha 1

TABLE 1: SUMMARY					Atty. Doctel No. 44924-0001W
					Doc. No. 1798897.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1601	1689	NM_013096	c.p	Rattus norvegicus Hemoglobin, alpha 1 (Hba1), mRNA. Length = 556	Hemoglobin, alpha 1
1601	1684	NM_013096	c.s,aa	Rattus norvegicus Hemoglobin, alpha 1 (Hba1), mRNA. Length = 556	Hemoglobin, alpha 1
1602	20886	NM_013097	u,x,bb	Rattus norvegicus Deoxyribonuclease I (Dnase1), mRNA. Length = 1143	Deoxyribonuclease I
1602	20887	NM_013097	u,x,bb	Rattus norvegicus Deoxyribonuclease I (Dnase1), mRNA. Length = 1143	Deoxyribonuclease I
1603	1321	NM_013098	c	Rattus norvegicus Glucose-6-phosphatase (G6pc), mRNA. Length = 2237	Glucose-6-phosphatase
1604	15296	NM_013102	l,m	Rattus norvegicus FK506-binding protein 1 (12kD) (FKbp1a), mRNA. Length = 654	FK506-binding protein 1 (12kD)
1606	23709	NM_013113	o,s,z,aa	Rattus norvegicus ATPase Na+/K+ transporting beta 1 polypeptide (Alp1b1), mRNA. Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
1606	23711	NM_013113	p	Rattus norvegicus ATPase Na+/K+ transporting beta 1 polypeptide (Alp1b1), mRNA. Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
1606	23710	NM_013113	s	Rattus norvegicus ATPase Na+/K+ transporting beta 1 polypeptide (Alp1b1), mRNA. Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
1607	1976	NM_013118	u	Rattus norvegicus Guanylate cyclase activator 2 (guanylin) (Guca2a), mRNA. Length = 567	Guanylate cyclase activator 2 (guanylin)
1609	870	NM_013130	h	Rattus norvegicus MAD (mothers against decapentaplegic, Drosophila) homolog 1 (Madh1), mRNA. Length = 2002	MAD (mothers against decapentaplegic, Drosophila) homolog 1
1610	16650	NM_013132	u,General	Rattus norvegicus Annexin V (Anx5), mRNA. Length = 1417	Annexin V
1611	650	NM_013134	h	Rattus norvegicus 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (Hmgcr), mRNA. Length = 2664	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
1611	651	NM_013134	h,j,l	Rattus norvegicus 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (Hmgcr), mRNA. Length = 2664	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
1612	1712	NM_013138	General	Rattus norvegicus Inositol 1, 4, 5-triphosphate receptor 3 (Itp3), mRNA. Length = 8806	Inositol 1, 4, 5-triphosphate receptor 3
1613	16982	NM_013144	o,v, General	Rattus norvegicus Insulin-like growth factor binding protein 1 (Igfbp1), mRNA. Length = 1500	Insulin-like growth factor binding protein 1

TABLE 1: SUMMARY					Atty. Docket No. 44924-5083WC Doc. No. 179237/1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq ID	Model Code	Gene Name	Unigene Cluster Title
1614	21683	NM_013154	Loc, General	Rattus norvegicus CCAAT/enhancerbinding, protein (C/EBP) delta (Cebpd), mRNA. Length = 1200	CCAAT/enhancerbinding, protein (C/EBP) delta
1614	21682	NM_013154	cc	Rattus norvegicus CCAAT/enhancerbinding, protein (C/EBP) delta (Cebpd), mRNA. Length = 1200	CCAAT/enhancerbinding, protein (C/EBP) delta
1615	3431	NM_013156	b,g,n	Rattus norvegicus Cathepsin L (Ctsl), mRNA. Length = 1386	Cathepsin L
1615	25567	NM_013156	v,General	Rattus norvegicus Cathepsin L (Ctsl), mRNA. Length = 1386	
1615	3430	NM_013156	General	Rattus norvegicus Cathepsin L (Ctsl), mRNA. Length = 1386	Cathepsin L
1616	1309	NM_013159	w	Rattus norvegicus Insulin degrading enzyme (Ide), mRNA. Length = 4276	Insulin degrading enzyme
1616	1310	NM_013159	w	Rattus norvegicus Insulin degrading enzyme (Ide), mRNA. Length = 4276	Insulin degrading enzyme
1617	21723	NM_013174	w	Rattus norvegicus Transforming growth factor, beta 3 (Tgfb3), mRNA. Length = 2633	Transforming growth factor, beta 3
1618	1314	NM_013181	m	Rattus norvegicus Protein kinase, cAMP dependent, regulatory, type 1 (Prkar1a), mRNA. Length = 1433	Protein kinase, cAMP dependent, regulatory, type 1
1619	17357	NM_013183	p.bb, General	Rattus norvegicus Meprin 1 beta (Mep1b), mRNA. Length = 2290	Meprin 1 beta
1620	1300	NM_013190	y	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkfb), mRNA. Length = 2740	Phosphofructokinase, liver, B-type
1621	16448	NM_013197	c	Rattus norvegicus Aminolevulinatase synthase 2, delta (Aldas2), mRNA. Length = 1899	Aminolevulinatase synthase 2, delta
1622	20856	NM_013200	b	Rattus norvegicus Camitine palmitoyltransferase 1 beta, muscle isoform (Cpt1b), mRNA. Length = 2826	Camitine palmitoyltransferase 1 beta, muscle isoform
1623	397	NM_013214	f	Rattus norvegicus acyl-CoA hydrolase (RBACH), mRNA. Length = 1523	Rattus norvegicus brain cytosolic acyl coenzyme A thioester hydrolase mRNA, complete cds, acyl-CoA hydrolase
1624	20864	NM_013215	g,n,y	Rattus norvegicus aflatoxin B1 aldehyde reductase (AFAR), mRNA. Length = 1272	aflatoxin B1 aldehyde reductase
1625	20728	NM_013217	v	Rattus norvegicus afadin (AF6), mRNA. Length = 5957	afadin
1626	1396	NM_013222	j	Rattus norvegicus augmentor of liver regeneration (ALR), mRNA. Length = 1226	augmentor of liver regeneration
1627	815	NM_013224	w	Rattus norvegicus ribosomal protein S26 (Rps26), mRNA. Length = 435	ribosomal protein S26

TABLE 1. SUMMARY					
Atty. Doctel No. 43921-503WO					
Doc. No. 179897.1					
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1628	16305	NM_013226	v	Rattus norvegicus ribosomal protein L32 (RpL32), mRNA. Length = 465	
1629	21076	NM_016986	d	Rattus norvegicus Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain (Acadm), mRNA. Length = 1866	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain
1630	24649	NM_016988	v	Rattus norvegicus Acid phosphatase 2, lysosomal (Acp2), mRNA. Length = 2009	Acid phosphatase 2, lysosomal
1631	15239	NM_016989	q,w	Rattus norvegicus adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA. Length = 2681	R.norvegicus (Sprague Dawley) ribosomal protein L15 mRNA
1632	45	NM_016996	General	Rattus norvegicus Calcium-sensing receptor (hypocalcemic hypercalcemia 1, severe neonatal hyperparathyroidism) (Casr), mRNA. Length = 4113	Calcium-sensing receptor (hypocalcemic hypercalcemia 1, severe neonatal hyperparathyroidism)
1633	20714	NM_016999	t	Rattus norvegicus Cytochrome P450, subfamily IVB, polypeptide 1 (Cyp4b1), mRNA. Length = 2462	Cytochrome P450, subfamily IVB, polypeptide 1
1633	20713	NM_016999	t	Rattus norvegicus Cytochrome P450, subfamily IVB, polypeptide 1 (Cyp4b1), mRNA. Length = 2462	Cytochrome P450, subfamily IVB, polypeptide 1
1633	20711	NM_016999	q,t	Rattus norvegicus Cytochrome P450, subfamily IVB, polypeptide 1 (Cyp4b1), mRNA. Length = 2462	Cytochrome P450, subfamily IVB, polypeptide 1
1633	20715	NM_016999	q,t	Rattus norvegicus Cytochrome P450, subfamily IVB, polypeptide 1 (Cyp4b1), mRNA. Length = 2462	Cytochrome P450, subfamily IVB, polypeptide 1
1634	1698	NM_017000	e,n,p, General	Rattus norvegicus Diaphorase (NADH/NADPH) (Dia4), mRNA. Length = 1396	Diaphorase (NADH/NADPH)
1635	1399	NM_017006	h,n, General	Rattus norvegicus Glucose-6-phosphate dehydrogenase (G6pd), mRNA. Length = 2324	Glucose-6-phosphate dehydrogenase
1637	18989	NM_017013	n	Rattus norvegicus Glutathione-S-transferase, alpha type (Yc?) (Gsta2), mRNA. Length = 830	Glutathione-S-transferase, alpha type (Yc?)
1638	21013	NM_017014	e,f	Rattus norvegicus Glutathione-S-transferase, mu type 2 (Yb2) (Gstm2), mRNA. Length = 1055	Glutathione-S-transferase, mu type 2 (Yb2)
1638	21015	NM_017014	e,General	Rattus norvegicus Glutathione-S-transferase, mu type 2 (Yb2) (Gstm2), mRNA. Length = 1055	Glutathione-S-transferase, mu type 2 (Yb2)

TABLE 1: SUMMARY					Atty. Bocket No. 4:9974-5089WO
					Doc. No. 1199247.1
Sequence ID No.	Identifier	GenBank Acc# Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title
1639	11636	NM_017023	b	Rattus norvegicus Potassium inwardly-rectifying channel, subfamily J (Kcnj1), mRNA. Length = 2059	Potassium inwardly-rectifying channel, subfamily J
1639	5475	NM_017023	b	Rattus norvegicus Potassium inwardly-rectifying channel, subfamily J (Kcnj1), mRNA. Length = 2059	ESTs, Potassium inwardly-rectifying channel, subfamily J
1639	25546	NM_017023	b,bb	Rattus norvegicus Potassium inwardly-rectifying channel, subfamily J (Kcnj1), mRNA. Length = 2059	
1640	17807	NM_017025	l,General	Rattus norvegicus Lactate dehydrogenase A (Ldha), mRNA. Length = 1609	Lactate dehydrogenase A
1641	24597	NM_017040	u	Rattus norvegicus Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (Ppp2cb), mRNA. Length = 1843	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
1642	24696	NM_017048	f,j,z	Rattus norvegicus Solute carrier family 4, member 2, anion exchange protein 2 (Slc4a2), mRNA. Length = 4057	Solute carrier family 4, member 2, anion exchange protein 2
1643	24695	NM_017049	u	Rattus norvegicus Solute carrier family 4, member 3, anion exchange protein 3 (Slc4a3), mRNA. Length = 3877	Solute carrier family 4, member 3, anion exchange protein 3
1644	20876	NM_017050	j,n,z	Rattus norvegicus Superoxide dismutase 1, soluble (Sod1), mRNA. Length = 650	Superoxide dismutase 1, soluble
1645	910	NM_017059	f,j,m	Rattus norvegicus Bcl2-associated X protein (Bax), mRNA. Length = 579	Bcl2-associated X protein
1645	912	NM_017059	i	Rattus norvegicus Bcl2-associated X protein (Bax), mRNA. Length = 579	Bcl2-associated X protein
1646	1946	NM_017061	h	Rattus norvegicus Lysyl oxidase (Lox), mRNA. Length = 4557	Lysyl oxidase
1646	1942	NM_017061	l,General	Rattus norvegicus Lysyl oxidase (Lox), mRNA. Length = 4557	Lysyl oxidase
1646	1943	NM_017061	t	Rattus norvegicus Lysyl oxidase (Lox), mRNA. Length = 4557	Lysyl oxidase
1647	6062	NM_017066	d	Rattus norvegicus Pleiotrophin (Heparine binding factor, Hbfn, in the mouse) (Ptn), mRNA. Length = 1246	Pleiotrophin (Heparine binding factor, Hbfn, in the mouse)
1648	6654	NM_017068	w	Rattus norvegicus Lysosomal-associated membrane protein 2 (Lamp2), mRNA. Length = 1548	Lysosomal-associated membrane protein 2
1649	11153	NM_017073	s	Rattus norvegicus Glutamine synthetase (glutamate-ammonia ligase) (Glu), mRNA. Length = 2793	Glutamine synthetase (glutamate-ammonia ligase)

TABLE 1: SUMMARY					
Atty. Docket No. 44924-3089VG Doc. No. 1798897.1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq ID	Model Code	Gene Name	Ligase Cluster Title
1650	923	NM_017076	General	Rattus norvegicus Tumor-associated glycoprotein pE4 (Tagp4), mRNA. Length = 2171	Tumor-associated glycoprotein pE4
1651	1523	NM_017079	s	Rattus norvegicus CD1D antigen (Cd1d), mRNA. Length = 1835	CD1D antigen
1652	23660	NM_017080	s	Rattus norvegicus Hydroxysteroid dehydrogenase, 11 beta type 1 (Hsd11b1), mRNA. Length = 1265	Hydroxysteroid dehydrogenase, 11 beta type 1
1653	275	NM_017081	b,d, General	Rattus norvegicus Hydroxysteroid dehydrogenase, 11 beta type 2 (Hsd11b2), mRNA. Length = 1864	Hydroxysteroid dehydrogenase, 11 beta type 2
1654	16211	NM_017082	i,s,z	Rattus norvegicus Uromodulin (Tamm-Horsfall protein) (Umod), mRNA. Length = 2227	Uromodulin (Tamm-Horsfall protein)
1655	1552	NM_017084	j	Rattus norvegicus Glycine methyltransferase (Gnmt), mRNA. Length = 988	Glycine methyltransferase
1655	1550	NM_017084	y	Rattus norvegicus Glycine methyltransferase (Gnmt), mRNA. Length = 988	Glycine methyltransferase
1656	22552	NM_017087	a,k,x	Rattus norvegicus Small proteoglycan 1 (biglycan), bone (BSPG1) (bone/cartilage proteoglycan 1 precursor) (Bgn), mRNA. Length = 2446	Small proteoglycan 1 (biglycan), bone (BSPG1) (bone/cartilage proteoglycan 1 precursor)
1657	8888	NM_017090	m	Rattus norvegicus guanylate cyclase 1, soluble, alpha 3 (Gucy1a3), mRNA. Length = 4775	Guanylate cyclase, soluble, alpha 1 (GTP pyrophosphate - lyase)
1658	10887	NM_017094	a,General	Rattus norvegicus Growth hormone receptor (Ghr), mRNA. Length = 2950	Growth hormone receptor
1659	4393	NM_017101	s,y	Rattus norvegicus Peptidylprolyl isomerase A (cyclophilin A) (Ppia), mRNA. Length = 743	Peptidylprolyl isomerase A (cyclophilin A)
1660	24770	NM_017111	d	Rattus norvegicus solute carrier family (organic anion transporter) member 1 (Slc21a1), mRNA. Length = 2758	solute carrier family (organic anion transporter) member 1
1661	20745	NM_017113	e	Rattus norvegicus granulins (Gm), mRNA. Length = 2113	granulins
1661	20746	NM_017113	a	Rattus norvegicus granulins (Gm), mRNA. Length = 2113	granulins
1662	1375	NM_017122	w	Rattus norvegicus hippocalcin (Hpcac), mRNA. Length = 1561	hippocalcin
1663	12903	NM_017124	k	Rattus norvegicus CD37 antigen (Cd37), mRNA. Length = 1158	CD37 antigen
1664	24885	NM_017138	r	Rattus norvegicus laminin receptor 1 (Lamr1), mRNA. Length = 1018	laminin receptor 1
1664	24886	NM_017138	d,g	Rattus norvegicus laminin receptor 1 (Lamr1), mRNA. Length = 1018	laminin receptor 1

TABLE 1: SUMMARY					Atty. Doctel No. 44924-6089WC
					Doc. No. 170897.1
Sequence ID No.	Identifier	GenBank/Ref. Seq ID	Mode Code	Gene Name	Unigene Cluster Title
1665	15363	NM_017147	n,u	Rattus norvegicus coflin 1, non-muscle (Cfl1), mRNA. Length = 1039	coflin 1, non-muscle
1666	13392	NM_017148	u,General	Rattus norvegicus cysteine rich protein 1 (Cspr1), mRNA. Length = 1403	cysteine rich protein
1667	5351	NM_017150	q	Rattus norvegicus ribosomal protein L29 (Rpl29), mRNA. Length = 630	ribosomal protein L29
1668	16954	NM_017151	a,n	Rattus norvegicus ribosomal protein S15 (Rps15), mRNA. Length = 487	ribosomal protein S15
1669	21643	NM_017152	g	Rattus norvegicus ribosomal protein S17 (Rps17), mRNA. Length = 466	ribosomal protein S17
1670	1694	NM_017153	a,q	Rattus norvegicus ribosomal protein S3a (Rps3a), mRNA. Length = 890	ribosomal protein S3a
1671	17104	NM_017160	bb, General	Rattus norvegicus ribosomal protein S6 (Rps6), mRNA. Length = 801	ribosomal protein S6
1671	17106	NM_017160	u	Rattus norvegicus ribosomal protein S6 (Rps6), mRNA. Length = 801	ribosomal protein S6
1671	17107	NM_017160	d,e	Rattus norvegicus ribosomal protein S6 (Rps6), mRNA. Length = 801	ribosomal protein S6
1672	17686	NM_017165	n,q	Rattus norvegicus glutathione peroxidase 4 (Gpx4), mRNA. Length = 872	glutathione peroxidase 4
1673	20702	NM_017166	c	Rattus norvegicus Leukemia-associated cytosolic phosphoprotein stathmin (Lap18), mRNA. Length = 1054	Leukemia-associated cytosolic phosphoprotein stathmin
1674	3513	NM_017177	r	Rattus norvegicus choline/ethanolamine kinase (Chetk), mRNA. Length = 1679	choline/ethanolamine kinase
1675	19031	NM_017180	v,General	Rattus norvegicus T-cell death associated gene (Tdag), mRNA. Length = 1353	T-cell death associated gene
1676	15437	NM_017187	x,z	Rattus norvegicus high mobility group box 2 (Hmgb2), mRNA. Length = 1072	high mobility group protein 2
1676	15433	NM_017187	y	Rattus norvegicus high mobility group box 2 (Hmgb2), mRNA. Length = 1072	high mobility group protein 2
1676	15434	NM_017187	x,z	Rattus norvegicus high mobility group box 2 (Hmgb2), mRNA. Length = 1072	high mobility group protein 2
1677	24437	NM_017190	p	Rattus norvegicus Myelin-associated glycoprotein (Mag), mRNA. Length = 2474	Myelin-associated glycoprotein
1678	1542	NM_017193	jj,m,z	Rattus norvegicus kynurenine aminotransferase II (Kat2), mRNA. Length = 1826	kynurenine aminotransferase II

TABLE 1: SUMMARY					Atty. Doctel No. 44921-5033WG Doc. No. 170333v.1
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title
1679	14695	NM_017202	q,s	Rattus norvegicus cytochrome c oxidase, subunit IVa (Cox4a), mRNA. Length = 696	cytochrome c oxidase, subunit IV
1679	14694	NM_017202	s,z	Rattus norvegicus cytochrome c oxidase, subunit IVa (Cox4a), mRNA. Length = 696	cytochrome c oxidase, subunit IV
1680	1428	NM_017213	m	Rattus norvegicus outer dense fiber of sperm tails 2 (Odf2), mRNA. Length = 2451	outer dense fiber of sperm tails 2
1681	1622	NM_017216	g,j,s,z	Rattus norvegicus solute carrier family 3, member 1 (Slc3a1), mRNA. Length = 2305	solute carrier family 3, member 1
1682	13642	NM_017220	v	Rattus norvegicus 6-pyruvoyl tetrahydropterin synthase (Pts), mRNA. Length = 1176	ESTs
1682	19976	NM_017220	w	Rattus norvegicus 6-pyruvoyl tetrahydropterin synthase (Pts), mRNA. Length = 1176	ESTs
1683	1510	NM_017224	General	Rattus norvegicus organic cationic transporter-like 1 (Orc1), mRNA. Length = 2227	organic cationic transporter-like 1
1684	1811	NM_017226	j,l,m,z	Rattus norvegicus dentatorubral pallidolysian atrophy (Drlpa), mRNA. Length = 4387	dentatorubral pallidolysian atrophy
1686	17563	NM_017245	a,c,e,q	Rattus norvegicus eukaryotic translation elongation factor 2 (Eef2), mRNA. Length = 2626	eukaryotic translation elongation factor 2
1687	17502	NM_017248	r	Rattus norvegicus heterogeneous nuclear ribonucleoprotein A1 (Hnra1), mRNA. Length = 1696	heterogeneous nuclear ribonucleoprotein A1
1687	17501	NM_017248	x	Rattus norvegicus heterogeneous nuclear ribonucleoprotein A1 (Hnra1), mRNA. Length = 1696	heterogeneous nuclear ribonucleoprotein A1
1688	19	NM_017258	v,General	Rattus norvegicus B-cell translocation gene 1, anti-proliferative (Btg1), mRNA. Length = 1464	B-cell translocation gene 1, anti-proliferative
1689	15300	NM_017259	i,v,cc, General	Rattus norvegicus B-cell translocation gene 2, anti-proliferative (Btg2), mRNA. Length = 2519	B-cell translocation gene 2, anti-proliferative
1689	15301	NM_017259	i,m,v,aa,c, General	Rattus norvegicus B-cell translocation gene 2, anti-proliferative (Btg2), mRNA. Length = 2519	B-cell translocation gene 2, anti-proliferative
1689	15299	NM_017259	i,y,cc, General	Rattus norvegicus B-cell translocation gene 2, anti-proliferative (Btg2), mRNA. Length = 2519	B-cell translocation gene 2, anti-proliferative
1690	15224	NM_017264	d	Rattus norvegicus protease (prosome, macropain) 28 subunit, alpha (Psm1), mRNA. Length = 921	protease (prosome, macropain) 28 subunit, alpha

TABLE 1: SUMMARY					
Rat, Accession No. 44921-50839					
Doc. No. 1792847.1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title
1691	3987	NM_017280	bb	Rattus norvegicus proteasome (prosome, macropain) subunit, alpha type 3 (Pama3), mRNA. Length = 897	proteasome (prosome, macropain) subunit, alpha type 3
1692	1447	NM_017281	l	Rattus norvegicus proteasome (prosome, macropain) subunit, alpha type 4 (Pama4), mRNA. Length = 1121	proteasome (prosome, macropain) subunit, alpha type 4
1693	15535	NM_017283	s,bb	Rattus norvegicus proteasome (prosome, macropain) subunit, alpha type 6 (Pama6), mRNA. Length = 932	proteasome (prosome, macropain) subunit, alpha type 6
1694	12349	NM_017290	General	Rattus norvegicus ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (Alp2a2), mRNA. Length = 5548	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
1695	15519	NM_017298	p	Rattus norvegicus calcium channel, voltage-dependent, L type, alpha 1D subunit (Cacna1d), mRNA. Length = 7966	calcium channel, voltage-dependent, L type, alpha 1D subunit
1696	23825	NM_017299	v	Rattus norvegicus solute carrier family 19 (sodium/hydrogen exchanger), member 1 (Slc19a1), mRNA. Length = 2402	solute carrier family 19 (sodium/hydrogen exchanger), member 1
1696	23826	NM_017299	v	Rattus norvegicus solute carrier family 19 (sodium/hydrogen exchanger), member 1 (Slc19a1), mRNA. Length = 2402	solute carrier family 19 (sodium/hydrogen exchanger), member 1
1697	14003	NM_017305	j,l,m,y,z	Rattus norvegicus glutamate-cysteine ligase, modifier subunit (Gclm), mRNA. Length = 1382	Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory
1698	26109	NM_017306	q,s	Rattus norvegicus dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) (DCI), mRNA. Length = 972	EST
1698	18687	NM_017306	q,t	Rattus norvegicus dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) (DCI), mRNA. Length = 972	Rat mRNA for delta3, delta2-enoyl-CoA isomerase, dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
1699	18142	NM_017314	g,s,aa	Rattus norvegicus ubiquitin C (Ubc), mRNA. Length = 2545	ubiquitin C
1700	1894	NM_017320	t	Rattus norvegicus cathepsin S (Ctss), mRNA. Length = 1330	cathepsin S
1701	20809	NM_017326	u	Rattus norvegicus calmodulin (RCM3), mRNA. Length = 1112	calmodulin
1702	355	NM_017334	cc	Rattus norvegicus transcriptional repressor CREM (CREM), mRNA. Length = 436	

TABLE 1: SUMMARY					Atty. Docket No. 44921-0089WG Doc. No. 199997.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID	Model Code	Gene Name	Original Cluster Title
1703	16148	NM_017340	q,s	Rattus norvegicus acyl-coA oxidase (RATACO1), mRNA. Length = 3741	acyl-coA oxidase
1703	16150	NM_017340	a	Rattus norvegicus acyl-coA oxidase (RATACO1), mRNA. Length = 3741	acyl-coA oxidase
1704	20849	NM_017343	r,u, General	Rattus norvegicus myosin regulatory light chain (MRLCB), mRNA. Length = 1139	Rat mRNA for myosin regulatory light chain (RLC)
1704	20848	NM_017343	b, General	Rattus norvegicus myosin regulatory light chain (MRLCB), mRNA. Length = 1139	Rat mRNA for myosin regulatory light chain (RLC)
1705	606	NM_017350	b	Rattus norvegicus urinary plasminogen activator receptor 2 (uPAR-2), mRNA. Length = 1272	urinary plasminogen activator receptor 2
1706	1581	NM_017365	General	Rattus norvegicus PDZ and LIM domain 1 (ellfin) (Ptim1), mRNA. Length = 1392	LIM protein
1707	455	NM_019131	x	Rattus norvegicus Tropomyosin 1 (alpha) (Tpm1), mRNA. Length = 1004	Tropomyosin 1 (alpha)
1707	456	NM_019131	y,z	Rattus norvegicus Tropomyosin 1 (alpha) (Tpm1), mRNA. Length = 1004	Tropomyosin 1 (alpha)
1708	4532	NM_019134	b	Rattus norvegicus Solute carrier family 12, member 1 (bumetanide-sensitive sodium-[potassium]-chloride cotransporter) (Slc12a1), mRNA. Length = 4595	Solute carrier family 12, member 1 (bumetanide-sensitive sodium-[potassium]-chloride cotransporter)
1709	1608	NM_019166	j,y,z	Rattus norvegicus synaptogyrin 1 (Syng1), mRNA. Length = 879	ESTs. Moderately similar to synaptogyrin [R.norvegicus], synaptogyrin 1
1710	7489	NM_019169	c, General	Rattus norvegicus synuclein, alpha (Snca), mRNA. Length = 1018	synuclein, alpha
1711	17066	NM_019170	p	Rattus norvegicus carbonyl reductase (Cbr), mRNA. Length = 1018	carbonyl reductase
1712	23924	NM_019174	bb	Rattus norvegicus carbonic anhydrase 4 (Ca4), mRNA. Length = 1205	ESTs. Highly similar to CARBONIC ANHYDRASE IV PRECURSOR [R.norvegicus]
1713	24019	NM_019186	l	Rattus norvegicus ADP-ribosylation-like 4 (Ar4), mRNA. Length = 1067	ADP-ribosylation-like 4
1714	22063	NM_019195	d	Rattus norvegicus integrin-associated protein (Cd47), mRNA. Length = 1053	integrin-associated protein
1715	2079	NM_019220	j,k,z	Rattus norvegicus amino-terminal enhancer of split (Aes), mRNA. Length = 1356	related to Drosophila groucho gene
1716	16284	NM_019229	l,m	Rattus norvegicus solute carrier family 12, member 4 (Slc12a4), mRNA. Length = 3725	solute carrier family 12, member 4
1717	985	NM_019233	b,cc	Rattus norvegicus small inducible cytokine subfamily A20 (Scya20), mRNA. Length = 816	small inducible cytokine subfamily A20

TABLE 1. SUMMARY						Ally Doclet No. 43924-5093WC
						Doc No. 1798897.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title	
1718	15503	NM_019237	k,x	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcolce), mRNA. Length = 1547	procollagen C-proteinase enhancer protein	
1718	15504	NM_019237	k,x	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcolce), mRNA. Length = 1547	procollagen C-proteinase enhancer protein	
1719	17908	NM_019242	l,v,cc, General	Rattus norvegicus interferon-related developmental regulator 1 (ifrd1), mRNA. Length = 1736	interferon-related developmental regulator 1	
1720	11218	NM_019247	c	Rattus norvegicus paired-like homeodomain transcription factor 3 (Pitx3), mRNA. Length = 1253	paired-like homeodomain transcription factor 3	
1721	15259	NM_019259	d,f	Rattus norvegicus complement component 1, q subcomponent binding protein (C1qb), mRNA. Length = 1124	complement component 1, q subcomponent binding protein	
1722	21443	NM_019262	aa, General	Rattus norvegicus complement component 1, q subcomponent, beta polypeptide (C1qb), mRNA. Length = 1136	complement component 1, q subcomponent, beta polypeptide	
1722	21444	NM_019262	l, General	Rattus norvegicus complement component 1, q subcomponent, beta polypeptide (C1qb), mRNA. Length = 1136	complement component 1, q subcomponent, beta polypeptide	
1723	117	NM_019266	o,bb	Rattus norvegicus sodium channel, voltage-gated, type VIII, alpha polypeptide (Scn8a), mRNA. Length = 6586	sodium channel, voltage-gated, type VIII, alpha polypeptide	
1724	1145	NM_019280	w	Rattus norvegicus gap junction membrane channel protein alpha 5 (Gja5), mRNA. Length = 3115	gap junction membrane channel protein alpha 5	
1725	22220	NM_019286	c	Rattus norvegicus Alcohol dehydrogenase 3 (Acdh3), mRNA. Length = 1131	Alcohol dehydrogenase (class I), alpha polypeptide	
1726	10015	NM_019289	l,m,Lx, General	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA. Length = 1430	Actin-related protein complex 1b	
1726	10016	NM_019289	bb, General	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA. Length = 1430	Actin-related protein complex 1b	
1727	21651	NM_019296	c,f,x	Rattus norvegicus Cell division cycle control protein 2 (Cdc2a), mRNA. Length = 1184	Cell division cycle control protein 2	
1728	20751	NM_019301	s	Rattus norvegicus Complement receptor related protein (Cr1), mRNA. Length = 1811	Complement receptor related protein	
1729	645	NM_019345	bb	Rattus norvegicus solute carrier family 12, member 3 (Slc12a3), mRNA. Length = 4361	solute carrier family 12, member 3	

TABLE 1: SUMMARY					Atty. Bocket No. 44921-6060W
					Doc. No. 199387.1
Sequence ID No.	Identify	GenBank Acc. Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title
1730	1301	NM_019349	c	Rattus norvegicus Serine/threonine kinase 2 (Slk2), mRNA. Length = 4194	Rat liver stearyl-CoA desaturase mRNA, complete cds
1731	3776	NM_019354	a,u	Rattus norvegicus Uncoupling protein 2, mitochondrial (Ucp2), mRNA. Length = 1575	Uncoupling protein 2, mitochondrial
1732	4592	NM_019356	General	Rattus norvegicus eukaryotic translation initiation factor 2, subunit 1 (alpha) (eIF2s1), mRNA. Length = 1377	eukaryotic translation initiation factor 2, subunit 1 (alpha)
1733	1324	NM_019371	w	Rattus norvegicus factor-responsive smooth muscle protein (SM-20), mRNA. Length = 2625	factor-responsive smooth muscle protein
1734	19577	NM_019377	e	Rattus norvegicus 14-3-3 protein beta-subtype (Ywhab), mRNA. Length = 2756	ESTs, Moderately similar to S12207 hypothetical protein [M.musculus]
1735	24626	NM_019381	s	Rattus norvegicus Testis enhanced gene transcript (Teg1), mRNA. Length = 940	Testis enhanced gene transcript
1736	744	NM_019622	p	Rattus norvegicus espin (Espn), mRNA. Length = 2786	espin
1737	20716	NM_019623	c	Rattus norvegicus cytochrome P450 4F1 (Cyp4f1), mRNA. Length = 1977	cytochrome P450 4F1
1738	20709	NM_019904	x	Rattus norvegicus beta-galactoside-binding lectin (Lgals1), mRNA. Length = 519	beta-galactoside-binding lectin
1739	574	NM_019905	u,General	Rattus norvegicus calpactin I heavy chain (Anxa2), mRNA. Length = 1395	Rattus norvegicus clone BB.1.4.1 unknown Glu-Pro dipeptide repeat protein mRNA, complete cds, calpactin I heavy chain, hydroxyacid oxidase 3 (medium-chain)
1740	9096	NM_019908	j	Rattus norvegicus hypothetical protein LOC56728 (LOC56728), mRNA. Length = 858	hypothetical protein LOC56728
1741	20457	NM_020073	i,General	Rattus norvegicus parathyroid hormone receptor (LOC56813), mRNA. Length = 2065	parathyroid hormone receptor
1741	20458	NM_020073	General	Rattus norvegicus parathyroid hormone receptor (LOC56813), mRNA. Length = 2065	parathyroid hormone receptor
1741	20460	NM_020073	General	Rattus norvegicus parathyroid hormone receptor (LOC56813), mRNA. Length = 2065	parathyroid hormone receptor
1742	18713	NM_020075	r	Rattus norvegicus eukaryotic initiation factor 5 (eIF-5) (eIF5), mRNA. Length = 3504	eukaryotic initiation factor 5 (eIF-5)
1742	18715	NM_020075	r	Rattus norvegicus eukaryotic initiation factor 5 (eIF-5) (eIF5), mRNA. Length = 3504	eukaryotic initiation factor 5 (eIF-5)

TABLE 1: SUMMARY					
Atty. Docket No. 44924-5035WO					
Doc No. 979897.1					
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1743	20493	NM_020076	p	Rattus norvegicus 3-hydroxyanthranilate 3,4-dioxygenase (Haoa), mRNA. Length = 1254	3-hydroxyanthranilate 3,4-dioxygenase
1744	16375	NM_020976	g	Rattus norvegicus kidney-specific membrane protein (NX-17), mRNA. Length = 1181	kidney-specific membrane protein
1745	20816	NM_021261	k, General	Rattus norvegicus thymosin, beta 10 (Tmsb10), mRNA. Length = 539	thymosin beta-10
1746	15335	NM_021264	a	Rattus norvegicus ribosomal protein L35a (Rpl35), mRNA. Length = 348	ribosomal protein L35a
1747	18729	NM_021578	k, z	Rattus norvegicus transforming growth factor beta-1 gene (Tgfb1), mRNA. Length = 1595	transforming growth factor beta-1 gene
1748	19060	NM_021587	cc	Rattus norvegicus transforming growth factor-beta (TGF-beta) masking protein large subunit (Ltbp1), mRNA. Length = 6244	transforming growth factor-beta (TGF-beta) masking protein large subunit
1749	17324	NM_021593	o, General	Rattus norvegicus kynurenine 3-hydroxylase (Kmo), mRNA. Length = 1733	kynurenine 3-hydroxylase
1750	19679	NM_021653	General	Rattus norvegicus Thyroxine deiodinase, type I (Dio1), mRNA. Length = 2106	Thyroxine deiodinase, type I
1750	19678	NM_021653	a, v, General	Rattus norvegicus Thyroxine deiodinase, type I (Dio1), mRNA. Length = 2106	Thyroxine deiodinase, type I
1751	19665	NM_021688	u, General	Rattus norvegicus putative potassium channel TWIK (Kcnk1), mRNA. Length = 1582	putative potassium channel TWIK
1752	19667	NM_021690	m	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) (Epac), mRNA. Length = 3373	cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI)
1754	22916	NM_021740	a	Rattus norvegicus prothymosin alpha (Ptma), mRNA. Length = 1182	prothymosin alpha
1755	19710	NM_021744	t	Rattus norvegicus CD14 antigen (Cd14), mRNA. Length = 1591	CD14 antigen
1755	19711	NM_021744	t	Rattus norvegicus CD14 antigen (Cd14), mRNA. Length = 1591	CD14 antigen
1756	19712	NM_021745	r	Rattus norvegicus farnesoid X activated receptor (LOC60351), mRNA. Length = 2070	farnesoid X activated receptor
1757	1982	NM_021750	j, k, y, z	Rattus norvegicus cysteine-sulfinate decarboxylase (Csd), mRNA. Length = 2413	Rattus norvegicus ccs2 mRNA, complete cds
1757	19824	NM_021750	a, bb	Rattus norvegicus cysteine-sulfinate decarboxylase (Csd), mRNA. Length = 2413	cysteine-sulfinate decarboxylase
1758	25198	NM_021754	h	Rattus norvegicus Nopp140 associated protein (Nap65), mRNA. Length = 1980	Nopp140 associated protein

TABLE 1 SUMMARY					Atty. Docket No. 44921-5089WO
					Doc. No. 1799397.1
Sequence ID No.	Identifier	GenBank Acc./Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title
1758	20035	NM_021754	b,n,s,v, General	Rattus norvegicus Nopp140 associated protein (Nap65), mRNA. Length = 1689	Nopp140 associated protein
1759	20090	NM_021757	m	Rattus norvegicus pleiotropic regulator 1 (Plrg1), mRNA. Length = 1545	pleiotropic regulator 1
1760	17885	NM_021765	aa	Rattus norvegicus beta prime COP (Copb), mRNA. Length = 3025	beta prime COP
1762	20161	NM_021836	cc, General	Rattus norvegicus jun B proto-oncogene (Junb), mRNA. Length = 1035	jun B proto-oncogene
1764	1203	NM_021997	k,z	Rattus norvegicus cytoplasmic linker 2 (Cyln2), mRNA. Length = 4847	cytoplasmic linker 2
1765	23151	NM_022005	b	Rattus norvegicus FXD domain-containing ion transport regulator 6 (Fxyd6), mRNA. Length = 1711	FXD domain-containing ion transport regulator 6
1767	17101	NM_022179	bb	Rattus norvegicus Hexokinase 3 (Hk3), mRNA. Length = 3692	Hexokinase 3
1767	17100	NM_022179	bb	Rattus norvegicus Hexokinase 3 (Hk3), mRNA. Length = 3692	Hexokinase 3
1768	20257	NM_022180	w, General	Rattus norvegicus Hepatic nuclear factor 4 (alpha transcription factor 4) (Hnf4a), mRNA. Length = 1446	Hepatic nuclear factor 4 (alpha transcription factor 4)
1768	25699	NM_022180	i	Rattus norvegicus Hepatic nuclear factor 4 (alpha transcription factor 4) (Hnf4a), mRNA. Length = 1446	Hepatic nuclear factor 4 (alpha transcription factor 4)
1768	10860	NM_022180	p	Rattus norvegicus Hepatic nuclear factor 4 (alpha transcription factor 4) (Hnf4a), mRNA. Length = 1446	ESTs
1769	23780	NM_022183	k,x	Rattus norvegicus topoisomerase (DNA) II alpha (Top2a), mRNA. Length = 6052	topoisomerase (DNA) II alpha
1770	20312	NM_022224	o	Rattus norvegicus resiniferatoxin-binding, phosphotriesterase-related protein (Rpr1), mRNA. Length = 1050	resiniferatoxin-binding, phosphotriesterase-related protein
1771	6585	NM_022266	d,p,cc	Rattus norvegicus connective tissue growth factor (Ctgf), mRNA. Length = 2345	connective tissue growth factor
1772	17161	NM_022298	i,v,cc, General	Rattus norvegicus alpha-tubulin (Tuba1), mRNA. Length = 1617	alpha-tubulin
1772	17162	NM_022298	u	Rattus norvegicus alpha-tubulin (Tuba1), mRNA. Length = 1617	alpha-tubulin
1772	17160	NM_022298	u	Rattus norvegicus alpha-tubulin (Tuba1), mRNA. Length = 1617	alpha-tubulin
1772	17158	NM_022298	q	Rattus norvegicus alpha-tubulin (Tuba1), mRNA. Length = 1617	alpha-tubulin

TABLE 1: SUMMARY					Atty. Docket No. 44821-8883WG Doc. No. 1298457.1
Sequence ID No.	Identifier	GenBank/ Acc/ Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title
1773	11454	NM_022381	I,aa, General	Rattus norvegicus Proliferating cell nuclear antigen (Pcna), mRNA. Length = 1160	Proliferating cell nuclear antigen
1773	11455	NM_022381	I,General	Rattus norvegicus Proliferating cell nuclear antigen (Pcna), mRNA. Length = 1160	Proliferating cell nuclear antigen
1774	13460	NM_022390	s	Rattus norvegicus quinoid dihydropteridine reductase (Qdpr), mRNA. Length = 1307	quinoid dihydropteridine reductase
1775	15184	NM_022391	z	Rattus norvegicus pituitary tumor-transforming 1 (Pitg1), mRNA. Length = 974	pituitary tumor transforming gene
1776	22413	NM_022392	h	Rattus norvegicus growth response protein (CL-6) (LOC64194), mRNA. Length = 2410	growth response protein (CL-6)
1776	22414	NM_022392	n	Rattus norvegicus growth response protein (CL-6) (LOC64194), mRNA. Length = 2410	growth response protein (CL-6)
1777	22499	NM_022393	t	Rattus norvegicus macrophage galactose N-acetyl-galactosamine specific lectin (Mgl), mRNA. Length = 1358	Gal/GalNAc-specific lectin
1779	24537	NM_022399	e	Rattus norvegicus calreticulin (Calr), mRNA. Length = 1882	calreticulin
1779	24539	NM_022399	y	Rattus norvegicus calreticulin (Calr), mRNA. Length = 1882	calreticulin
1780	1141	NM_022401	o,General	Rattus norvegicus plectin (Plect1), mRNA. Length = 15,231	plectin
1781	1069	NM_022402	g	Rattus norvegicus acidic ribosomal protein P0 (Arbp), mRNA. Length = 1046	acidic ribosomal protein P0
1782	8211	NM_022500	i,n,s	Rattus norvegicus ferritin light chain 1 (Ftl1), mRNA. Length = 552	ferritin light chain 1
1782	8212	NM_022500	n,s	Rattus norvegicus ferritin light chain 1 (Ftl1), mRNA. Length = 552	ferritin light chain 1
1783	6615	NM_022503	s	Rattus norvegicus cytochrome c oxidase subunit VIIa 3 (Cox7a3), mRNA. Length = 460	cytochrome c oxidase subunit VIIa 3
1784	4259	NM_022504	q,w	Rattus norvegicus ribosomal protein L36 (Rpl36), mRNA. Length = 364	ribosomal protein L36
1785	1611	NM_022509	j	Rattus norvegicus survival motor neuron (Snm), mRNA. Length = 1243	survival motor neuron
1786	2236	NM_022512	y,z	Rattus norvegicus short chain acyl-coenzyme A dehydrogenase (Acads), mRNA. Length = 1749	short chain acyl-coenzyme A dehydrogenase
1787	3026	NM_022514	a	Rattus norvegicus ribosomal protein L27 (Rpl27), mRNA. Length = 463	ribosomal protein L27

TABLE 1: SUMMARY				Atty. Docket No. 44921-5039WG Doc. No. 179367.1	
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Organic Cluster Title
1787	3027	NM_022514	a,q,r,aa	Rattus norvegicus ribosomal protein L27 (Rpl27), mRNA. Length = 463	ribosomal protein L27
1788	2696	NM_022515	a,d	Rattus norvegicus ribosomal protein L24 (Rpl24), mRNA. Length = 541	ribosomal protein L24
1788	2697	NM_022515	n,w,aa	Rattus norvegicus ribosomal protein L24 (Rpl24), mRNA. Length = 541	ribosomal protein L24
1789	3900	NM_022516	h	Rattus norvegicus polypyrimidine tract binding protein (Ptb), mRNA. Length = 2697	polypyrimidine tract binding protein
1790	4151	NM_022518	o	Rattus norvegicus ADP-ribosylation factor 1 (Arf1), mRNA. Length = 900	ADP-ribosylation factor 1
1791	4242	NM_022521	c	Rattus norvegicus ornithine aminotransferase (Oat), mRNA. Length = 1938	ornithine aminotransferase
1792	4412	NM_022523	o	Rattus norvegicus platelet endothelial tetraspan antigen-3 (Cd151), mRNA. Length = 1668	platelet endothelial tetraspan antigen-3
1793	6641	NM_022533	General	Rattus norvegicus plasmolipin (Z49658), mRNA. Length = 1475	plasmolipin
1794	8097	NM_022536	a	Rattus norvegicus cyclophilin B (Pbib), mRNA. Length = 840	cyclophilin B
1795	8597	NM_022538	c,r,u	Rattus norvegicus phosphatidate phosphohydrolase type 2 (Ppap2), mRNA. Length = 871	phosphatidate phosphohydrolase type 2
1795	8598	NM_022538	u	Rattus norvegicus phosphatidate phosphohydrolase type 2 (Ppap2), mRNA. Length = 871	phosphatidate phosphohydrolase type 2
1796	9296	NM_022541	o	Rattus norvegicus small zinc finger-like protein DDP2 (Ddp2), mRNA. Length = 494	small zinc finger-like protein DDP2
1797	21063	NM_022585	h	Rattus norvegicus ornithine decarboxylase antizyme inhibitor (Oazi), mRNA. Length = 4269	ornithine decarboxylase antizyme inhibitor
1799	20781	NM_022591	z	Rattus norvegicus telomerase protein component 1 (Ttp1), mRNA. Length = 8216	telomerase protein component 1
1800	20803	NM_022592	n	Rattus norvegicus transketolase (Tkt), mRNA. Length = 2098	transketolase
1801	20925	NM_022594	q	Rattus norvegicus enoyl hydratase-like protein, peroxisomal (Ech1), mRNA. Length = 1097	enoyl hydratase-like protein, peroxisomal
1802	20944	NM_022597	aa	Rattus norvegicus cathepsin B (Ctsb), mRNA. Length = 1904	cathepsin B
1803	21024	NM_022599	o,General	Rattus norvegicus synaptobrevin 2 binding protein (Synj2bp), mRNA. Length = 5215	outer membrane protein

TABLE 1: SUMMARY				Atty. Docket No. 43921-5639WG Doc. No. 199997-1	
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID	Model Gene	Gene Name	UniGene Cluster Title
1804	2250	NM_022643	General	Rattus norvegicus Testis-specific histone 2b (Th2b), mRNA. Length = 470	ESTs, Highly similar to 0506206A histone H2B (R.norvegicus)
1805	17567	NM_022672	a,y	Rattus norvegicus ribosomal protein S14 (Rps14), mRNA. Length = 492	ribosomal protein S14
1806	17561	NM_022674	bb	Rattus norvegicus H2A histone family, member Z (H2afz), mRNA. Length = 811	H2A histone family, member Z
1807	24563	NM_022676	b	Rattus norvegicus protein phosphatase 1, regulatory (inhibitor) subunit 1A (Ppp1r1a), mRNA. Length = 619	protein phosphatase 1, regulatory (inhibitor) subunit 1A
1807	24564	NM_022676	b,x	Rattus norvegicus protein phosphatase 1, regulatory (inhibitor) subunit 1A (Ppp1r1a), mRNA. Length = 619	protein phosphatase 1, regulatory (inhibitor) subunit 1A
1808	20506	NM_022686	l	Rattus norvegicus germinal histone H4 gene (Hist4), mRNA. Length = 377	germinal histone H4 gene
1809	20508	NM_022688	g	Rattus norvegicus preoptic regulatory factor-1 (Porf1), mRNA. Length = 689	preoptic regulatory factor-1
1810	17586	NM_022694	k	Rattus norvegicus p105 coactivator (U83883), mRNA. Length = 3166	p105 coactivator
1811	17730	NM_022697	a	Rattus norvegicus ribosomal protein L28 (Rpl28), mRNA. Length = 466	ribosomal protein L28
1811	17729	NM_022697	q	Rattus norvegicus ribosomal protein L28 (Rpl28), mRNA. Length = 466	ribosomal protein L28
1812	154	NM_022849	t	Rattus norvegicus crp-ductin (Cprd), mRNA. Length = 4344	crp-ductin
1813	127	NM_022855	h	Rattus norvegicus casein kinase 1 gamma 3 isoform (Cskn1g3), mRNA. Length = 2547	casein kinase 1 gamma 3 isoform
1814	152	NM_022858	j	Rattus norvegicus HNF-3/forkhead homolog-1 (Hnf1), mRNA. Length = 1760	HNF-3/forkhead homolog-1
1816	18101	NM_022948	z	Rattus norvegicus tricarboxylate carrier-like protein (Loc65042), mRNA. Length = 2699	tricarboxylate carrier-like protein
1816	18103	NM_022948	u	Rattus norvegicus tricarboxylate carrier-like protein (Loc65042), mRNA. Length = 2699	tricarboxylate carrier-like protein
1817	21491	NM_022951	w	Rattus norvegicus putative protein phosphatase 1 nuclear targeting subunit (Ppp1r10), mRNA. Length = 4131	putative protein phosphatase 1 nuclear targeting subunit
1818	15742	NM_022958	y	Rattus norvegicus phosphatidylinositol 3-kinase (Pik3c3), mRNA. Length = 2752	phosphatidylinositol 3-kinase

TABLE 1: SUMMARY					Ally, Docket No. 44921-5069WG Doc. No. 106937
Sequence ID No.	Identifier	GenBank Accession No.	Model Code	Gene Name	Unigene Cluster Title
1819	9286	NM_023027	Lw	Rattus norvegicus tRNA selenocysteine associated protein (Secp43), mRNA. Length = 864	tRNA selenocysteine associated protein
1820	23215	NM_023102	z	Rattus norvegicus casein kinase 1 gamma 2 isoform (Csk1g2), mRNA. Length = 1572	casein kinase 1 gamma 2 isoform
1821	21238	NM_024125	cc, General	Rattus norvegicus Liver activating protein (LAP), also NF-IL6, nuclear factor-IL6, previously designated TCF5 (Cebpb), mRNA. Length = 1408	Liver activating protein (LAP), also NF-IL6, nuclear factor-IL6, previously designated TCF5
1821	21239	NM_024125	cc, General	Rattus norvegicus Liver activating protein (LAP), also NF-IL6, nuclear factor-IL6, previously designated TCF5 (Cebpb), mRNA. Length = 1408	Liver activating protein (LAP), also NF-IL6, nuclear factor-IL6, previously designated TCF5
1822	353	NM_024127	i,n, General	Rattus norvegicus DNA-damage-inducible transcript 1 (Gadd45a), mRNA. Length = 711	DNA-damage-inducible transcript 1
1822	354	NM_024127	i,n, General	Rattus norvegicus DNA-damage-inducible transcript 1 (Gadd45a), mRNA. Length = 711	DNA-damage-inducible transcript 1
1822	352	NM_024127	h, General	Rattus norvegicus DNA-damage-inducible transcript 1 (Gadd45a), mRNA. Length = 711	DNA-damage-inducible transcript 1
1823	17227	NM_024131	x	Rattus norvegicus D-dopachrome tautomerase (Ddt), mRNA. Length = 628	D-dopachrome tautomerase
1824	1598	NM_024134	i	Rattus norvegicus DNA-damage inducible transcript 3 (Ddit3), mRNA. Length = 806	DNA-damage inducible transcript 3
1825	1162	NM_024153	d	Rattus norvegicus adrenodoxin reductase (Fdxr), mRNA. Length = 1786	adrenodoxin reductase
1826	7863	NM_024156	c	Rattus norvegicus annexin VI (Anxa6), mRNA. Length = 2739	Rattus norvegicus mRNA for H(+)-transporting ATPase, complete cds
1827	22079	NM_024157	x	Rattus norvegicus complement factor I (Cfi), mRNA. Length = 2021	complement factor I
1828	16476	NM_024162	General	Rattus norvegicus heart fatty acid binding protein (Fabp3), mRNA. Length = 666	heart fatty acid binding protein
1829	17765	NM_024351	b,s,v	Rattus norvegicus heat shock 70KD protein 8 (Hspa8), mRNA. Length = 2073	Heat shock cognate protein 70
1830	8879	NM_024360	h	Rattus norvegicus hairy and enhancer of split 1, (Drosophila) (Hes1), mRNA. Length = 1453	hairy and enhancer of split 1, (Drosophila)

TABLE 1: SUMMARY						Atty. Docket No. 44921-5689WC	
						Doc. No. 179337.1	
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title		
1831	20772	NM_024363	x	Rattus norvegicus heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae) (Hmt112), mRNA. Length = 1201	heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae)		
1832	2812	NM_024366	c	Rattus norvegicus 3-hydroxy-3-methylglutaryl CoA lyase (Hmgcl), mRNA. Length = 1590	3-hydroxy-3-methylglutaryl CoA lyase		
1833	335	NM_024367	i,y	Rattus norvegicus heme oxygenase-2 non-reducing isoform (Hmox2), mRNA. Length = 1815	heme oxygenase-2 non-reducing isoform		
1834	21	NM_024388	cc	Rattus norvegicus immediate early gene transcription factor NGFI-B (Nr4a1), mRNA. Length = 2488	immediate early gene transcription factor NGFI-B		
1834	22	NM_024388	cc	Rattus norvegicus immediate early gene transcription factor NGFI-B (Nr4a1), mRNA. Length = 2488	immediate early gene transcription factor NGFI-B		
1836	9929	NM_024392	f	Rattus norvegicus peroxisomal multifunctional enzyme type II (Hsd17b4), mRNA. Length = 2535	peroxisomal multifunctional enzyme type II		
1837	3582	NM_024396	aa	Rattus norvegicus ATP-binding cassette, sub-family A (ABC1), member 2 (Abca2), mRNA. Length = 8040	ATP-binding cassette, sub-family A (ABC1), member 2		
1838	19993	NM_024398	e,p,s,aa	Rattus norvegicus mitochondrial aconitase (nuclear aco2 gene) (Aco2), mRNA. Length = 2744	mitochondrial aconitase (nuclear aco2 gene)		
1839	10789	NM_024399	o	Rattus norvegicus aspartoacylase (Aspa), mRNA. Length = 1552	aspartoacylase		
1840	22626	NM_024400	cc, General	Rattus norvegicus a disintegrin and metalloproteinase with thrombospondin motifs 1 (ADAMTS-1) (Adams1), mRNA. Length = 4878	a disintegrin and metalloproteinase with thrombospondin motifs 1 (ADAMTS-1)		
1841	13633	NM_024403	g,General	Rattus norvegicus activating transcription factor ATF-4 (Atf4), mRNA. Length = 1173	activating transcription factor ATF-4		
1841	13634	NM_024403	g,General	Rattus norvegicus activating transcription factor ATF-4 (Atf4), mRNA. Length = 1173	activating transcription factor ATF-4		
1842	23387	NM_024404	b,General	Rattus norvegicus RNA binding protein p45AUF1 (Hnrpd), mRNA. Length = 1240	RNA binding protein p45AUF1		
1843	21038	NM_024484	h	Rattus norvegicus aminotetralin acid synthase 1 (Alas1), mRNA. Length = 2052	aminotetralin acid synthase 1		
1844	1853	NM_030826	s	Rattus norvegicus Glutathione peroxidase 1 (Gpx1), mRNA. Length = 1539	ESTs, Glutathione peroxidase 1		

TABLE 1: SUMMARY					Atty. Docket No. 44324-SUSW02
					Doc. No. 179833-1
Sequence ID No.	Identifier	GenBank Acc./Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title
1845	15111	NM_030827	e, General	Rattus norvegicus glycoprotein 330 (Lrp2), mRNA. Length = 15,438	glycoprotein 330
1845	15112	NM_030827	y, z	Rattus norvegicus glycoprotein 330 (Lrp2), mRNA. Length = 15,438	glycoprotein 330
1845	15110	NM_030827	General	Rattus norvegicus glycoprotein 330 (Lrp2), mRNA. Length = 15,438	glycoprotein 330
1846	808	NM_030837	k, m	Rattus norvegicus kidney specific organic anion transporter (Slc21a4), mRNA. Length = 2772	kidney specific organic anion transporter
1847	4057	NM_030844	k	Rattus norvegicus islet cell autoantigen 1, 69 kDa (Ica1), mRNA. Length = 2094	islet cell autoantigen 1, 69 kDa
1848	1221	NM_030845	t	Rattus norvegicus gro (Gro1), mRNA. Length = 929	gro
1849	21509	NM_030847	x	Rattus norvegicus epithelial membrane protein 3 (Emp3), mRNA. Length = 737	epithelial membrane protein 3
1850	1928	NM_030872	v	Rattus norvegicus pyruvate dehydrogenase kinase 2 subunit p45 (PDK2) (Pdk2), mRNA. Length = 2207	pyruvate dehydrogenase kinase 2 subunit p45 (PDK2)
1851	17342	NM_030873	u	Rattus norvegicus profilin II (Pfn2), mRNA. Length = 1966	profilin II
1852	24648	NM_030985	u	Rattus norvegicus Angiotensin II receptor, type 1 (AT1A) (Agt1a), mRNA. Length = 1450	Angiotensin II receptor, type 1 (AT1A)
1852	25453	NM_030985	General	Rattus norvegicus Angiotensin II receptor, type 1 (AT1A) (Agt1a), mRNA. Length = 1450	
1853	21802	NM_030987	h	Rattus norvegicus Guanine nucleotide-binding protein beta 1 (Gnb1), mRNA. Length = 2537	Guanine nucleotide-binding protein beta 1
1854	23109	NM_031000	f, s, z	Rattus norvegicus aldo-keto reductase family 1, member A1 (aldohyde reductase) (Akr1a1), mRNA. Length = 1124	aldo-keto reductase family 1, member A1 (aldohyde reductase)
1855	134	NM_031003	a, u	Rattus norvegicus 4-aminobutyrate aminotransferase (Abat), mRNA. Length = 1726	4-aminobutyrate aminotransferase
1856	25461	NM_031009	o	Rattus norvegicus angiotensin II type-1 receptor (Agt1r), mRNA. Length = 2156	angiotensin II type-1 receptor
1857	1845	NM_031010	t	Rattus norvegicus arachidonate 12-lipoxygenase (Alox12), mRNA. Length = 2048	arachidonate 12-lipoxygenase
1857	25517	NM_031010	c, t	Rattus norvegicus arachidonate 12-lipoxygenase (Alox12), mRNA. Length = 2048	arachidonate 12-lipoxygenase
1858	16562	NM_031020	f	Rattus norvegicus p38 mitogen activated protein kinase (Mapk14), mRNA. Length = 3132	p38 mitogen activated protein kinase

TABLE 1: SUMMARY					Atty. Docket No. 4424-368WG
					Doc. No. 1792697.1
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID	Mode Code	Gene Name	UniGene Cluster Title
1859	1480	NM_031021	f	Rattus norvegicus casein kinase II beta subunit (Cenk2b), mRNA. Length = 1954	casein kinase II beta subunit
1860	1719	NM_031024	n	Rattus norvegicus drebrin A (Dbn1), mRNA. Length = 2697	drebrin A
1861	1350	NM_031030	h	Rattus norvegicus cyclin G-associated kinase (Gak), mRNA. Length = 4454	cyclin G-associated kinase
1862	16775	NM_031031	General	Rattus norvegicus L-arginine: glycine amidinotransferase (Gatm), mRNA. Length = 2260	L-arginine: glycine amidinotransferase
1863	691	NM_031034	w	Rattus norvegicus guanine nucleotide binding protein (G protein) alpha 12 (Gna12), mRNA. Length = 1423	guanine nucleotide binding protein (G protein) alpha 12
1864	15886	NM_031035	z	Rattus norvegicus GTP-binding protein (G-alpha-12) (Gna12), mRNA. Length = 1748	GTP-binding protein (G-alpha-12)
1866	3608	NM_031044	k, General	Rattus norvegicus histamine N-methyltransferase (Hnmt), mRNA. Length = 1225	histamine N-methyltransferase
1866	3610	NM_031044	d, General	Rattus norvegicus histamine N-methyltransferase (Hnmt), mRNA. Length = 1225	histamine N-methyltransferase
1867	15137	NM_031051	s	Rattus norvegicus macrophage migration inhibitory factor (Mif), mRNA. Length = 551	macrophage migration inhibitory factor
1868	514	NM_031056	General	Rattus norvegicus matrix metalloproteinase 14, membrane-inserted (Mmp14), mRNA. Length = 2448	matrix metalloproteinase 14, membrane-inserted
1869	17269	NM_031057	General	Rattus norvegicus methylmalonate semialdehyde dehydrogenase gene (Mmsdh), mRNA. Length = 2059	methylmalonate semialdehyde dehydrogenase gene
1870	11849	NM_031065	a	Rattus norvegicus ribosomal protein L10a (Rpl10a), mRNA. Length = 710	ribosomal protein L10a
1871	1855	NM_031074	h	Rattus norvegicus nucleoporin 98 (Nup98), mRNA. Length = 3237	nucleoporin 98
1872	4683	NM_031083	d	Rattus norvegicus phosphatidylinositol 4-kinase (Pik4cb), mRNA. Length = 3205	phosphatidylinositol 4-kinase
1873	15202	NM_031093	a	Rattus norvegicus -ral simian leukemia viral oncogene homolog A (ras related) (Rala), mRNA. Length = 952	#NAME?
1873	15201	NM_031093	a, n	Rattus norvegicus -ral simian leukemia viral oncogene homolog A (ras related) (Rala), mRNA. Length = 952	#NAME?
1874	12639	NM_031099	aa	Rattus norvegicus ribosomal protein L5 (Rpl5), mRNA. Length = 1069	ribosomal protein L5

TABLE 1: SUMMARY					Atty. Docket No. 44324-5489WC
					Doc. No. 179839C-1
Sequence ID No.	Identifier	GenBank Accession No.	Model Code	Cyto Name	Unigene Cluster Title
1875	20812	NM_031100	a	Rattus norvegicus ribosomal protein L10 (Rpl10), mRNA. Length = 769	ribosomal protein L10
1876	16638	NM_031103	w	Rattus norvegicus ribosomal protein L19 (Rpl19), mRNA. Length = 703	ribosomal protein L19
1877	19268	NM_031104	q	Rattus norvegicus ribosomal protein L22 (Rpl22), mRNA. Length = 465	ribosomal protein L22
1878	16629	NM_031108	q	Rattus norvegicus mRNA for ribosomal protein S9 (Rps9), mRNA. Length = 688	mRNA for ribosomal protein S9
1879	10878	NM_031110	q.bb	Rattus norvegicus ribosomal protein S11 (Rps11), mRNA. Length = 534	ribosomal protein S11
1880	19162	NM_031111	aa	Rattus norvegicus ribosomal protein S21 (Rps21), mRNA. Length = 359	ribosomal protein S21
1880	19161	NM_031111	a.bb	Rattus norvegicus ribosomal protein S21 (Rps21), mRNA. Length = 359	ribosomal protein S21
1881	24615	NM_031112	a.y	Rattus norvegicus ribosomal protein S24 (Rps24), mRNA. Length = 466	ribosomal protein S24
1882	20839	NM_031113	a.q	Rattus norvegicus ribosomal protein S27a (Rps27a), mRNA. Length = 552	ribosomal protein S27a
1883	19040	NM_031114	l.m. General	Rattus norvegicus S-100 related protein, clone 42C (S100A10), mRNA. Length = 573	S-100 related protein, clone 42C
1884	16349	NM_031115	u	Rattus norvegicus secretin receptor (Scir), mRNA. Length = 1796	secretin receptor
1885	14970	NM_031127	General	Rattus norvegicus sulfite oxidase (Suox), mRNA. Length = 1777	sulfite oxidase
1886	1814	NM_031134	n.q	Rattus norvegicus thyroid hormone receptor alpha (Thra1), mRNA. Length = 2460	thyroid hormone receptor
1887	13359	NM_031135	General	Rattus norvegicus TGFβ inducible early growth response (Tieg), mRNA. Length = 3115	TGFβ inducible early growth response
1888	15052	NM_031136	a	Rattus norvegicus thymosin beta-4 (Tmsb4x), mRNA. Length = 686	thymosin beta-4
1888	19359	NM_031136	a	Rattus norvegicus thymosin beta-4 (Tmsb4x), mRNA. Length = 686	EST
1889	15185	NM_031140	General	Rattus norvegicus vimentin (Vim), mRNA. Length = 1796	vimentin
1890	21625	NM_031144	a.e	Rattus norvegicus cytoplasmic beta-actin (Actb), mRNA. Length = 1128	cytoplasmic beta-actin
1891	238	NM_031152	bb	Rattus norvegicus RAB11a, member RAS oncogene family (Rab11a), mRNA. Length = 895	RAB11a, member RAS oncogene family
1891	240	NM_031152	bb	Rattus norvegicus RAB11a, member RAS oncogene family (Rab11a), mRNA. Length = 895	RAB11a, member RAS oncogene family

TABLE 1: SUMMARY					
Atty. Docket No. 43921-5883WG					
Doc. No. 196937.1					
Sequence ID No.	Identifier	GenBank Acc# Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1892	15277	NM_031237	g	Rattus norvegicus ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5) (Ubc2d3), mRNA. Length = 1531	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
1893	18083	NM_031315	q	Rattus norvegicus acyl-CoA thioesterase 1, cytosolic (Cte1), mRNA. Length = 1591	R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase
1893	1858	NM_031315	q	Rattus norvegicus acyl-CoA thioesterase 1, cytosolic (Cte1), mRNA. Length = 1591	R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase, acyl-CoA thioesterase 1, cytosolic
1894	15663	NM_031318	General	Rattus norvegicus t-complex testis expressed 1 (Tctex1), mRNA. Length = 698	t-complex testis expressed 1
1895	1422	NM_031324	bb, General	Rattus norvegicus prolly endopeptidase (Prep), mRNA. Length = 2743	prolyl endopeptidase
1896	18597	NM_031325	g,bb	Rattus norvegicus UDP-glucose dehydrogenase (Ugdh), mRNA. Length = 2318	UDP-glucose dehydrogenase
1897	11259	NM_031327	l,cc, General	Rattus norvegicus cysteine rich protein 61 (Cyr61), mRNA. Length = 1871	cysteine rich protein 61
1898	4235	NM_031330	General	Rattus norvegicus heterogeneous nuclear ribonucleoprotein A/B (Hnnpab), mRNA. Length = 3061	heterogeneous nuclear ribonucleoprotein A/B
1899	18375	NM_031331	l,m	Rattus norvegicus proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 (Psm4), mRNA. Length = 1334	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
1900	3519	NM_031334	cc	Rattus norvegicus E-cadherin (Cdh1), mRNA. Length = 4396	E-cadherin
1901	20698	NM_031357	b	Rattus norvegicus ceroid- lipofuscinosis, neuronal 2 (Cln2), mRNA. Length = 2485	
1903	634	NM_031509	n	Rattus norvegicus Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. Length = 1178	Glutathione-S-transferase, alpha type (Ya)
1903	25525	NM_031509	n	Rattus norvegicus Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. Length = 1178	Glutathione-S-transferase, alpha type (Ya)
1903	25069	NM_031509	b,n,w	Rattus norvegicus Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. Length = 1178	
1903	635	NM_031509	z	Rattus norvegicus Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. Length = 1178	Glutathione-S-transferase, alpha type (Ya)
1904	848	NM_031517	t	Rattus norvegicus Met proto-oncogene (Met), mRNA. Length = 4189	Met proto-oncogene
1905	1872	NM_031523	a	Rattus norvegicus Nerve growth factor, gamma polypeptide (Ngf), mRNA. Length = 873	Nerve growth factor, gamma polypeptide

TABLE 1: SUMMARY						Atty. Docket No. 41921-5637WO Doc. No. 1766897.1	
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title		
1905	16245	NM_031523	a,d,u	Rattus norvegicus Nerve growth factor, gamma polypeptide (Ngf), mRNA. Length = 873	Rattus norvegicus (clone RSKG50) kallikrein mRNA, 3' end		
1905	16244	NM_031523	a	Rattus norvegicus Nerve growth factor, gamma polypeptide (Ngf), mRNA. Length = 873	Rattus norvegicus (clone RSKG50) kallikrein mRNA, 3' end		
1906	9370	NM_031527	w	Rattus norvegicus Protein phosphatase type 1 alpha, catalytic subunit (Ppp1ca), mRNA. Length = 1392	Protein phosphatase type 1 alpha, catalytic subunit		
1907	20448	NM_031530	General	Rattus norvegicus Small inducible gene JE (Scya2), mRNA. Length = 780	Small Inducible gene JE		
1907	20449	NM_031530	General	Rattus norvegicus Small inducible gene JE (Scya2), mRNA. Length = 780	Small inducible gene JE		
1908	14633	NM_031533	u	Rattus norvegicus Androstere UDP-glucuronosyltransferase (Ugt2b2), mRNA. Length = 1593	Androstere UDP-glucuronosyltransferase		
1909	16048	NM_031541	f	Rattus norvegicus CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 (scavenger receptor class B type 1) (Cd36f1), mRNA. Length = 2497	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 (scavenger receptor class B type 1)		
1910	4011	NM_031543	c,q	Rattus norvegicus Cytochrome P450, subfamily 2e1 (ethanol-inducible) (Cyp2e1), mRNA. Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)		
1910	4010	NM_031543	c,q	Rattus norvegicus Cytochrome P450, subfamily 2e1 (ethanol-inducible) (Cyp2e1), mRNA. Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)		
1910	4012	NM_031543	q	Rattus norvegicus Cytochrome P450, subfamily 2e1 (ethanol-inducible) (Cyp2e1), mRNA. Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)		
1911	28	NM_031546	General	Rattus norvegicus Regucalcin (Rgn), mRNA. Length = 1605	Regucalcin		
1912	24640	NM_031548	h,cc	Rattus norvegicus Sodium channel, nonvoltage-gated 1, alpha (epithelial) (Scn11a), mRNA. Length = 3081	Sodium channel, nonvoltage-gated 1, alpha (epithelial)		
1913	17149	NM_031549	x	Rattus norvegicus Transgelin (Smooth muscle 22 protein) (Tagln), mRNA. Length = 1186	Transgelin (Smooth muscle 22 protein)		
1913	17151	NM_031549	x	Rattus norvegicus Transgelin (Smooth muscle 22 protein) (Tagln), mRNA. Length = 1186	Transgelin (Smooth muscle 22 protein)		
1914	13105	NM_031552	w	Rattus norvegicus Adducin 3, gamma (Add3), mRNA. Length = 2246	Adducin 3, gamma		

TABLE 1: SUMMARY				Atty. Docket No. 44924-36839C Doc. No. 4728839.1	
Sequence ID No.	Identifier	GenBank, AF01 Ref. Seq ID	Model Code	Gene Name	Unigene Cluster Title
1915	15411	NM_031559	d,r	Rattus norvegicus Camitine palmitoyltransferase 1 alpha, liver isoform (Cpl1a), mRNA. Length = 4377	Camitine palmitoyltransferase 1 alpha, liver isoform
1916	16164	NM_031563	a,y	Rattus norvegicus Y box protein 1 (Ybx1), mRNA. Length = 1489	Y box protein 1
1917	9621	NM_031570	bb	Rattus norvegicus ribosomal protein S7 (Rps7), mRNA. Length = 650	ribosomal protein S7
1917	9620	NM_031570	w,bb	Rattus norvegicus ribosomal protein S7 (Rps7), mRNA. Length = 650	ribosomal protein S7
1918	546	NM_031573	f	Rattus norvegicus Phosphorylase kinase, gamma 1 (Phkg1), mRNA. Length = 1388	phosphorylase kinase gamma
1919	1921	NM_031576	f	Rattus norvegicus P450 (cytochrome) oxidoreductase (Por), mRNA. Length = 2441	P450 (cytochrome) oxidoreductase
1919	1920	NM_031576	r	Rattus norvegicus P450 (cytochrome) oxidoreductase (Por), mRNA. Length = 2441	P450 (cytochrome) oxidoreductase
1920	24219	NM_031579	i,General	Rattus norvegicus protein tyrosine phosphatase 4a1 (Ptp4a1), mRNA. Length = 2638	protein tyrosine phosphatase 4a1
1921	770	NM_031584	k,x	Rattus norvegicus solute carrier family 22, member 2 (Slc22a2), mRNA. Length = 2152	solute carrier family 22, member 2
1922	18008	NM_031588	cc	Rattus norvegicus neuregulin 1 (Nrg1), mRNA. Length = 3272	potassium channel, subfamily K, member 3
1922	18005	NM_031588	h	Rattus norvegicus neuregulin 1 (Nrg1), mRNA. Length = 3272	potassium channel, subfamily K, member 3
1922	18011	NM_031588	cc, General	Rattus norvegicus neuregulin 1 (Nrg1), mRNA. Length = 3272	potassium channel, subfamily K, member 3
1923	1584	NM_031595	k	Rattus norvegicus proteasome (prosome, macropain) 26S subunit, ATPase 3 (Psmc3), mRNA. Length = 1627	proteasome (prosome, macropain) 26S subunit, ATPase 3
1924	24235	NM_031614	v	Rattus norvegicus thioredoxin reductase 1 (Txnrd1), mRNA. Length = 3360	thioredoxin reductase 1
1924	24234	NM_031614	General	Rattus norvegicus thioredoxin reductase 1 (Txnrd1), mRNA. Length = 3360	thioredoxin reductase 1
1925	1639	NM_031627	j,j,v	Rattus norvegicus nuclear receptor subfamily 1, group H, member 3 (Nr1h3), mRNA. Length = 1723	nuclear receptor subfamily 1, group H, member 3
1926	1727	NM_031642	m, General	Rattus norvegicus core promoter element binding protein (Copeb), mRNA. Length = 1356	core promoter element binding protein

TABLE 1: SUMMARY					
Atty. Docket No. 44921-5083WG					
Doc. No. 1793897.1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1927	20766	NM 031643	y	Rattus norvegicus mitogen activated protein kinase kinase 2 (Map2k2), mRNA. Length = 1152	mitogen activated protein kinase kinase 2
1929	1993	NM 031655	k,j,m, General	Rattus norvegicus latexin (Lxn), mRNA. Length = 1087	latexin
1930	2057	NM 031660	e	Rattus norvegicus cyclic AMP phosphoprotein, 19kD (Arpp19-pending), mRNA. Length = 339	cyclic AMP phosphoprotein, 19kD
1931	15039	NM 031672	k, General	Rattus norvegicus solute carrier family 15 (H <sup>+</sup> /peptide transporter), member 2 (Slc15a2), mRNA. Length = 3923	solute carrier family 15 (H <sup>+</sup> /peptide transporter), member 2
1932	15175	NM 031682	bb	Rattus norvegicus hydroxyacyl-Coenzyme A dehydrogenase, type II (Hadh2), mRNA. Length = 917	hydroxyacyl-Coenzyme A dehydrogenase, type II
1933	1004	NM 031685	v	Rattus norvegicus golgi SNAP receptor complex member 2 (Gosr2), mRNA. Length = 683	golgi SNAP receptor complex member 2
1934	19727	NM 031687	a,q,s	Rattus norvegicus ubiquitin A S2 residue ribosomal protein fusion product 1 (Ubsa2), mRNA. Length = 467	ubiquitin A-S2 residue ribosomal protein fusion product 1
1935	20404	NM 031700	j,r,y	Rattus norvegicus claudin 3 (Cldn3), mRNA. Length = 1192	claudin 3
1935	20405	NM 031700	o,r	Rattus norvegicus claudin 3 (Cldn3), mRNA. Length = 1192	claudin 3
1936	811	NM 031705	General	Rattus norvegicus dihydropyrimidinase (Dpys), mRNA. Length = 2091	dihydropyrimidinase
1936	812	NM 031705	o,v,bb, General	Rattus norvegicus dihydropyrimidinase (Dpys), mRNA. Length = 2091	dihydropyrimidinase
1937	16204	NM 031706	q,bb	Rattus norvegicus ribosomal protein S8 (Rps8), mRNA. Length = 696	ribosomal protein S8
1937	16205	NM 031706	a,y	Rattus norvegicus ribosomal protein S8 (Rps8), mRNA. Length = 696	ribosomal protein S8
1938	24081	NM 031708	m	Rattus norvegicus glycoprotein 110 (Gp110-pending), mRNA. Length = 1444	glycoprotein 110
1939	16918	NM 031709	a,q	Rattus norvegicus ribosomal protein S12 (Rps12), mRNA. Length = 499	ribosomal protein S12
1940	1081	NM 031712	General	Rattus norvegicus PDZ domain containing 1 (Pdzk1), mRNA. Length = 2005	PDZ domain containing 1
1941	1340	NM 031715	b,n,u,cc, General	Rattus norvegicus phosphofructokinase, muscle (Pfkcm), mRNA. Length = 2757	phosphofructokinase, muscle
1942	23884	NM 031731	j,s	Rattus norvegicus alcohol dehydrogenase family 3, subfamily A2 (Aldh3a2), mRNA. Length = 2977	alcohol dehydrogenase family 3, subfamily A2

TABLE 1: SUMMARY					Atty. Docket No. 44924-008W0
					Date Rec. 1766397.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title
1943	10241	NM_031740	d	Rattus norvegicus UDP-Gal:betaGlcNAc:beta 1,4-galactosyltransferase, polypeptide 6 (B4galt6), mRNA. Length = 5729	UDP-Gal:betaGlcNAc:beta 1,4-galactosyltransferase, polypeptide 6
1944	1214	NM_031741	r	Rattus norvegicus solute carrier family 2 (facilitated glucose transporter), member 5 (Slc2a5), mRNA. Length = 2160	solute carrier family 2 (facilitated glucose transporter), member 5
1944	1215	NM_031741	r	Rattus norvegicus solute carrier family 2 (facilitated glucose transporter), member 5 (Slc2a5), mRNA. Length = 2160	solute carrier family 2 (facilitated glucose transporter), member 5
1945	20724	NM_031753	h	Rattus norvegicus activated leukocyte cell adhesion molecule (Alcam), mRNA. Length = 2866	activated leukocyte cell adhesion molecule
1946	20753	NM_031763	h	Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) (Pafah1b1), mRNA. Length = 1233	platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta)
1946	20752	NM_031763	y	Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) (Pafah1b1), mRNA. Length = 1233	platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta)
1947	14953	NM_031774	p	Rattus norvegicus rab acceptor 1 (prenylated) (Rabact1), mRNA. Length = 861	rab acceptor 1 (prenylated)
1948	14184	NM_031776	t, General	Rattus norvegicus guanine deaminase (Gda), mRNA. Length = 1568	guanine deaminase
1948	14185	NM_031776	d,o,t, General	Rattus norvegicus guanine deaminase (Gda), mRNA. Length = 1568	guanine deaminase
1949	1160	NM_031789	c	Rattus norvegicus NF-E2-related factor 2 (Nfe2l2), mRNA. Length = 2307	NF-E2-related factor 2
1950	16155	NM_031810	d,x	Rattus norvegicus defensin beta 1 (Defb1), mRNA. Length = 416	defensin beta 1
1950	16156	NM_031810	d	Rattus norvegicus defensin beta 1 (Defb1), mRNA. Length = 416	defensin beta 1
1951	17194	NM_031814	z	Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein (GIT1) (Git1), mRNA. Length = 3236	G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein (GIT1)
1952	17535	NM_031816	bb	Rattus norvegicus retinoblastoma binding protein 7 (Rbp7), mRNA. Length = 1917	retinoblastoma binding protein 7
1953	2655	NM_031821	i,j,m,aa	Rattus norvegicus serum-inducible kinase (Snk), mRNA. Length = 2781	serum-inducible kinase
1954	10167	NM_031830	i	Rattus norvegicus reggie1-1 (Flo2), mRNA. Length = 2629	reggie1-1

TABLE 1: SUMMARY					
Affy. Beadlet No. 44921-506396					
Doc. No. 179399.1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq ID	Model Code	Gene Name	Uniform Cluster Title
1955	22321	NM 031632	o.t.u. General	Rattus norvegicus IgE binding protein (Lgals3), mRNA. Length = 948	IgE binding protein
1956	4748	NM 031834	e.t	Rattus norvegicus sulfotransferase family 1A, phenol-preferring, member 1 (Sult1a1), mRNA. Length = 1227	minoxidil sulfotransferase
1956	4749	NM 031834	e.t	Rattus norvegicus sulfotransferase family 1A, phenol-preferring, member 1 (Sult1a1), mRNA. Length = 1227	minoxidil sulfotransferase
1957	7914	NM 031835	e	Rattus norvegicus beta-alanine-pyruvate aminotransferase (AGT2), mRNA. Length = 2151	beta-alanine-pyruvate aminotransferase
1958	8385	NM 031836	h	Rattus norvegicus vascular endothelial growth factor (Vegf), mRNA. Length = 645	vascular endothelial growth factor
1958	8384	NM 031836	h	Rattus norvegicus vascular endothelial growth factor (Vegf), mRNA. Length = 645	vascular endothelial growth factor
1959	10268	NM 031838	a	Rattus norvegicus ribosomal protein S2 (Rps2), mRNA. Length = 819	ribosomal protein S2
1959	10269	NM 031838	aa	Rattus norvegicus ribosomal protein S2 (Rps2), mRNA. Length = 819	ribosomal protein S2
1959	10267	NM 031838	n,aa	Rattus norvegicus ribosomal protein S2 (Rps2), mRNA. Length = 819	ribosomal protein S2
1960	15077	NM 031841	b	Rattus norvegicus stearyl-CoA desaturase 2 (Scd2), mRNA. Length = 5055	stearyl-CoA desaturase 2
1961	16726	NM 031855	x	Rattus norvegicus Ketohexokinase (Khk), mRNA. Length = 1342	Ketohexokinase
1962	25802	NM 031969	a	Rattus norvegicus Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
1962	19191	NM 031969	c	Rattus norvegicus Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
1962	19195	NM 031969	r	Rattus norvegicus Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
1962	19190	NM 031969	p	Rattus norvegicus Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
1963	17734	NM 031970	v,General	Rattus norvegicus Heat shock 27 kDa protein (Hsp27), mRNA. Length = 787	ESTs, Heat shock 27 kDa protein
1964	1475	NM 031971	v	Rattus norvegicus Heat shock protein 70-1 (Hsp70-1), mRNA. Length = 2455	ESTs, Highly similar to S10A RAT S-100 PROTEIN, ALPHA CHAIN [R. norvegicus], Heat shock protein 70-1

TABLE 1: SUMMARY					Atty. Docket No. 44924-5061WG
					Doc. No. 1988997.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title
1965	15470	NM_031978	f	Rattus norvegicus 26S proteasome, subunit p112 (PSMD1), mRNA. Length = 3089	26S proteasome, subunit p112
1966	18502	NM_031984	c	Rattus norvegicus cerebellar Ca-binding protein, spot 35 protein (Calb1), mRNA. Length = 2280	cerebellar Ca-binding protein, spot 35 protein
1967	19768	NM_031986	v.a.a., General	Rattus norvegicus syntenin (Sdcbp), mRNA. Length = 2077	syntenin
1968	723	NM_032084	n	Rattus norvegicus chimerin (chimaerin) 2 (Chn2), mRNA. Length = 1118	chimerin (chimaerin) 2
1969	17935	NM_032615	a	Rattus norvegicus membrane interacting protein of RGS16 (Mir16), mRNA. Length = 1203	membrane interacting protein of RGS16
1970	16831	NM_033095	n	Rattus norvegicus Crystallin, gamma polypeptide 4 (Crygd), mRNA. Length = 634	
1971	25468	NM_033234	c.z	Rattus norvegicus Hemoglobin, beta (Hbb), mRNA. Length = 620	
1971	25469	NM_033234	c	Rattus norvegicus Hemoglobin, beta (Hbb), mRNA. Length = 620	
1971	17832	NM_033234	c.p	Rattus norvegicus Hemoglobin, beta (Hbb), mRNA. Length = 620	Rat major beta-globin mRNA, complete cds
1971	17829	NM_033234	c.z	Rattus norvegicus Hemoglobin, beta (Hbb), mRNA. Length = 620	Rat major beta-globin mRNA, complete cds
1972	4723	NM_033235	z	Rattus norvegicus Malate dehydrogenase-like enzyme (Mdh1), mRNA. Length = 1266	Rattus norvegicus cytosolic malate dehydrogenase (Mdh) mRNA, complete cds
1973	1409	NM_033349	p.General	Rattus norvegicus Hydroxyacyl glutathione hydrolase (Haghl), mRNA. Length = 783	Rattus norvegicus round spermatid protein RSP29 gene, complete cds
1974	19998	NM_033352	General	Rattus norvegicus ATP-binding cassette, sub-family D (ALD), member 2 (Abcd2), mRNA. Length = 5531	PDZ domain containing 1
1975	1410	NM_052798	d	Rattus norvegicus Kidney 1 (Kd1), mRNA. Length = 2563	Rat zinc finger protein (kid-1) mRNA, complete cds
1976	15028	NM_052809	f	Rattus norvegicus cytosolic cysteine dioxygenase 1 (Cdo1), mRNA. Length = 1458	Rat cysteine dioxygenase mRNA, complete cds
1977	5176	NM_053297	u	Rattus norvegicus Pyruvate kinase 3 (Pkm2), mRNA. Length = 1973	Rat mRNA for pituitary pyruvate kinase
1978	7660	NM_053299	i	Rattus norvegicus ubiquitin D (Ubq), mRNA. Length = 584	ESTs, Weakly similar to polyubiquitin [R.norvegicus]
1979	5117	NM_053310	p	Rattus norvegicus homer, neuronal immediate early gene, 3 (Homer3), mRNA. Length = 1207	Rattus norvegicus mRNA for Vest-3, complete cds

TABLE 1: SUMMARY					
Atty. Docket No. 44924-6031W					
Doc. No. 1732897.1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
1981	17473	NM 053319	a,v	Rattus norvegicus dynein, cytoplasmic, light chain 1 (Pin), mRNA. Length = 505	Rattus norvegicus protein inhibitor of neuronal nitric oxide synthase (PIN) mRNA, complete cds
1982	25480	NM 053329	g	Rattus norvegicus insulin-like growth factor binding protein, acid labile subunit (Igfals), mRNA. Length = 1812	
1982	21977	NM 053329	y	Rattus norvegicus insulin-like growth factor binding protein, acid labile subunit (Igfals), mRNA. Length = 1812	Rattus norvegicus insulin-like growth factor binding protein complex acid-labile subunit gene, complete cds
1983	14926	NM 053330	f	Rattus norvegicus ribosomal protein L21 (RpL21), mRNA. Length = 554	Rattus norvegicus ribosomal protein L21 mRNA, complete cds
1983	14929	NM 053330	e,General	Rattus norvegicus ribosomal protein L21 (RpL21), mRNA. Length = 554	Rattus norvegicus ribosomal protein L21 mRNA, complete cds
1984	16407	NM 053332	c,e	Rattus norvegicus cubilin (intrinsic factor-cobalamin receptor) (Cubn), mRNA. Length = 10,872	Rattus norvegicus intrinsic factor-B12 receptor precursor (CUBILIN) mRNA, complete cds
1985	15790	NM 053341	j,x	Rattus norvegicus regulator of G-protein signalling 19 (Rgs19), mRNA. Length = 1607	regulator of G-protein signaling 19
1986	6154	NM 053356	p	Rattus norvegicus procollagen, type I, alpha 2 (Col1a2), mRNA. Length = 4474	procollagen, type I, alpha 2
1987	9215	NM 053374	i	Rattus norvegicus interferon gamma inducing factor binding protein (Igfbp), mRNA. Length = 626	interferon gamma inducing factor binding protein
1988	6416	NM 053380	General	Rattus norvegicus solute carrier family 34 (sodium phosphate), member 2 (Slc34a2), mRNA. Length = 3950	solute carrier family 34 (sodium phosphate), member 2
1989	19113	NM 053395	a	Rattus norvegicus small muscle protein, X-linked (Smpx), mRNA. Length = 892	Rattus norvegicus SMPX protein (Smpx) mRNA, complete cds
1990	2242	NM 053433	n,General	Rattus norvegicus flavin-containing monooxygenase 3 (Fmo3), mRNA. Length = 2037	flavin-containing monooxygenase 3
1991	5561	NM 053438	y	Rattus norvegicus zinc finger protein 103 (Zfp103), mRNA. Length = 3258	zinc finger protein 103
1992	14670	NM 053439	n,General	Rattus norvegicus RAN, member RAS oncogene family (Ran), mRNA. Length = 1064	RAN, member RAS oncogene family
1993	17102	NM 053440	w	Rattus norvegicus superiorocervical ganglia, neural specific 10 (Scgn10), mRNA. Length = 1654	superiorocervical ganglia, neural specific 10
1994	24762	NM 053442	General	Rattus norvegicus solute carrier family 8 (cationic amino acid transporter, y <sup>+</sup> system), member 7 (Lat4), mRNA. Length = 4117	solute carrier family 8 (cationic amino acid transporter, y <sup>+</sup> system), member 7

TABLE 1: SUMMARY					Atty. Docket No. 44924-0039W0
					Seq. No. 1798897.1
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title
1995	8085	NM_053453	General	Rattus norvegicus regulator of G-protein signaling protein 2 (Rgs2), mRNA. Length = 1629	regulator of G-protein signaling protein 2
1996	4622	NM_053463	d	Rattus norvegicus nucleobindin (Nucb), mRNA. Length = 2303	nucleobindin
1997	21866	NM_053472	p	Rattus norvegicus cytochrome c oxidase subunit IV isoform 2 precursor (CoxIV-2), mRNA. Length = 704	cytochrome c oxidase subunit IV isoform 2 precursor
1998	9573	NM_053475	h	Rattus norvegicus protein tyrosine phosphatase type IVA, member 2 (Ptp4a2), mRNA. Length = 1095	protein tyrosine phosphatase type IVA, member 2
1999	16137	NM_053480	k	Rattus norvegicus DNA polymerase alpha subunit II (Pola2), mRNA. Length = 1836	DNA polymerase alpha subunit II
2000	15556	NM_053483	y	Rattus norvegicus karyopherin (importin) alpha 2 (Kpna2), mRNA. Length = 1886	karyopherin (importin) alpha 2
2001	16394	NM_053485	General	Rattus norvegicus calcium binding protein A6 (calcyclin) (S100a6), mRNA. Length = 291	calcium binding protein A6 (calcyclin)
2002	4290	NM_053487	j,y	Rattus norvegicus peroxisomal membrane protein Pmp26p (Peroxin-11) (Pex11a), mRNA. Length = 1194	peroxisomal membrane protein Pmp26p (Peroxin-11)
2004	18826	NM_053523	d	Rattus norvegicus homocysteine-inducible, endoplasmic reticulum stress inducible, ubiquitin-like domain member 1 (Herpud1), mRNA. Length = 1857	Rattus norvegicus SUP mRNA, complete cds
2005	7764	NM_053525	aa	Rattus norvegicus ATP-dependent, RNA helicase (Rok1), mRNA. Length = 2175	Rattus norvegicus rROK1L mRNA for ROK1-like protein, complete cds
2006	14199	NM_053538	c	Rattus norvegicus lysosomal-associated protein transmembrane 5 (Laptm5), mRNA. Length = 1309	Rattus norvegicus gcd-10S mRNA, complete cds
2007	1058	NM_053539	c,d	Rattus norvegicus isopentenyl-diphosphate delta isomerase (Idi1), mRNA. Length = 1182	Rattus norvegicus isopentenyl diphosphate:dimethylallyl diphosphate isomerase mRNA, complete cds
2008	4327	NM_053563	General	Rattus norvegicus nuclear RNA helicase, DECD variant of DEAD box family (Ddx1), mRNA. Length = 1511	Rattus norvegicus nuclear RNA helicase mRNA, complete cds
2009	1342	NM_053573	h	Rattus norvegicus olfactomedin related ER localized protein (Olfml1), mRNA. Length = 2759	Rattus norvegicus neuronal olfactomedin-related ER localized protein (D2Sut1e) mRNA, complete cds
2010	19254	NM_053576	h,s	Rattus norvegicus thiol-specific antioxidant protein (Prdx5), mRNA. Length = 1414	Rattus norvegicus mRNA for thiol-specific antioxidant protein (t-Cys peroxidoxin)

TABLE 1: SUMMARY					
Atty. Docket No. 44921-5089WG					
Doc. No. 1793897.1					
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
2010	19253	NM_053576	h	Rattus norvegicus thiol-specific antioxidant protein (Prox5), mRNA. Length = 1414	Rattus norvegicus mRNA for thiol-specific antioxidant protein (1-Cys peroxiredoxin)
2011	3049	NM_053582	p,cc, General	Rattus norvegicus glucocorticoid-inducible protein (gis5), mRNA. Length = 1869	Rattus norvegicus gis5 mRNA for glucocorticoid-inducible protein, complete cds
2011	3050	NM_053582	o, General	Rattus norvegicus glucocorticoid-inducible protein (gis5), mRNA. Length = 1869	Rattus norvegicus gis5 mRNA for glucocorticoid-inducible protein, complete cds
2012	21423	NM_053586	s,y	Rattus norvegicus cytochrome c oxidase subunit Vb (Cox5b), mRNA. Length = 485	Rat mRNA for cytochrome c oxidase subunit Vb
2013	21445	NM_053587	l,v	Rattus norvegicus S100 calcium-binding protein A9 (calgranulin B) (S100a9), mRNA. Length = 494	Rattus norvegicus intracellular calcium binding protein (MRP14) mRNA, complete cds
2014	20871	NM_053591	j,l	Rattus norvegicus dipeptidase 1 (Dpep1), mRNA. Length = 2179	Rat dipeptidase (dpep1) mRNA, complete cds
2014	20870	NM_053591	l	Rattus norvegicus dipeptidase 1 (Dpep1), mRNA. Length = 2179	Rat dipeptidase (dpep1) mRNA, complete cds
2015	21044	NM_053594	d	Rattus norvegicus protein tyrosine phosphatase, receptor type, R (Ptprr), mRNA. Length = 3565	Rattus norvegicus mRNA for tyrosine phosphatase CBPTP, complete cds
2016	21709	NM_053596	k	Rattus norvegicus endothelin converting enzyme 1 (Ece1), mRNA. Length = 4469	Rat mRNA for endothelin-converting enzyme, complete cds
2016	21708	NM_053596	z	Rattus norvegicus endothelin converting enzyme 1 (Ece1), mRNA. Length = 4469	Rat mRNA for endothelin-converting enzyme, complete cds
2017	1597	NM_053611	t	Rattus norvegicus nuclear protein 1 (Nupr1), mRNA. Length = 602	Rattus norvegicus p8 mRNA, complete cds
2018	5565	NM_053618	General	Rattus norvegicus Bardet-Biedl syndrome 2 (human) (Bbs2), mRNA. Length = 2573	Rattus norvegicus BBS2 (Bbs2) mRNA, complete cds
2019	13004	NM_053623	t	Rattus norvegicus fatty acid-Coenzyme A ligase, long chain 4 (Fac4), mRNA. Length = 4862	Rattus norvegicus mRNA for Acyl-CoA synthetase, complete cds
2020	1127	NM_053626	g	Rattus norvegicus D-amino acid oxidase (Dao1), mRNA. Length = 1646	Rattus norvegicus mRNA for D-amino acid oxidase, complete cds
2021	18644	NM_053648	n	Rattus norvegicus beta-carotene 15, 15'-dioxygenase (Bdo), mRNA. Length = 2207	Rattus norvegicus mRNA for beta-carotene 15,15'-dioxygenase, complete cds
2022	21637	NM_053653	p	Rattus norvegicus vascular endothelial growth factor C (Vegfc), mRNA. Length = 1596	ESTs, Highly similar to VEGC MOUSE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR [M.musculus]
2023	3454	NM_053662	cc	Rattus norvegicus cyclin L (Ccnl), mRNA. Length = 2092	Rattus norvegicus cyclin ania-6a mRNA, complete cds

TABLE 1: SUMMARY					Atly, Doclet No. 4:024-6089WG (Doc. No. 199889-1)
Sequence ID No.	Identifier	GenBank/Accession Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title
2024	16121	NM_053698	h,j,z	Rattus norvegicus Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (Cited2), mRNA. Length = 1155	Rattus norvegicus transcription factor MRG1 mRNA, complete cds
2024	16122	NM_053698	h,j,z	Rattus norvegicus Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (Cited2), mRNA. Length = 1155	Rattus norvegicus transcription factor MRG1 mRNA, complete cds
2025	25379	NM_053713	General	Rattus norvegicus Kruppel-like factor 4 (gut) (Klf4), mRNA. Length = 2393	
2025	13622	NM_053713	General	Rattus norvegicus Kruppel-like factor 4 (gut) (Klf4), mRNA. Length = 2393	ESTs, Moderately similar to zinc finger protein [R. norvegicus]
2026	15376	NM_053747	h	Rattus norvegicus ubiquitin 1 (Ubain1), mRNA. Length = 2131	Rattus norvegicus mRNA for DA41, complete cds
2027	1218	NM_053748	b	Rattus norvegicus dipeptidylpeptidase III (Dpp3), mRNA. Length = 2632	Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds
2028	1137	NM_053763	y	Rattus norvegicus cytochrome P450, 40 (25-hydroxyvitamin D3 1-alpha-hydroxylase) (Cyp40), mRNA. Length = 2426	Rattus norvegicus 25-hydroxyvitamin D 1-hydroxylase (CYP1) mRNA, complete cds
2029	15996	NM_053769	cc	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 16 (Ptpn16), mRNA. Length = 1104	Rattus norvegicus protein tyrosine phosphatase mRNA, complete cds
2030	8652	NM_053774	g	Rattus norvegicus ubiquitin specific protease 2 (Usp2), mRNA. Length = 1857	Rattus norvegicus deubiquitinating enzyme Ubp69 (ubp69) mRNA, complete cds
2031	14664	NM_053806	General	Rattus norvegicus potassium channel, subfamily K, member 6 (TWIK-2) (Kcnk6), mRNA. Length = 2243	ESTs
2032	4361	NM_053812	k	Rattus norvegicus BCL2-antagonist/killer 1 (Bak1), mRNA. Length = 1923	Rattus norvegicus BAK protein (Bak) mRNA, complete cds
2034	15002	NM_053819	b,x,bb, General	Rattus norvegicus tissue inhibitor of metalloproteinase 1 (Timp1), mRNA. Length = 740	Rattus norvegicus tissue inhibitor of metalloproteinase-1 (TIMP1), mRNA, complete cds
2034	15003	NM_053819	b,i,x,bb, General	Rattus norvegicus tissue inhibitor of metalloproteinase 1 (Timp1), mRNA. Length = 740	Rattus norvegicus tissue inhibitor of metalloproteinase-1 (TIMP1), mRNA, complete cds
2035	16173	NM_053822	t	Rattus norvegicus S100 calcium-binding protein A8 (calgranulin A) (S100a8), mRNA. Length = 361	Rattus norvegicus intercellular calcium binding protein (MRP8) mRNA, complete cds
2036	17154	NM_053835	j,z	Rattus norvegicus clathrin, light polypeptide (Lcb) (Cltb), mRNA. Length = 882	Rat clathrin light chain (LCB2) mRNA, complete cds, Rat clathrin light chain (LCB3) mRNA, complete cds
2037	20868	NM_053843	t	Rattus norvegicus Fc receptor, IgG, low affinity III (Fcgr3), mRNA. Length = 1318	Rat Fc-gamma receptor mRNA, complete cds
2037	20869	NM_053843	t	Rattus norvegicus Fc receptor, IgG, low affinity III (Fcgr3), mRNA. Length = 1318	Rat Fc-gamma receptor mRNA, complete cds

TABLE 1: SUMMARY					Atty. Docket No. 43924-5683WG Doc. No. 1798397.1
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID	Model Code	Gene Name	Unigene Cluster Title
2040	714	NM_053863	y	Rattus norvegicus solute carrier family 28 (sodium-coupled nucleoside transporter), member 1 (Slc28a1), mRNA. Length = 2401	Rattus norvegicus Sprague-Dawley sodium-dependent nucleoside transporter (CNT1) mRNA, complete cds
2041	19781	NM_053883	b	Rattus norvegicus dual specificity phosphatase 6 (Dusp6), mRNA. Length = 2104	Rattus norvegicus dual-specificity protein tyrosine phosphatase (vH6) mRNA, complete cds
2041	19780	NM_053883	b	Rattus norvegicus dual specificity phosphatase 6 (Dusp6), mRNA. Length = 2104	Rattus norvegicus dual-specificity protein tyrosine phosphatase (vH6) mRNA, complete cds
2042	1454	NM_053887	General	Rattus norvegicus mitogen activated protein kinase kinase kinase 1 (Map3k1), mRNA. Length = 5180	Rattus norvegicus MAP kinase kinase 1 (MEKK1) mRNA, complete cds
2043	1660	NM_053891	g	Rattus norvegicus cyclin-dependent kinase 5, regulatory subunit 1 (p35) (Cdk5r), mRNA. Length = 1208	Rattus norvegicus P35 mRNA, complete cds
2044	712	NM_053896	k	Rattus norvegicus aldehyde dehydrogenase family 1, subfamily A2 (Aldh1a2), mRNA. Length = 2240	Rattus norvegicus aldehyde dehydrogenase mRNA, complete cds
2045	753	NM_053897	k	Rattus norvegicus coagulation factor II (thrombin) receptor-like 1 (F2r1), mRNA. Length = 1428	Rattus norvegicus proteinase-activated receptor-2 mRNA, complete cds
2046	794	NM_053902	General	Rattus norvegicus kynureninase (L-kynurenine hydrolase) (Kynu), mRNA. Length = 1765	Rattus norvegicus L-kynurenine hydrolase mRNA, complete cds
2047	17937	NM_053911	f	Rattus norvegicus pleckstrin homology, Sec7 and coiled-coil domains 2 (Pscd2), mRNA. Length = 1561	Rattus norvegicus sec7B mRNA, complete cds
2048	8188	NM_053927	General	Rattus norvegicus erythrocyte membrane protein band 4.1-like 3 (Ep41l3), mRNA. Length = 4543	Rattus norvegicus mRNA for type II brain 4.1, complete cds
2050	1628	NM_053936	h	Rattus norvegicus endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (Edg2), mRNA. Length = 1543	Rattus norvegicus putative G-protein coupled receptor GPCR91 (Gpcr91) mRNA, complete cds
2051	13954	NM_053955	General	Rattus norvegicus crystallin, mu (Crym), mRNA. Length = 1227	Rattus norvegicus CDK108 mRNA
2052	408	NM_053961	General	Rattus norvegicus endoplasmic reticulum protein 29 (Erp29), mRNA. Length = 4529	R. norvegicus mRNA encoding 45kDa protein which binds to heymann nephritis antigen gp330
2052	19991	NM_053961	a	Rattus norvegicus endoplasmic reticulum protein 29 (Erp29), mRNA. Length = 4529	mitochondrial aconitase (nuclear aco2 gene)

TABLE 1: SUMMARY					
Atty. Ref. No. 4-024-0001WO					
Doc. No. 179897.1					
Sequence ID No.	Identifier	GenBank Acc'd Ref. Seq ID	Model Code	Gene Name	UniGene Cluster Title
2052	16190	NM_053961	q	Rattus norvegicus endoplasmic reticulum protein 29 (Erp29), mRNA. Length = 4529	ESTs, Weakly similar to ECHM RAT ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR [R.norvegicus]
2052	21355	NM_053961	j.l.y.z	Rattus norvegicus endoplasmic reticulum protein 29 (Erp29), mRNA. Length = 4529	ESTs
2055	15136	NM_053971	aa	Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. Length = 963	R.norvegicus mRNA for ribosomal protein L6
2055	15135	NM_053971	d	Rattus norvegicus ribosomal protein L6 (Rpl6), mRNA. Length = 963	R.norvegicus mRNA for ribosomal protein L6
2056	1764	NM_053974	h	Rattus norvegicus eukaryotic translation initiation factor 4E (Eif4e), mRNA. Length = 1647	R.norvegicus mRNA eIF-4E
2057	1292	NM_053980	i	Rattus norvegicus ADP-ribosylation factor related protein 1 (Arf1p1), mRNA. Length = 943	R.norvegicus (Sprague Dawley) ARP1 mRNA for ARF-related protein
2058	15468	NM_053982	q	Rattus norvegicus ribosomal protein S15a (Rps15a), mRNA. Length = 449	R.norvegicus mRNA for ribosomal protein S15a
2059	15642	NM_053985	General	Rattus norvegicus H3 histone, family 3B (H3f3b), mRNA. Length = 1107	R.norvegicus mRNA for histone H3.3
2060	21066	NM_054001	t	Rattus norvegicus CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (Cd36l2), mRNA. Length = 1938	Rat lysosomal membrane protein (LIMP1) mRNA, complete cds
2061	17326	NM_054008	o	Rattus norvegicus Rgc32 protein (Rgc32), mRNA. Length = 889	Rattus norvegicus RGC-32 (RGC-32) mRNA, complete cds
2061	17327	NM_054008	cc	Rattus norvegicus Rgc32 protein (Rgc32), mRNA. Length = 889	Rattus norvegicus RGC-32 (RGC-32) mRNA, complete cds
2061	17329	NM_054008	g.o.cc	Rattus norvegicus Rgc32 protein (Rgc32), mRNA. Length = 889	Rattus norvegicus RGC-32 (RGC-32) mRNA, complete cds
2062	25253	NM_057099	j.l.m.p.z	Rattus norvegicus proteasome (prosome, macropain) subunit, beta type 6 (Psm6), mRNA. Length = 760	ESTs, Highly similar to PROTEASOME DELTA CHAIN PRECURSOR [R.norvegicus]
2062	22849	NM_057099	j.l	Rattus norvegicus A kinase (PRKA) anchor protein (gravin) 12 (Akap12), mRNA. Length = 5236	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
2063	19657	NM_057103	b.cc	Rattus norvegicus UDP-glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. Length = 1593	ESTs, UDP-glucuronosyltransferase 1 family, member 1
2064	5492	NM_057105	w	Rattus norvegicus UDP-glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. Length = 1593	Rattus norvegicus UDP-glucuronosyltransferase UGT1A7 mRNA, complete cds, UDP-glucuronosyltransferase 1 family, member 1
2064	15126	NM_057105	r	Rattus norvegicus UDP-glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. Length = 1593	Rattus norvegicus UDP-glucuronosyltransferase UGT1A7 mRNA, complete cds, UDP-glucuronosyltransferase 1 family, member 1

TABLE 1: SUMMARY					
Atty. Docket No. 44921-5093WO					
Doc. No. 176627.1					
Sequence ID No.	Identifier	GenBank Acc./Ref. Seq. ID	Model Code	Gene Name	Unique Cluster Title
2064	15125	NM_057105	s	Rattus norvegicus UDP-glucuronosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. Length = 1593	Rattus norvegicus UDP-glucuronosyltransferase UGT1A7 mRNA, complete cds, UDP-glucuronosyltransferase 1 family, member 1
2066	15391	NM_057114	n	Rattus norvegicus peroxiredoxin 1 (Prdx1), mRNA. Length = 882	Rat mRNA for HBP23 (heme-binding protein 23 kDa), complete cds
2067	727	NM_057123	m	Rattus norvegicus protease (prosome, macropain) 26S subunit, ATPase 1 (Psmc1), mRNA. Length = 1556	Rattus norvegicus mRNA for proteasomal ATPase (S4), complete cds
2068	915	NM_057124	s	Rattus norvegicus pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2ry6), mRNA. Length = 1922	Rat mRNA for novel G protein-coupled P2 receptor, complete cds
2069	15151	NM_057131	k	Rattus norvegicus phosphoribosyl pyrophosphate synthetase-associated protein 2 (Prpsap2), mRNA. Length = 1612	Rattus norvegicus mRNA for 41-kDa phosphoribosylpyrophosphate synthetase-associated protein, complete cds
2070	1892	NM_057144	b	Rattus norvegicus cysteine-rich protein 3 (Carp3), mRNA. Length = 853	R. norvegicus mRNA for muscle LIM protein
2071	12333	NM_057155	f	Rattus norvegicus X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound (Xprp2), mRNA. Length = 2828	Rattus norvegicus membrane-bound aminopeptidase P mRNA, complete cds
2071	12331	NM_057155	v, General	Rattus norvegicus X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound (Xprp2), mRNA. Length = 2828	Rattus norvegicus membrane-bound aminopeptidase P mRNA, complete cds
2071	12332	NM_057155	f, General	Rattus norvegicus X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound (Xprp2), mRNA. Length = 2828	Rattus norvegicus membrane-bound aminopeptidase P mRNA, complete cds
2072	17477	NM_057194	a, General	Rattus norvegicus phospholipid scramblase 1 (Plscr1), mRNA. Length = 1569	Rattus norvegicus phospholipid scramblase PLSCR mRNA, complete cds
2073	15408	NM_057197	p, l	Rattus norvegicus 2,4-dienoyl CoA reductase 1, mitochondrial (Decr1), mRNA. Length = 1109	Rattus norvegicus mRNA for 2,4-dienoyl-CoA reductase precursor, complete cds
2073	15409	NM_057197	t	Rattus norvegicus 2,4-dienoyl CoA reductase 1, mitochondrial (Decr1), mRNA. Length = 1109	Rattus norvegicus mRNA for 2,4-dienoyl-CoA reductase precursor, complete cds
2074	7866	NM_057198	h	Rattus norvegicus phosphoribosyl pyrophosphate amidotransferase (Ppat), mRNA. Length = 2934	Rattus norvegicus mRNA for amidophosphoribosyltransferase

TABLE 1: SUMMARY					Atty. Docket No. 44924-000000 Doc. No. 1098367.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title
2075	14125	NM_057208	h,j,y,z	Rattus norvegicus tropomyosin 3, gamma (Tpm3), mRNA. Length = 1101	Rattus norvegicus tropomyosin non-muscle isoform NM1 (TPM-gamma) mRNA, complete cds; Rattus norvegicus tropomyosin non-muscle isoform NM3 (TPM-gamma) mRNA, complete cds
2076	1743	NM_057210	k,s	Rattus norvegicus synaptic vesicle glycoprotein 2 a (SV2a), mRNA. Length = 3844	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2077	10498	NM_078617	a	Rattus norvegicus ribosomal protein S23 (Rps23), mRNA. Length = 432	R. norvegicus (Sprague-Dawley) ribosomal protein S23 mRNA
2078	8820	NM_080399	n	Rattus norvegicus Smhs1 protein (Smhs1), mRNA. Length = 1107	ESTs
2079	15701	NM_080581	j,m,y,z	Rattus norvegicus ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (Abcc3), mRNA. Length = 5174	Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-2 (MLP-2), complete cds
2079	20105	NM_080581	aa	Rattus norvegicus ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (Abcc3), mRNA. Length = 5174	ESTs
2080	16109	NM_080585	c	Rattus norvegicus N-ethylmaleimide sensitive fusion protein attachment protein alpha (Napa), mRNA. Length = 1505	Rattus norvegicus mRNA for alpha-soluble NSF attachment protein
2081	1757	NM_080766	d	Rattus norvegicus Neuroblastoma RAS viral (v-ras) oncogene homolog (N-ras), mRNA. Length = 3350	R. norvegicus N-ras gene for p21 protein
2082	7108	NM_080778	y	Rattus norvegicus nuclear receptor subfamily 2, group F, member 2 (Nr2f2), mRNA. Length = 1572	Rattus norvegicus ovalbumin upstream promoter beta nuclear receptor rCOUPb mRNA, complete cds
2083	132	NM_080782	k	Rattus norvegicus cyclin-dependent kinase inhibitor 1A (P21) (Cdkn1a), mRNA. Length = 495	Rattus norvegicus p21 (WAF1) mRNA, complete cds
2083	133	NM_080782	l	Rattus norvegicus cyclin-dependent kinase inhibitor 1A (P21) (Cdkn1a), mRNA. Length = 495	Rattus norvegicus p21 (WAF1) mRNA, complete cds
2084	20122	NM_080887	a General	Rattus norvegicus thioredoxin-like (32kD) (Txn), mRNA. Length = 1061	ESTs, Highly similar to thioredoxin-related protein [M.musculus]
2085	6143	NM_080892	e	Rattus norvegicus selenium binding protein 2 (Selenbp2), mRNA. Length = 1685	ESTs, Moderately similar to selenium-binding protein [H.sapiens]
2086	9952	NM_080902	h	Rattus norvegicus hypoxia induced gene 1 (Hig1), mRNA. Length = 355	ESTs, Moderately similar to AF077034.1 HSPC010 [H.sapiens]
2087	17546	NM_130401	b	Rattus norvegicus membrane-associated protein 17 (Map17), mRNA. Length = 816	ESTs, Moderately similar to DD96 homolog [R.norvegicus]

TABLE 1: SUMMARY					Atty. DocId: No. 44921-6039WG Doc. No. 1760397.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq ID	Mode Code	Gene Name	Uniprot Cluster Title
2088	21695	NM_130411	c,x	Rattus norvegicus coronin, actin binding protein 1A (Coro1a), mRNA. Length = 1386	ESTs, Weakly similar to coronin-like protein [R.norvegicus]
2089	21391	NM_130416	x,General	Rattus norvegicus annexin A7 (Anxa7), mRNA. Length = 2912	ESTs, Weakly similar to ANX4 RAT ANNEXIN IV [R.norvegicus]
2090	20694	NM_130430	General	Rattus norvegicus proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 (Psm9), mRNA. Length = 1448	EST
2090	19818	NM_130430	cc	Rattus norvegicus proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 (Psm9), mRNA. Length = 1448	EST
2090	18810	NM_130430	e,s	Rattus norvegicus proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 (Psm9), mRNA. Length = 1448	mitochondrial H <sup>+</sup> -ATP synthase alpha subunit
2091	18293	NM_130433	q	Rattus norvegicus acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (Acaa2), mRNA. Length = 1619	Rat mRNA for 3-oxoacyl-CoA thiolase
2092	25064	S45392	a,n		
2093	3244	S63519	u		ESTs
2094	25501	S63521	q		
2095	16248	S68135	h		Rat brain glucose-transporter protein mRNA, complete cds
2096	18647	S69316	q		ESTs, Weakly similar to H98B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]
2097	24351	S74257	v		ESTs, Weakly similar to ABD4 MOUSE ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 4 [M.musculus]
2098	25066	S75280	d		
2099	1460	S76054	j,l,m,x,y,General		ESTs, Highly similar to K2C8 RAT KERATIN, TYPE II CYTOSKELETAL 8 [R.norvegicus]
2100	25539	S76742	v		
2101	16400	S76779	c		Rat apolipoprotein e mRNA
2102	24469	S77858	n		ESTs, Highly similar to MLES RAT MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM [R.norvegicus]
2103	25545	S77900	k,s		
2103	21583	S77900	k		ESTs
2104	10260	S81497	s		ESTs
2105	3609	S82579	k	histamine N-methyltransferase	histamine N-methyltransferase
2106	111	U02506	u	Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats	Rattus norvegicus Sprague Dawley protein kinase C receptor mRNA, complete cds
2107	14959	U03390	a,q,General		Rattus norvegicus Sprague-Dawley fibrinogen B beta chain mRNA, complete cds
2109	2010	U05675	b,x,bb		protein S
2110	15462	U06230	d	protein S	

TABLE 1: SUMMARY						Atty. Docket No. 44824-5689WG
						Doc. No. 1789397.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title	
2112	1583	U07201	s, General	Asparagine synthetase	Asparagine synthetase	
2113	627	U09229	h		Rattus norvegicus New England Deaconess transcription factor mRNA, partial cds	
2114	809	U17035	General		Rattus norvegicus interferon inducible protein 10 (IP-10) mRNA, complete cds	
2115	16675	U17565	h, x, bb	mini chromosome maintenance deficient 6 (S. cerevisiae)	mini chromosome maintenance deficient 6 (S. cerevisiae)	
2116	25587	U20110	r		Rattus norvegicus nuclear receptor Rev-Erba-beta mRNA, partial cds	
2117	90	U20796	r			
2118	25589	U21718	h, aa			
2119	22196	U21719	h		ESTs	
2120	17118	U25746	s		Rattus norvegicus RNA helicase with arginine-serine-rich domain mRNA, complete cds	
2121	1537	U27518	g, h, n		Rattus norvegicus UDP-glucuronosyltransferase mRNA, complete cds	
2122	1558	U28504	bb		Rattus norvegicus Na+/PI cotransporter-1 mRNA, complete cds	
2123	16193	U30831	n		Rattus norvegicus B/K protein mRNA, complete cds	
2124	17480	U31598	z		R. norvegicus mRNA for R11.Ma	
2125	18302	U33500	General		Rattus norvegicus retinol dehydrogenase type II mRNA, complete cds	
2126	25599	U34897	y			
2127	1394	U37099	h		Rattus norvegicus GTP-binding protein (rab 3C) mRNA, complete cds	
2128	244	U38376	n		EST, Weakly similar to actin-filament binding protein Frabin [R. norvegicus], Rattus norvegicus cytosolic phospholipase A2 mRNA, complete cds	
2129	1623	U41164	h		Rattus norvegicus Cya2/His2 zinc finger protein (Rkr1) mRNA, complete cds	
2130	15851	U42719	f, l, x, General	Complement component 4	Complement component 4	
2131	17886	U47315	s, z		Rattus norvegicus apoptosis-regulating basic protein mRNA, complete cds	
2132	21654	U53184	i, t, General	estrogen-responsive uterine transcript	estrogen-responsive uterine transcript	
2133	1439	U57391	w		Rattus norvegicus FcεRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds	
2134	725	U62316	bb	solute carrier family 16 (monocarboxylic acid transporters), mem	solute carrier family 16 (monocarboxylic acid transporters), member 7	
2137	2153	U75404	b, cc, General		ESTs	
2139	4956	U76714	j, y		Rattus norvegicus cell adhesion regulator (CAR1) mRNA, complete cds	
2140	4477	U77829	i, m		ESTs	
2141	21703	U82591	z		Rattus norvegicus RCL (Rci) mRNA, complete cds	
2142	977	U89744	s		Rattus norvegicus putative cell surface antigen mRNA, complete cds	
2143	23282	U90725	n	lipoprotein-binding protein	lipoprotein-binding protein	
2144	22005	U96490	m		Rattus norvegicus liver mRNA, complete cds	

TABLE 1: SUMMARY						Atty. Docket No. 44921-5893V6
						Doc. No. 198997.4
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID	Model Code	Gene Name	UniGene Cluster Title	
2146	819	X02284	j,z	Aldolase B, fructose-biphosphate	Aldolase B, fructose-biphosphate	
2147	818	X02291	a,j,z	Aldolase B, fructose-biphosphate	Aldolase B, fructose-biphosphate	
2148	20818	X02904	n,q	glutathione S-transferase, pi 2	glutathione S-transferase, pi 2	
2149	16401	X04979	c	Rat apolipoprotein e mma		
2150	20513	X05684	o,r	Pyruvate kinase, liver and RBC	Pyruvate kinase, liver and RBC	
2151	25084	X06769	cc			
2152	672	X13722	h		Rat mRNA for LDL-receptor	
2153	25675	X14181	n			
2153	20810	X14181	n,q,w		ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L18A [R.norvegicus]	
2154	18541	X14671	y		ESTs, Highly similar to RL26 RAT 60S RIBOSOMAL PROTEIN L26 [R.norvegicus]	
2155	25679	X15013	q			
2155	19244	X15013	c,q,w		ESTs, Highly similar to RL7A, HUMAN 60S RIBOSOMAL PROTEIN L7A [R.norvegicus]	
2156	15626	X17665	a		ESTs, Highly similar to RS16, HUMAN 40S RIBOSOMAL PROTEIN S1 [R.norvegicus]	
2157	1893	X51529	t	phospholipase A2, group IIA (platelets, synovial fluid)	phospholipase A2, group IIA (platelets, synovial fluid)	
2158	25666	X51536	bb			
2158	10819	X51536	aa,bb		ESTs, Highly similar to RS3 MOUSE 40S RIBOSOMAL PROTEIN S3 [R.norvegicus]	
2158	18250	X51706	a,q,w	ribosomal protein L9	ESTs, Highly similar to RL9 RAT 60S RIBOSOMAL PROTEIN L9 [R.norvegicus]	
2160	20872	X51707	a	ribosomal protein S19	ESTs, Highly similar to RS19 RAT 40S RIBOSOMAL PROTEIN S19 [R.norvegicus]	
2161	516	X52711	c		Rat mRNA for Mx1 protein	
2162	25669	X52815	g			
2163	20427	X53378	w		Rattus norvegicus ribosomal protein S13 (RPS13) mRNA, 3' end	
2164	18606	X53504	General		ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L12 [R.norvegicus]	
2165	1463	X54467	d,u, General		Rat mRNA for preprocathepsin D (EC 3.4.23.5)	
2166	24577	X55153	a,v		ESTs, Highly similar to 60S ACIDIC RIBOSOMAL PROTEIN P2 [R.norvegicus]	
2167	10344	X57405	j,m	Drosophila Notch homolog 1	LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR [R.norvegicus]	
2168	15106	X57529	g,n,q		ESTs, Highly similar to RS18, HUMAN 40S RIBOSOMAL PROTEIN S18 [R.norvegicus]	
2169	5667	X58200	q,bb	ribosomal protein L23		
2169	18511	X58200	a,v	ribosomal protein L23	ESTs, Highly similar to RL23, HUMAN 60S RIBOSOMAL PROTEIN L23 [R.norvegicus]	
2170	17175	X58389	w		R.norvegicus ASI mRNA for mammalian equivalent of bacterial large ribosomal subunit protein L22	
2171	25702	X58465	w			
2171	10109	X58465	c,q	Ribosomal protein S5	Ribosomal protein S5	
2172	25705	X59375	c,i,aa, General			

TABLE 1: SUMMARY						Atty. Doctel No. 44924-0001VG
						Doc. No. 1728697.1
Sequence ID No.	Identifier	GenBank Acc/Ref Seq ID	Insert Size	Gene Name	UniGene Cluster Title	
2173	25709	X59737	u			
2174	18354	X59859	General	decorin	decorin	
2174	18355	X59859	l	decorin	decorin	
2175	21657	X61381	General		Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds	
2176	25718	X62145	bb, General	ribosomal protein L8		
2176	15875	X62145	a,q,v	ribosomal protein L8		ESTs, Highly similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L [R.norvegicus]
2177	13646	X62166	bb			ESTs, Highly similar to RL3 RAT 60S RIBOSOMAL PROTEIN L3 [R.norvegicus]
2178	25721	X62325	p			
2179	16012	X62875	m,s,x			ESTs, Highly similar to HIGH MOBILITY GROUP PROTEIN HMG-Y [M.musculus]
2180	25730	X63369	cc			
2181	25089	X63594	General			
2181	25090	X63594	cc, General			
2182	20844	X65228	n,w			ESTs, Highly similar to RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [R.norvegicus]
2183	20879	X65296	l,y	carboxylesterase 1	carboxylesterase 1	
2184	25736	X68782	c			
2185	16426	X70369	c	procollagen, type III, alpha 1	procollagen, type III, alpha 1	
2186	16300	X70706	u	plastin 3 (T-isoform)	plastin 3 (T-isoform)	
2187	24232	X75207	c	cyclin D1	cyclin D1	
2188	16272	X76456	n,p		R.norvegicus (Sprague Dawley) alpha albumin gene	
2189	25741	X76489	u			
2190	23302	X78949	h	prolyl 4-hydroxylase alpha subunit	prolyl 4-hydroxylase alpha subunit	
2191	25747	X81448	General			
2192	24115	X81449	u			ESTs, Highly similar to K1CS RAT KERATIN, TYPE I CYTOSKELETAL 19 [R.norvegicus]
2193	25754	X89696	g			
2194	25097	X90642	y,z			
2195	12978	X96437	cc, General			ESTs, Highly similar to RADIATION-INDUCIBLE IMMEDIATE-EARLY GENE IEX-1 [M.musculus]
2197	4594	Y07704	c		Rattus norvegicus mRNA Best5 protein	
2198	25777	Y08355	g,p, General	oxidative stress induced	oxidative stress induced	
2199	15986	Y09945	bb, General		Rattus norvegicus mRNA for putative integral membrane transport protein (UST1)	
2200	20890	Y13275	k		Rattus norvegicus mRNA for D6.1A protein	
2201	21914	Y13336	d		Rattus norvegicus DAD-1 gene	
2202	406	Z11895	o,General		R.norvegicus mRNA encoding 45kDa protein which binds to heymann nephritis antigen gp330	
2203	18352	Z12298	t	decorin	decorin	
2204	17481	Z49761	k		R.norvegicus mRNA for RT1 Ma	
2205	8664	Z75029	r,v	Heat shock protein 70-1	ESTs, Moderately similar to T17342 hypothetical protein DKFP586K1924.1 [H.sapiens], Heat shock protein 70-1	
2206	2459	AA964755	cc		ESTs	
2207	23830	AA956638	aa		ESTs	
2208	6100	X73524	x	desmin	desmin	

TABLE 1: SUMMARY					
Atty. Docket No. 44324-5089WG					
Seq. No. 1798357.1					
Sequence ID No.	Identifier	GenBank/Acc./Ref. Seq ID	Model Code	Gene Name	Unigene/Start/End
2209	439	Z22607	w	Bone morphogenetic protein 4	Bone morphogenetic protein 4
					ESTs, Moderately similar to T17342 hypothetical protein DKFZp586K1924.1 (H.sapiens), Heat shock protein 70-1
2210	8665	A1071965	v	Heat shock protein 70-1	Heat shock protein 70-1
2211	155	U32681	t	crp-ductin	crp-ductin
					Rattus norvegicus mRNA for thiol-specific antioxidant protein (1-Cys peroxiredoxin)
2212	19252	AA892041	s	Hmm:peroxiredoxin 5	Hmm:peroxiredoxin 5
					Rat mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase mRNA, complete cds
2213	15582	A1232320	q		
				Epoxide hydrolase 1 (microsomal xenobiotic hydrolase)	Epoxide hydrolase 1 (microsomal xenobiotic hydrolase)
2214	17541	M26125	n		Rat Ly6-B antigen mRNA, complete cds
2215	18609	M30669	i		ESTs
2216	6262	A1177125	g		ESTs
2217	23859	A1072161	f		ESTs
				Glutathione-S-transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)
2218	21011	H32189	e		ESTs
2220	2572	A1177143	b		ESTs
2221	25419	M22922	a		ESTs

TABLE 2: PATHWAYS				Atty. Locked No. 44921-5030 WO Doc. No. 1792827.1	
Sequence ID No.	Identifier	GenBank Ref. Seq. ID No.	Model Code	Pathways	
1	6949	AA012765	q		
2	25096	AA108277	h,v		
3	17312	AA108305	r		
4	16882	AA684537	o		
5	6049	AA685176	y		
6	4426	AA685074	l,m		
7	21815	AA686423	g		
8	1600	AA686470	i		
8	1599	AA686470	i		
9	21997	AA799325	u		
10	18396	AA799330	v		
11	6561	AA799412	f,j		
12	16536	AA799449	k		
13	23294	AA799472	u		
14	18290	AA799497	r		
15	16981	AA799523	e		
16	20843	AA799545	h		
17	16993	AA799560	b		
18	16576	AA799570	d		
19	18361	AA799591	i		
20	17712	AA799596	z		
22	18346	AA799716	f		
23	8768	AA799726	l		
24	11667	AA799732	w		
25	18349	AA799744	u		
26	17494	AA799751	n		
27	18360	AA799771	General		
28	18660	AA799801	w		
29	20998	AA799803	z		
30	21006	AA799861	c		
31	15011	AA799893	General		
32	20611	AA799899	a		
33	23202	AA799971	General		
34	4632	AA800190	b		
35	21656	AA800202	d		
36	18433	AA800218	j,y,z		
37	6366	AA800235	u		
38	18442	AA800258	h,k		
39	21092	AA800360	y		
40	17325	AA800567	General		
41	13930	AA800613	cc, General		
42	21372	AA800693	v		
43	21373	AA800693	s		
44	18161	AA800701	k		
44	6696	AA800753	w		
45	13346	AA800928	General		
46	23115	AA801165	o,y		
47	12399	AA801307	General		
48	7543	AA801395	General		
49	24237	AA817726	t, General		
50	11215	AA817921	o		
51	5985	AA818005	g		
52	11338	AA818016	x		
53	2845	AA818026	k, General		
54	16756	AA818089	l,k, General		
55	17771	AA818224	e,g,p, General		
56	6522	AA818261	g,m		
57	5924	AA818359	y		
58	7866	AA818421	b,aa		
59	8237	AA818512	v		
60	17434	AA818574	h		
61	8726	AA818615	General		
62	6054	AA818656	b,v,cc, General		

TABLE 2. PATHWAYS					Atty. blocket No. 449215088W0 Doc. No. 1290837.4
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID No.	Model Code	Pathways	
63	11590	AA818721	d		
64	4291	AA818741	q,General		
65	4330	AA818747	o,General		
66	19723	AA818761	v,General		
67	13684	AA818770	h,j,m		
68	6322	AA818801	k		
69	7690	AA818875	General		
70	4952	AA818907	q,General		
71	6094	AA818911	t		
72	10985	AA818998	o,General		
73	6120	AA819008	t		
74	2586	AA819081	c		
76	6438	AA819269	o		
77	24721	AA819306	d,w		
78	6250	AA819376	o,y		
80	6281	AA819517	j		
81	10141	AA819526	j		
82	6551	AA819558	t		
83	6723	AA819653	r		
84	14958	AA819744	aa		
85	19433	AA819776	v		
86	6204	AA819889	aa		
87	22820	AA848315	General	Purine metabolism	
88	6614	AA848389	bb		
89	21125	AA848437	General		
90	23504	AA848496	q		
91	18532	AA848675	g		
92	21140	AA848738	c		
93	16128	AA848807	o		
94	22923	AA848929	g		
95	17339	AA849497	General		
96	11127	AA849518	l		
97	21275	AA849796	l,m,General		
98	16678	AA849827	aa		
99	8515	AA849917	e		
100	18447	AA849939	General		
101	12130	AA850037	p		
102	23981	AA850040	x,aa		
103	13615	AA850364	t		
105	2637	AA850893	x		
106	22093	AA850909	d		
107	21766	AA850916	c		
108	2847	AA850919	w		
109	12162	AA850975	h		
110	9514	AA850978	General		
111	3924	AA851017	e,q		
111	3925	AA851017	o,General		
112	4490	AA851184	s,k		
113	19187	AA851230	General		
114	19189	AA851237	c		
115	15386	AA851241	m		
116	21462	AA851261	g,l,General		
117	21471	AA851343	General		
118	16902	AA851379	p	Oxidative phosphorylation,Ubiquinone biosynthesis	
119	23376	AA851392	i,x		
119	23377	AA851392	x		
120	13349	AA851417	General		
121	21527	AA851733	r,u		
122	4048	AA851814	l,o,u,General		
123	10561	AA851871	bb		
124	17411	AA858621	l,y		
125	1801	AA858636	k,s,x,bb		

TABLE 2: PATHWAYS				Atty. Docket No. 44921-5089WC Doc. No. 1 72447 1	
Sequence ID No.	Identifier	SubPart, Acc. Ref. Seq. ID No.	Model Code	Pathways	
126	18350	AA858674	p		
127	19484	AA858693	e		
128	6360	AA858696	d		
129	17334	AA858704	p		
130	6360	AA858758	q		
131	13219	AA858759	a		
132	6384	AA858786	l,m,General		
134	13412	AA858830	p		
135	7279	AA858892	t		
136	16217	AA858930	t		
137	5667	AA858953	v,General	Alanine and aspartate metabolism,Aminoacyl-tRNA biosynthesis	
138	14479	AA858969	r		
139	6431	AA859085	t		
140	17361	AA859114	o,General		
141	21025	AA859241	General		
142	10076	AA859271	c		
143	21791	AA859333	k		
144	16314	AA859348	cc,General		
145	18662	AA859520	f		
146	15059	AA859545	r		
147	19694	AA859581	e		
148	14353	AA859585	h		
149	16318	AA859648	h		
150	17316	AA859652	General		
151	19067	AA859663	n,q		
152	22406	AA859680	n		
153	20599	AA859690	x		
154	14261	AA859693	u		
155	14138	AA859700	v	Porphyrin and chlorophyll metabolism	
155	14139	AA859700	v	Porphyrin and chlorophyll metabolism	
157	22374	AA859804	l		
158	22385	AA859805	b,k		
159	22773	AA859885	n		
160	22816	AA859898	k,x,z		
161	11891	AA859926	x		
162	23070	AA859942	k		
163	23121	AA859948	k		
164	23166	AA859954	cc,General		
165	18468	AA859966	aa		
166	23336	AA859981	q	Inositol phosphate metabolism	
167	4222	AA860024	a,bb		
168	13974	AA860030	u,x,General		
169	7090	AA860039	x		
170	23769	AA860055	k,x		
171	16323	AA860240	w		
172	4462	AA860264	General		
173	15884	AA860276	k		
174	17742	AA860302	c,y	Phenylalanine metabolism, Tyrosine metabolism	
175	16333	AA860414	a,h		
176	18918	AA860444	p,q		
177	16853	AA860454	p,l,m,y,z		
178	18995	AA860459	h,m		
179	16013	AA860482	s		
180	26036	AA874849	r		
181	16059	AA874857	h		
182	16089	AA874873	r		
183	21633	AA874951	f		
184	16192	AA874995	w		
185	16254	AA875025	j		
186	16312	AA875032	cc,General		
187	20701	AA875097	b		

TABLE 2: PATHWAYS					Atty. Pocket No. 44921-5089WO Doc. No. 1798897.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathway	
188	15416	AA875098	bb		
189	15419	AA875102	bb		
190	15313	AA875126	l,m,General		
191	10936	AA875146	w		
192	18084	AA875186	h		
193	15371	AA875205	u		
194	15401	AA875257	x,z		
195	15410	AA875268	p,s	Oxidative phosphorylation,Ubiquinone biosynthesis	
196	15420	AA875286	f		
197	15446	AA875327	s,w		
198	7936	AA875495	b,General		
199	17314	AA875509	l,l,m		
200	24472	AA875523	k		
201	15587	AA875577	j		
202	15517	AA875620	General		
202	15618	AA875620	General		
203	5384	AA891041	f,cc,General		
204	24814	AA891209	f,p		
205	21930	AA891322	d		
206	17225	AA891553	h		
207	7522	AA891571	j,m		
208	9071	AA891578	b		
209	19321	AA891666	u		
210	17693	AA891737	j,l,m,n,y,z		
211	17256	AA891739	General		
213	18269	AA891769	General		
214	9905	AA891774	s,bb,General		
215	17081	AA891812	d		
216	7050	AA891824	h		
217	4463	AA891831	General		
218	14289	AA891838	i		
219	20523	AA891842	r,cc		
220	17779	AA891914	g,s,z		
221	17438	AA891943	General		
222	22862	AA891944	p		
223	1159	AA891949	e,z		
224	4473	AA891965	General		
225	6362	AA892053	f,j,l,m		
226	9037	AA892066	y		
227	19469	AA892112	General		
228	14595	AA892128	o,t,v		
229	15527	AA892154	cc		
230	4482	AA892173	bb		
231	20917	AA892238	h		
232	2357	AA892268	d		
233	18183	AA892271	h		
234	6523	AA892299	d		
236	13647	AA892367	a		
237	3473	AA892378	v		
238	17682	AA892382	j,p,s,x, General		
239	820	AA892395	g,s	Carbon fixation,Fructose and mannose metabolism,Glycolysis / Gluconeogenesis,Inositol metabolism,Pentose phosphate cycle	
240	14754	AA892414	u		
241	17439	AA892446	f		
242	15469	AA892462	p		
243	13609	AA892468	i,General		
243	13610	AA892468	n,v,General		
244	9254	AA892470	n,u		
245	11991	AA892483	s		
246	1522	AA892486	f		

TABLE 2: PATHWAYS				Atty. Doctel No. 41921-5009 V0
				Doc. No. 1792897 1
Sequence ID No.	Identifer	GenBank Acc/ Ref. Seq. ID No.	Metab. Code	Pathway
247	11994	AA892507	aa	
248	23888	AA892520	w	
248	23889	AA892520	h	
249	8599	AA892522	p	
250	15154	AA892532	p	
251	17468	AA892545	r	
252	11203	AA892554	f,h	
253	18906	AA892561	a,bb,General	
254	19327	AA892562	f,i,y,z	
255	18274	AA892572	p	
256	4512	AA892578	cc	
257	15876	AA892582	w	
258	19085	AA892598	General	
258	19086	AA892598	General	
259	20065	AA892647	i	
260	20088	AA892666	a,n	
261	23783	AA892773	n	
262	17549	AA892776	f,z	
263	13542	AA892798	b	
264	22537	AA892799	General	Glyoxylate and dicarboxylate metabolism,Pyruvate metabolism
264	22539	AA892799	v	Glyoxylate and dicarboxylate metabolism,Pyruvate metabolism
264	22538	AA892799	General	Glyoxylate and dicarboxylate metabolism,Pyruvate metabolism
265	6951	AA892820	h	
266	23322	AA892821	i,z	
267	17923	AA892843	f	
268	22871	AA892859	m	
269	9053	AA892861	p,v,General	
270	16482	AA892940	w	
271	12020	AA893035	i,y	
272	3563	AA893060	General	
273	13332	AA893080	i,General	
274	21305	AA893082	General	
275	16591	AA893191	i,z	
276	17447	AA893192	General	
277	3876	AA893205	n	
278	3878	AA893230	General	
279	20986	AA893242	q	Fatty acid metabolism
280	16168	AA893280	i,z,General	
281	3886	AA893289	i,m,y	
282	15209	AA893327	y	
283	17800	AA893436	cc	
284	17836	AA893626	h	
285	9084	AA893717	x	
286	22731	AA893743	d	
287	12031	AA893860	v	Aminoacyl-tRNA biosynthesis,Glycine, serine and threonine metabolism
288	17897	AA893905	k	
289	3447	AA893982	d	
290	22583	AA894009	n	
291	10540	AA894027	i	
292	4569	AA894059	x	
293	18419	AA894130	d	
294	17336	AA894297	i	
295	19120	AA894318	f,j	
296	19762	AA899113	i	
297	18286	AA899219	u	
298	22051	AA899498	w	
298	22052	AA899498	q	
299	21528	AA899563	aa	
300	4262	AA899590	i	

TABLE 2: PATHWAYS					Atty. General No. 44921-5000 WO Doc. No. 1790007
Seq. Name	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Pathways	
301	4661	AA899709	l,General		
302	21354	AA899721	q		
303	17905	AA899762	General		
304	18231	AA899840	r		
305	23778	AA899854	c,k,x		
306	22060	AA899898	b		
307	9114	AA899951	v,General		
308	8988	AA900148	f		
309	11841	AA900247	v		
310	4725	AA900290	cc		
311	4747	AA900465	General		
312	20988	AA900562	o		
313	3822	AA900863	b,g,General		
315	12420	AA901017	b		
316	4849	AA901155	s		
317	3959	AA901338	General		
318	22846	AA923862	a,d		
319	4895	AA923995	k		
320	21546	AA924188	cc,General		
321	24192	AA924210	n,General		
322	4933	AA924301	g,l,General		
323	4944	AA924405	l,General		
324	4948	AA924428	r		
325	4949	AA924432	General		
326	18891	AA924598	e		
327	22540	AA924630	v,General	Glyoxylate and dicarboxylate metabolism,Pyruvate metabolism	
327	22541	AA924630	General	Glyoxylate and dicarboxylate metabolism,Pyruvate metabolism	
328	14759	AA924786	k		
329	23123	AA924794	x		
330	4067	AA924813	g,p		
331	2888	AA924902	r,General		
332	18130	AA924964	d		
333	23141	AA925019	r		
334	23195	AA925026	General		
335	21458	AA925049	f,aa,General		
336	5073	AA925061	m		
337	14790	AA925087	o,General		
338	5089	AA925126	g		
339	23261	AA925145	k,General		
340	17363	AA925150	a		
341	23448	AA925167	l		
342	23159	AA925318	e		
343	21500	AA925353	x		
344	22479	AA925418	t		
345	21151	AA925539	b		
346	16944	AA925541	f		
346	16945	AA925541	f		
347	17514	AA925554	bb	Oxidative phosphorylation	
348	5183	AA925662	i,General		
349	23189	AA925844	r		
350	23190	AA925863	aa		
351	5252	AA926051	General		
352	22967	AA926080	h,cc		
353	17157	AA926129	b		
354	13411	AA926196	u,General		
355	5295	AA926247	General		
356	22928	AA926262	General		
357	8949	AA926316	r		
358	21798	AA926365	aa		
359	9942	AA942697	s		
360	6039	AA942716	x,General		

TABLE 2. PATHWAYS					Atty. Doc. ref. No. 44921-5009W
					Doc. No. 179937.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Metabolic Code	Pathway	
361	11174	AA942745	g,o,w		
362	23005	AA942770	g		
363	21318	AA942774	General		
364	6615	AA942889	v		
365	6691	AA943028	c		
366	22142	AA943066	p		
367	21993	AA943149	v,General		
368	9061	AA943508	General		
369	24390	AA943531	b,j,n,y		
370	13976	AA943532	f,s,x		
371	22248	AA943537	cc,General		
372	22257	AA943558	m		
373	12673	AA943773	u,cc,General		
374	13641	AA944154	u		
375	2658	AA944155	f		
376	12770	AA944161	d		
377	20903	AA944180	l,x		
378	13507	AA944244	v		
379	15596	AA944353	General		
380	22681	AA944413	i,v,cc,General		
381	6711	AA944439	General		
382	14763	AA944481	l,q,General		
383	22466	AA944605	h		
384	12301	AA944727	b		
385	7023	AA944792	d,m,aa	Purine metabolism,Pyrimidine metabolism,RNA polymerase	
386	22536	AA944803	bb		
387	22501	AA944811	g,l		
388	23967	AA944831	s		
389	26084	AA944822	f		
390	11974	AA944958	General		
391	22547	AA944970	aa		
392	22554	AA945076	z,General		
393	14352	AA945181	General		
395	1798	AA945569	General		
396	22050	AA945604	i,aa		
397	19731	AA945615	d,o		
398	22612	AA945624	a,General		
399	22618	AA945656	aa		
400	11871	AA945679	v		
401	22656	AA945818	General		
402	6720	AA945828	p		
403	22351	AA945867	m		
404	22665	AA945877	f		
405	24243	AA945950	b		
406	22689	AA945962	General		
407	22692	AA945986	d		
408	22696	AA945996	c,General		
408	22697	AA945996	c,o		
409	22658	AA945998	w		
410	20832	AA946040	s	Oxidative phosphorylation	
411	18337	AA946046	General		
412	825	AA946108	General		
413	8639	AA946221	e,cc,General		
414	23237	AA946224	f		
415	15600	AA946250	o,aa		
416	19387	AA946275	t		
417	6351	AA946344	d		
418	22067	AA946348	e		
419	22069	AA946349	aa		
420	13962	AA946351	General		
421	18280	AA946361	g		
422	18944	AA946391	v		

TABLE 2: PATHWAYS			Atty. Docket No. 44245-5029/W/	
			Doc. No. 179337.1	
Sequence ID No.	Identifier	GenBank Acc. No.	Model Code	Pathways
424	21410	AA946408	t	
425	643	AA946439	o,y	
426	20736	AA946443	x	
427	21878	AA946448	r	
428	21947	AA946451	bb	
429	17499	AA946467	General	
430	1809	AA946503	x,General	
431	23360	AA955104	f	
432	23471	AA955162	General	
433	9452	AA955206	b,General	
434	23512	AA955282	General	
435	22596	AA955298	General	
436	23283	AA955391	h	
437	23546	AA955393	General	
438	12404	AA955408	b	
439	23626	AA955540	aa	
441	17540	AA955914	bb	
442	24277	AA955962	General	
443	19939	AA955980	General	
444	24000	AA956005	i	
445	11050	AA956164	s,v	
446	498	AA956278	a,General	
447	23409	AA956294	q	
449	23773	AA956476	f,x	
450	23799	AA956530	d	
451	23800	AA956534	aa	
452	23834	AA956659	cc,General	
453	16425	AA956688	f,x	
454	23847	AA956723	s	
455	23852	AA956746	j,l,m,z	
456	5989	AA956907	g,s	
458	5990	AA956907	General	
457	23957	AA957123	u,General	
458	22357	AA957264	General	
			g,l,m,p,v,cc,	
459	23314	AA957270	General	
460	23995	AA957292	a,b	
461	2702	AA957307	General	Aminoacyl-tRNA biosynthesis, Glycine, serine and threonine metabolism
462	24040	AA957422	c	
463	12478	AA957554	m	
464	21308	AA957811	v	
465	24183	AA957889	t	
466	24178	AA957905	d	
467	17034	AA963071	e	
468	24053	AA963092	General	
469	2767	AA963201	o	
470	2022	AA963259	g	
471	2126	AA963488	d	
472	24246	AA963703	b	
473	2195	AA963746	General	
474	19370	AA963797	i	
475	2282	AA964147	e	
476	2284	AA964152	x	
478	2350	AA964368	g,General	
479	18630	AA964496	aa	
480	2392	AA964541	b	
481	2395	AA964554	General	
482	2410	AA964589	i,aa	
483	19145	AA964613	t	
484	2424	AA964617	g	
485	3107	AA964687	General	
486	2457	AA964752	q,t	

TABLE 2: PATHWAYS				Atty. Doc. No. 44921-5069WG Doc. No. 1793397	
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways	
487	6778	AA964763	b		
489	2468	AA964807	i		
490	2469	AA964814	w	Glutamate metabolism, Glutathione metabolism	
491	12561	AA964815	General		
492	2326	AA964882	aa		
493	21339	AA964982	General		
494	21390	AA964988	General		
495	12569	AA965023	g		
496	2583	AA965166	bb		
497	15885	AA965207	r		
499	2905	AA96727	b,l,m,u,General		
500	2915	AA96782	u,bb		
501	2920	AA96813	d		
502	19525	AA96856	aa,General		
503	2984	AA997015	c		
504	2986	AA997028	General		
505	3145	AA997237	General		
506	19249	AA997342	m		
507	16863	AA997345	General		
508	12598	AA997382	s		
509	3470	AA997374	p		
510	3180	AA997425	l		
511	3245	AA997608	General		
512	3020	AA997656	t		
513	3269	AA997800	x,aa		
514	3288	AA997877	f		
515	23992	AA998164	k,x		
516	17470	AA998264	b		
517	3773	AA998356	General		
518	19623	AA998422	General		
519	3572	AA998516	x		
520	2782	AA998565	c		
521	26119	AA998576	l,r,w,General		
522	22737	AA998660	aa		
523	3696	AA999030	e		
524	3079	AA999169	k,x,General		
525	3081	AA999171	e,p,r		
526	3082	AA999172	General	Glutamate metabolism, Purine metabolism	
527	17337	AB000717	k		
528	1535	AB000778	a		
529	1382	AB002406	k		
530	20184	AB003753	d		
531	4312	AB010635	c,l,j,k,y,z		
532	21666	AB012214	k	Methionine metabolism	
533	15772	AB015645	g		
534	1183	AF013144	h		
535	1582	AF015911	h,z		
536	11483	AF020618	u,cc,General		
537	20295	AF024712	aa		
538	19077	AF030358	y,z		
539	23044	AF034218	General		
540	25178	AF035955	d		
541	1564	AF035963	x,bb,General		
542	8426	AF036335	f		
543	21817	AF036537	k		
544	21145	AF038571	General		
545	22602	AF044574	General		
546	13464	AF047707	h		
547	24024	AF052695	x		
548	12259	AF061286	h		
549	4589	AF062369	y,z		
550	18007	AF062594	t		

TABLE 2: PATHWAYS					Aty. Doc. No. 44934-5069 WO Doc. No. 9793397.1
Sequence ID No.	Identifier	GenBank Acc. Ref. Seq. ID No.	Model Code	Pathways	
551	15761	AF062741	u		
552	17426	AF073839	p		
553	18615	AF074608	s		
554	15797	AF084205	f		
555	12932	AF102552	s		
556	18603	AI007649	x		
557	22733	AI007658	r		
558	22746	AI007672	r		
559	24109	AI007725	General		
560	15848	AI007820	n,v		
561	10108	AI007857	f		
562	6804	AI007877	General		
563	20099	AI007893	f,u		
564	11368	AI007948	d		
565	15849	AI008074	h		
566	3121	AI008160	General		
567	16646	AI008190	t		
568	12683	AI008203	x		
569	22018	AI008309	b		
570	23877	AI008441	n		
571	22599	AI008458	General		
572	22698	AI008578	p,General		
573	14405	AI008579	f,x		
574	4086	AI008629	x		
575	3808	AI008643	i,v,General		
576	3931	AI008697	l		
577	7785	AI008758	aa		
578	16701	AI008838	q		
579	21769	AI008930	k		
580	21895	AI008971	General		
581	410	AI008974	l,aa,General		
582	21632	AI009167	General		
583	21596	AI009168	General		
584	22801	AI009167	General		
585	11876	AI009321	cc,General		
586	2506	AI009341	General		
587	6382	AI009362	General		
588	14370	AI009427	k		
589	19275	AI009460	x		
590	4154	AI009467	g		
591	3464	AI009589	cc		
592	3926	AI009592	e		
593	19358	AI009675	c		
594	22545	AI009747	g		
595	15089	AI009752	cc,General		
596	5458	AI009756	h		
597	6844	AI009770	e,r,cc		
598	15627	AI009810	aa		
599	22619	AI009825	d		
600	7857	AI009898	l,l,m,z		
601	13259	AI009946	f		
602	21105	AI010067	General		
603	24627	AI010102	aa		
604	12716	AI010178	General		
605	18757	AI010216	aa		
606	2912	AI010220	aa,General		
607	3316	AI010237	t		
608	15644	AI010256	General		
609	657	AI010262	b		
610	3271	AI010303	b		
611	11081	AI010407	bb		
612	16521	AI010470	c,s,l,General	Porphyrin and chlorophyll metabolism	
613	6927	AI010542	General		

TABLE 2: PATHWAYS				Any DocId: No. 44991-50839
				Doc. No. 11796837.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways
614	17524	AI010568	a,j,y,General	
615	6946	AI010642	n	
616	23509	AI010962	aa	
617	6044	AI011285	t	
618	13865	AI011361	o	
619	21779	AI011380	cc	
621	12534	AI011460	cc	
622	12629	AI011492	e,f	
623	735	AI011560	f	
624	3941	AI011598	General	
625	17550	AI011607	j,General	
626	10636	AI011634	e	
627	3995	AI011678	General	
628	16112	AI011706	h	
629	13354	AI011757	c	
630	12745	AI011799	cc	
631	18684	AI011812	t	
632	4205	AI011982	b	
633	6618	AI012114	General	
634	17407	AI012145	General	
635	13093	AI012177	r	
636	15395	AI012216	f	
637	21796	AI012221	d,General	
638	3981	AI012235	i,General	
639	6606	AI012308	i,r	
640	3417	AI012337	w	
641	24200	AI012356	b,t,General	
642	7471	AI012379	cc	
643	7247	AI012438	g	
644	7127	AI012464	p,General	
645	3304	AI012471	b	
646	2311	AI012485	aa	
647	20817	AI012589	g,n,q	Glutathione metabolism
648	3483	AI012590	v,General	
649	8975	AI012613	General	
650	11335	AI012619	j	
651	21409	AI012637	General	
652	8015	AI012638	aa	
653	8476	AI012647	w	
654	4232	AI012958	e,p,General	
655	23128	AI013011	General	
656	20086	AI013260	General	
657	11969	AI013273	k	
658	26147	AI013387	aa	
659	8815	AI013437	p	
660	19722	AI013508	k	
661	8674	AI013568	General	
662	23145	AI013647	c,t	
663	15130	AI013676	w	
664	7274	AI013715	aa	
665	7276	AI013730	e	
666	7278	AI013738	y,z,aa	
667	22592	AI013740	s,x,bb,General	
668	16584	AI013765	w	
669	24143	AI013804	j,l	
670	15928	AI013829	a,General	
671	21950	AI013861	j	Valine, leucine and isoleucine degradation
672	3260	AI013875	t	
673	2708	AI013882	d,q	
674	8585	AI013886	i	
675	7299	AI013911	p,r,t,General	
676	15904	AI013971	General	
677	12781	AI014023	w	

TABLE 2: PATHWAYS				Att. Docket No. 44924-1039,70 Doc. No. 1793997.1	
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways	
678	19372	A1014135	aa		
679	4241	A1014140	w		
680	15247	A1014169	c,u		
681	7315	A1028831	n		
682	16631	A1028856	General		
683	23297	A1028953	x		
684	11326	A1029015	b		
685	2866	A1029058	n,y		
686	12812	A1029126	General		
687	17602	A1029156	p		
688	7392	A1029185	aa		
689	6517	A1029264	d,k,x		
690	7639	A1029292	b		
691	3874	A1029428	i,General		
692	12819	A1029437	f		
693	7452	A1029466	r		
694	7493	A1029608	b		
696	7537	A1029829	o,General		
697	2310	A1029969	v		
698	7585	A1030023	x		
699	7586	A1030024	b,n		
700	14492	A1030061	cc		
701	10673	A1030134	f		
702	7615	A1030163	o,r		
703	2370	A1030179	General		
704	7681	A1030449	n		
705	11559	A1030472	General		
706	7665	A1030668	t,bb		
707	24222	A1030704	k		
708	10740	A1030743	h		
709	10742	A1030773	e		
711	16169	A1030932	General		
712	19527	A1030961	f		
713	22814	A1031004	r		
714	3167	A1031012	e		
715	5350	A1043611	a		
716	7858	A1043654	t		
717	10784	A1043678	d		
718	9180	A1043694	aa		
719	7867	A1043695	aa	Glutamate metabolism,Purine metabolism	
720	7584	A1043724	General		
721	7895	A1043768	e		
722	7903	A1043805	General		
723	7913	A1043849	cc		
724	3899	A1043904	l		
725	6766	A1043914	f		
726	10818	A1043990	g,l,m,General		
727	7956	A1044018	f		
728	5393	A1044170	p		
729	5398	A1044177	q		
730	5425	A1044237	a,d		
731	8692	A1044247	r		
732	5430	A1044253	i		
733	5461	A1044338	g,p,General		
734	5464	A1044345	i		
735	3359	A1044347	aa		
737	2695	A1044396	b		
738	5494	A1044425	General		
740	9882	A1044588	j,m		
741	5575	A1044688	g		
742	2348	A1044794	General		
743	18205	A1044836	n		
744	5626	A1044864	u		

Sequence		GenBank Acc/		Model Code		Pathways	
ID No.		Ref. Seq. ID No.					
745	5630	AI044869		f			
746	5634	AI044883		General			
747	4047	AI044947		I,m			
748	5654	AI044976		w			
749	5684	AI045056		r			
750	19235	AI045074		General			
751	5689	AI045075		i,aa,General			
752	5711	AI045151		General			
753	19237	AI045153		c			
754	9964	AI045161		f			
755	5735	AI045223		f			
756	5474	AI045477		a,General			
757	5811	AI045502		d,e			
758	5819	AI045537		General			
759	5839	AI045594		i			
760	6808	AI045600		s			
761	17755	AI045608		y			
763	10020	AI045632		a			
764	5855	AI045669		General			
765	5881	AI045789		i			
766	5897	AI045862		General			
767	5900	AI045866		y,z			
768	7540	AI045882		o,i,General			
769	5329	AI045970		p			
770	15093	AI058285		d			
771	8002	AI058304		i			
772	8017	AI058341		c			
773	6628	AI058359		General			
774	8177	AI058603		aa			
775	3090	AI058730		aa			
776	10093	AI058746		g			
777	8143	AI058759		General			
778	18559	AI058762		f			
779	8163	AI058837		aa			
780	4739	AI058889		General			
781	8221	AI059061		General			
782	10159	AI059147		d			
783	8245	AI059154		b			
784	8283	AI059290		n			
785	8314	AI059386		g,General			
786	10200	AI059444		i			
787	8347	AI059519		s			
788	18359	AI059675		n			
789	10281	AI059947		b,t			
790	8494	AI059968		aa			
791	8495	AI059971		General			
792	8496	AI059974		General			
793	10289	AI060053		i			
794	8548	AI060176		k			
795	8565	AI060236		t			
796	18322	AI060279		i,y,z			
797	8745	AI069939		r			
798	8785	AI070067		o			
799	17506	AI070068		cc			
800	9067	AI070087		General			
801	3551	AI070122		e			
802	4967	AI070179		k			
803	18	AI070195		General			
804	24197	AI070314		General			
805	8869	AI070330		r			
806	8874	AI070336		b,cc			
807	10417	AI070410		m			
808	8901	AI070419		aa			

TABLE 2: PATHWAYS				App. Doc. No. 44924-5089.V0
				Doc. No. 1793397.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways
809	14424	AI070421	l,p,General	
810	10434	AI070497	General	
811	8927	AI070523	v	
812	8946	AI070611	q	
813	8950	AI070621	w	
814	8972	AI070673	General	
815	8981	AI070715	bb	
816	26184	AI070784	lj	
817	3007	AI070824	w	
818	8999	AI070839	p	
819	10477	AI070868	e,f	
820	24301	AI070911	k	
821	8721	AI071024	General	
822	9212	AI071098	x	
823	1831	AI071137	c	
824	11005	AI071139	r	
825	9104	AI071173	q,m	
826	9583	AI071185	General	
827	9644	AI071410	c	
828	16058	AI071490	General	Sphingoglycolipid metabolism
829	11067	AI071509	f,o	
831	5695	AI071566	bb	
832	9671	AI071568	w	
833	22929	AI071578	General	
834	9673	AI071581	General	
835	9699	AI071646	General	
837	9799	AI072008	q,y,z	
838	9608	AI072050	d	
839	22796	AI072213	General	
840	9271	AI072405	v	
841	10869	AI072425	w	
842	21797	AI072439	General	
843	9306	AI072521	r	
844	9312	AI072550	j	
845	10893	AI072559	k	
846	1501	AI072634	cc,General	
847	6548	AI072658	General	
848	9363	AI072695	d	
850	9409	AI072841	n	
851	9410	AI072842	w	
852	9468	AI073021	General	
853	9518	AI073223	f	
854	11183	AI100768	t	Nitrogen metabolism
855	9190	AI100835	e	
856	2029	AI100842	p	
857	5687	AI101006	e	
858	15192	AI101099	g,cc	
859	17399	AI101157	o	
860	9339	AI101160	l,m,o	
861	6321	AI101256	General	
862	5421	AI101270	c	
863	11910	AI101323	General	
864	23140	AI101608	e	
865	4119	AI101901	General	
866	16324	AI102009	b	
867	18642	AI102023	o	
868	19373	AI102044	a	
869	7051	AI102055	h	
870	6544	AI102064	c	
871	10227	AI102248	w	
872	23849	AI102318	e,q	
873	11954	AI102505	g,l,s	Oxidative phosphorylation
874	2125	AI102519	c,k	

TABLE 2: PATHWAYS				Atty. Docket No. 44921-5089 WO
				Doc. No. 1798897.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways
875	5967	AI102520	y	
875	5969	AI102520	p,w	
876	11563	AI102560	General	
877	15190	AI102562	b,g,n,p,v	
878	10769	AI102570	bb	
879	22487	AI102578	General	
880	19011	AI102618	General	
881	23837	AI102620	q,t	
882	23538	AI102727	g,General	
883	17234	AI102741	c	
884	5891	AI102745	k	
885	6796	AI102753	General	
886	8637	AI102849	o,p	
887	15861	AI102868	i	
888	3533	AI102877	g	
889	13222	AI102977	General	
890	6806	AI103018	o,u	
891	10659	AI103059	w,cc,General	
892	17400	AI103097	e	
893	3584	AI103106	x,aa	
894	13298	AI103143	r	
895	15981	AI103150	i,x	
896	3475	AI103245	w	
898	23619	AI103314	p	
899	24181	AI103320	e	
901	4355	AI103410	General	
902	7622	AI103472	General	
903	20918	AI103552	n	
904	21579	AI103572	General	
905	2222	AI103631	o	
906	2752	AI103641	e	
907	4856	AI103708	i	
908	8990	AI103719	i,m,y,z	
909	15942	AI103738	r	
910	22885	AI103828	e,General	
911	15853	AI103841	x	
912	15050	AI103911	j,y	Oxidative phosphorylation
913	12376	AI103939	u	
914	22271	AI103947	o,y	
915	20833	AI104035	f,q	Oxidative phosphorylation
916	7010	AI104099	w	
917	22101	AI104251	General	
918	22833	AI104258	General	
919	22211	AI104279	g,m	
920	10720	AI104296	i	
921	15416	AI104340	i	
922	10991	AI104342	a	
923	18831	AI104357	p	
924	7223	AI104373	e	
925	23574	AI104520	e,g,s	Oxidative phosphorylation
926	18509	AI104528	q	
927	11680	AI104605	v	
928	12342	AI104658	w	
929	23689	AI104685	r	
930	15377	AI104821	o,cc	
931	22957	AI104897	General	
932	18451	AI104953	o,s	Oxidative phosphorylation, Type III protein secretion system
933	24375	AI104979	n,General	
934	18278	AI105080	bb	
935	2196	AI105243	p	
936	5199	AI105272	bb,General	
937	12901	AI105301	o,s	

TABLE 2: PATHWAYS				Atty. Docket No. 44924-5081W0
				Doc. No. 4720387.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathway
936	7700	AI105383	cc,General	
939	13343	AI105396	u	
940	22931	AI105417	e,General	
941	23596	AI105435	bb	Fatty acid metabolism,Lysine degradation,Tryptophan metabolism
942	15863	AI105465	o	
943	12660	AI111492	c	
944	4479	AI111599	General	
945	24211	AI111853	k	
946	2539	AI111960	r	
947	5729	AI111990	k	
948	4049	AI112012	i,q,u,General	
949	12908	AI112043	i	
950	20041	AI112161	t	
951	12937	AI112462	General	
952	3713	AI112571	b	
953	12921	AI112636	General	
954	12965	AI112926	General	
955	7480	AI112966	General	
956	4969	AI113008	r	
957	11817	AI136295	f	
959	11165	AI136372	c	
960	4045	AI136460	cc	
961	12782	AI136493	k	
962	6850	AI136665	h	Purine metabolism,Pyrimidine metabolism
963	20920	AI136891	p,v	
964	6552	AI137062	o	
965	22722	AI137211	i	
966	13111	AI137224	o,General	
967	15969	AI137302	e	
968	14349	AI137303	d	
969	9166	AI137406	General	
970	8525	AI137516	r	
971	6638	AI137579	General	
972	7414	AI137596	General	
973	11321	AI137752	z	
974	23473	AI137932	l	
975	13158	AI138024	l	
976	13467	AI138034	cc	
977	11377	AI138105	y	
978	6790	AI144801	d,h	
979	6506	AI144919	j,l,y	
980	8027	AI144956	l	
982	14458	AI145095	General	
983	7476	AI145202	g	
984	17545	AI145394	e	
985	17479	AI145395	r	
986	4194	AI145387	r	
987	8634	AI145722	g	
988	8339	AI145761	y,General	
989	2059	AI146005	h,General	
990	23224	AI146033	o	
991	5232	AI168942	bb	Valine, leucine and isoleucine degradation
992	18472	AI168975	u	
992	18473	AI168975	u	
993	13235	AI169020	r	
994	11618	AI169115	o,y,General	
995	17386	AI169144	o	
996	10984	AI169156	o,u	
997	8205	AI169176	e	
998	12679	AI169177	e	
999	2607	AI169211	c	

TABLE 2: PATHWAYS				Atty. Booklet No. 4493-5039 WO Doc. No. 1793397.1	
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Pathway	
1000	22661	AI169265	s,z	Oxidative phosphorylation, Type III protein secretion system	
1001	13239	AI169278	g,l,y,z		
1002	24162	AI169279	m		
1003	15879	AI169284	o		
1004	24213	AI169289	p		
1005	13240	AI169311	cc		
1006	5931	AI169324	b		
1007	20891	AI169337	d		
1008	11979	AI169365	cc		
1009	10947	AI169372	s		
1010	20697	AI169494	o,u		
1011	8234	AI169517	z		
1012	18343	AI169648	o		
1013	10839	AI169655	l,m		
1014	24146	AI169668	j,l		
1015	22575	AI169728	r		
1016	804	AI169756	cc		
1017	6213	AI169883	p		
1018	3616	AI169947	l,bb		
1019	3733	AI170053	u, General		
1020	14179	AI170224	cc		
1021	11406	AI170263	r		
1022	3547	AI170279	General		
1023	11524	AI170340	j,y,z		
1024	2729	AI170363	e,i		
1025	18811	AI170525	i		
1026	22524	AI170542	h		
1027	24048	AI170570	a,g		
1028	5968	AI170692	y,aa		
1029	9757	AI170693	b		
1030	18905	AI170770	e,s		
1031	16170	AI170894	l		
1032	7069	AI171185	c		
1033	17591	AI171354	b		
1034	13265	AI171361	h		
1035	4428	AI171362	a	Oxidative phosphorylation, Ubiquinone biosynthesis	
1036	18126	AI171369	w		
1037	23253	AI171448	o		
1038	4584	AI171492	m, General		
1039	11158	AI171542	r,s		
1040	15345	AI171587	l		
1041	21183	AI171676	k		
1042	8215	AI171692	i		
1043	11437	AI171794	l		
1044	2625	AI171800	cc		
1045	23679	AI171802	v		
1046	11708	AI171807	l,l	Oxidative phosphorylation, Type III protein secretion system	
1047	17204	AI171844	s,y,z		
1048	4420	AI171916	m		
1049	3266	AI171948	l,m		
1050	19012	AI172056	l		
1051	11205	AI172057	a,q,bb		
1052	6057	AI172102	b		
1053	19128	AI172103	m		
1054	15673	AI172107	z		
1055	6630	AI172184	n		
1056	11968	AI172208	bb		
1057	6974	AI172263	l,m		
1058	23313	AI172271	d		
1059	2140	AI172272	General		

TABLE 2: PATHWAYS				Atty. Docket No. 44924-5009 WO Doc. No. 1998387.1	
Sequence- ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Metab. Code	Pathways	
1060	15382	AI172302	lp,General		
1061	18689	AI172329	l		
1062	17887	AI172414	o		
1063	3042	AI172447	General		
1064	17291	AI172491	bb	Citrate cycle (TCA cycle), Glutathione metabolism, Reductive carboxylate cycle (CO <sub>2</sub> fixation)	
1065	26222	AI172506	p		
1066	13095	AI172595	r		
1067	8795	AI172618	General		
1068	6454	AI175342	l,l,m,y		
1070	4445	AI175466	x		
1071	3418	AI175475	m		
1072	18507	AI175551	bb		
1073	10217	AI175628	w		
1074	7262	AI175833	l,m,x		
1075	19004	AI175875	r		
1076	22352	AI175959	l,General		
1077	7022	AI176041	h,n		
1078	21467	AI176061	t		
1079	18381	AI176160	General		
1080	14159	AI176169	g		
1081	21742	AI176172	w		
1082	10182	AI176185	v		
1083	22765	AI176265	General		
1084	6905	AI176275	a		
1085	12999	AI176276	cc		
1086	16438	AI176294	e		
1087	21130	AI176298	y		
1088	3014	AI176362	e		
1089	15015	AI176363	r		
1090	19006	AI176393	x		
1091	20001	AI176396	o		
1092	12174	AI176435	l,m		
1093	15191	AI176456	b,o,l,v,cc		
1094	24236	AI176473	d,General		
1095	16518	AI176546	v		
1096	2161	AI176592	General		
1097	12436	AI176610	General		
1098	2536	AI176616	l,l,v,General		
1099	18525	AI176792	u		
1100	23449	AI176828	g		
1101	23299	AI176839	General		
1102	3580	AI176848	e		
1103	22103	AI176849	d,General		
1104	16036	AI176855	f		
1105	15588	AI176916	General		
1106	16917	AI176951	t		
1107	16124	AI176963	cc		
1108	15146	AI176969	b,General		
1109	5786	AI177058	f		
1110	2852	AI177059	c		
1112	3156	AI177092	g		
1113	14384	AI177096	a	Purine metabolism	
1114	13310	AI177119	General		
1115	24049	AI177341	g,p,s,u		
1116	15964	AI177360	o,General		
1117	14989	AI177366	u		
1118	7975	AI177374	aa		
1119	3006	AI177395	k		
1120	17570	AI177683	r		
1121	9521	AI177706	b		
1122	14425	AI177755	g,General		

TABLE 2: PATHWAYS			Atty. Pocket No. 44921-5086W6 Doc. No. 1726837.1	
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways
1123	10611	AI177790	j,m	
1124	5356	AI177813	cc	
1125	11791	AI177843	General	
1126	14484	AI177867	General	
1127	6780	AI177868	General	
1128	19184	AI178025	General	
1129	6059	AI178245	c,General	
1130	23248	AI178267	y	
1131	4073	AI178272	o	
1132	7838	AI178291	e	
1133	18996	AI178326	y	
1134	22488	AI178392	b	
1135	18800	AI178504	n,p,aa	
1136	22197	AI178527	g,General	
1137	3401	AI178684	bb	
1138	17713	AI178700	m	
1139	14874	AI178735	e	
1140	23567	AI178748	v,General	
1141	18907	AI178871	c	
1142	20991	AI178979	i	
1143	5887	AI179099	q,t	
1144	8477	AI179167	b,e,General	
1145	3348	AI179288	u,v	
1146	13608	AI179314	e	
1147	8849	AI179315	g,p	
1148	13611	AI179378	v,General	
1149	15438	AI179399	m,x	
1150	13614	AI179407	e,t,General	
1151	15042	AI179422	b,General	
1152	2768	AI179481	i,General	
1153	24041	AI179580	b,i	
1154	19822	AI179599	o,General	
1155	23270	AI179601	q,General	
1156	5801	AI179605	e	
1157	16081	AI179610	g,j,p	Porphyrin and chlorophyll metabolism
1158	14564	AI179717	k	
1159	7918	AI179750	General	
1160	6647	AI179795	g	
1161	9097	AI179875	o,General	
1162	23989	AI179953	a	
1163	12899	AI179967	b	
1164	1687	AI179971	c	
1165	22569	AI179979	General	
1166	23514	AI179986	o,General	Glycine, serine and threonine metabolism
1167	15892	AI179988	c,General	
1168	12402	AI180004	g	
1169	5443	AI180065	General	
1170	5481	AI180170	General	
1171	24028	AI180239	i	
1172	17089	AI180281	g	
1173	3701	AI180306	aa	
1174	3352	AI180334	m	
1175	24368	AI180392	i,m	
1176	14337	AI180414	c	
1177	19080	AI227647	j,y,z	
1178	22838	AI227667	aa	
1179	6765	AI227761	i,General	
1180	24054	AI227867	General	
1181	7324	AI227885	i	
1182	23998	AI227997	d	
1183	1851	AI228068	n,w	
1184	14237	AI228128	e	
1185	14242	AI228197	General	

TABLE 2: PATHWAYS				Atty. Doc. No. 44924-5699WO Doc. No. 1793397.1	
Sequence ID No.	Identifier	SeqBank Acc/ Ref. Seq. ID No.	Model Code	Pathways	
1186	16913	AI228236	o		
1187	22915	AI228299	r		
1188	8917	AI228301	General		
1189	15879	AI228313	r,General		
1190	13727	AI228326	o,General		
1191	6102	AI228335	General		
1192	13730	AI228356	a		
1193	13745	AI228494	b,cc		
1194	4217	AI228587	s		
1195	16053	AI228596	cc		
1196	3557	AI228672	e		
1197	11605	AI228682	e		
1198	13203	AI228728	r		
1199	13771	AI228848	g		
1200	5918	AI229036	r		
1201	8235	AI229154	k		
1202	16203	AI229196	r		
1203	13626	AI229304	a		
1204	13144	AI229320	g		
1205	4640	AI229404	x,aa		
1206	23563	AI229421	j		
1207	15426	AI229497	s		
1208	15193	AI229508	bb		
1209	19243	AI229638	x		
1210	23078	AI229647	p		
1211	3099	AI229680	o	Oxidative phosphorylation, Ubiquinone biosynthesis	
1212	19508	AI229696	bb		
1213	13977	AI229707	x		
1214	23983	AI229708	v		
1215	2688	AI229793	e		
1216	13674	AI229832	g		
1217	12587	AI229879	General		
1218	20591	AI229993	i,m		
1219	24042	AI230002	a,b,d,General		
1220	13880	AI230042	u		
1221	17672	AI230074	d	Oxidative phosphorylation, Ubiquinone biosynthesis	
1222	3652	AI230113	General		
1223	18650	AI230121	aa		
1224	13025	AI230173	c		
1225	4280	AI230247	z		
1226	18528	AI230284	General		
1227	7084	AI230362	p		
1228	20895	AI230549	b,n		
1229	12961	AI230554	General		
1230	15636	AI230616	r		
1231	4121	AI230647	i,m		
1232	14388	AI230702	General		
1233	18529	AI230716	x,General		
1234	13618	AI230724	General		
1235	8304	AI230746	cc		
1236	4731	AI230773	e		
1237	14430	AI230798	c,k,x		
1238	16627	AI230822	bb	Glycoprotein biosynthesis	
1239	3125	AI231026	General		
1240	633	AI231127	k		
1241	20846	AI231140	p		
1242	6743	AI231219	d		
1244	26292	AI231381	k		
1245	12343	AI231433	w		
1246	7337	AI231465	aa		
1247	16321	AI231506	General		

TABLE 2: PATHWAYS					Art. Pocket No. 44921-5099WO Doc. No. 179997.1
Sequence ID No.	Identifier	GenBank Acc./Ref. Seq. ID No.	Model Code	Pathways	
1248	8004	AI231532	jj		
1249	15171	AI231792	g		
1250	6193	AI231797	l		
1252	14227	AI231999	u		
1253	24501	AI232006	w,y,bb		
1254	3434	AI232014	g,q,z,cc,General		
1255	19094	AI232021	n,General		
1256	14020	AI232076	u		
1257	6726	AI232157	d		
1258	11549	AI232174	lm		
1259	23125	AI232266	js		
1260	2085	AI232270	bb		
1261	2913	AI232272	o		
1262	14304	AI232281	g		
1263	15955	AI232294	u,bb,General		
1264	15122	AI232303	y		
1265	4716	AI232313	y		
1266	15246	AI232332	tu		
1267	24321	AI232340	o		
1268	16172	AI232341	d		
1269	14411	AI232346	h		
1270	16287	AI232379	f	pdf	
1271	5601	AI232461	n,General		
1272	14051	AI232489	lm		
1273	5572	AI232490	lt		
1274	11157	AI232494	cc		
1275	8709	AI232534	o		
1276	20350	AI232552	l,v,y		
1277	14069	AI232631	e		
1278	4440	AI232643	w		
1279	17695	AI232784	e		
1280	15796	AI232874	v		
1281	12467	AI232924	General		
1282	12873	AI232984	l		
1283	5355	AI233031	r		
1284	18794	AI233121	c		
1285	3823	AI233147	b,g,General		
1286	11967	AI233155	c,h,General		
1287	11561	AI233182	d		
1288	3471	AI233183	g		
1289	21948	AI233191	i		
1290	13598	AI233194	g,p,y		
1291	15552	AI233195	y		
1292	17907	AI233224	bb		
1293	14111	AI233269	cc		
1294	12894	AI233365	d		
1295	7161	AI233407	General		
1296	15306	AI233425	q		
1297	14120	AI233433	d		
1298	14095	AI233458	a,d		
1299	3075	AI233494	u,aa		
1300	6046	AI233530	General		
1301	18900	AI233570	General		
1302	7888	AI233583	General	Aminoacyl-tRNA biosynthesis,Arginine and proline metabolism	
1303	16709	AI233602	General	Purine metabolism	
1304	5163	AI233712	y		
1305	7243	AI233717	General		
1306	3816	AI233729	g		
1307	13023	AI233740	d,h,General		
1308	14871	AI233743	g		
1309	7469	AI233767	cc		

TABLE 2: PATHWAYS				Atty. Docket No. 4-92-5089WO Doc. No. 179887-1	
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Pathways	
1310	7804	AI233771	b		
1311	13563	AI233773	e		
1312	2154	AI233818	k,cc		
1313	16616	AI234079	h		
1314	13393	AI234100	a,d,General		
1315	7071	AI234162	r		
1316	14677	AI234620	General		
1317	4443	AI234629	m		
1318	22453	AI234678	b		
1319	23964	AI234748	t,General		
1320	19581	AI234753	f		
1321	22152	AI234822	o,General		
1322	18942	AI234865	d		
1323	22662	AI234939	aa	Oxidative phosphorylation, Type III protein secretion system	
1324	3875	AI235047	o,General		
1325	19479	AI235135	o		
1326	14906	AI235192	g		
1327	14718	AI235210	e		
1328	15004	AI235224	b,General		
1329	6632	AI235277	v		
1330	14722	AI235284	x,z		
1331	1462	AI235585	u,General		
1332	21061	AI235631	j,m		
1333	14665	AI235646	m	tgf-beta	
1334	19940	AI235689	General		
1335	5698	AI235692	u		
1336	23745	AI235732	k		
1337	11164	AI235739	General		
1338	5212	AI235745	d		
1339	14768	AI235912	h		
1340	14776	AI235950	m		
1341	3091	AI236027	n,General		
1342	14861	AI236045	r		
1343	14862	AI236048	e		
1344	16943	AI236097	p		
1345	8336	AI236101	i		
1346	23230	AI236146	v		
1347	22855	AI236150	e		
1348	14594	AI236152	i		
1349	18406	AI236168	r		
1350	15051	AI236332	General		
1351	19298	AI236338	bb		
1352	10667	AI236366	b		
1353	10774	AI236397	f		
1354	9407	AI236402	aa		
1355	26335	AI236460	General		
1356	17950	AI236500	t,General		
1357	18259	AI236601	h,v		
1358	11445	AI236613	j,y		
1359	17248	AI236635	o,aa		
1360	16859	AI236753	t,General		
1361	5206	AI236754	g		
1362	24368	AI236772	e,General		
1363	15850	AI236795	n,v,w		
1364	14800	AI236856	w		
1366	11404	AI237002	m		
1367	18151	AI237212	o,General		
1368	21653	AI237535	t,General		
1369	11208	AI237586	z		
1370	21863	AI237713	j,k,aa		
1371	14842	AI237724	r		
1372	3467	AI237835	General		

TABLE 2: PATHWAYS					Att'y. Docket No. 44921-50891W Doc. No. 179387
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways	
1373	25840	AI638972	u		
1374	17108	AI639017	n		
1375	16676	AI639082	c,k,x		
1376	12400	AI639107	k		
1377	19952	AI639108	q,v		
1379	25907	AI639167	q,w		
1381	18533	AI639231	n		
1382	18353	AI639233	l,aa		
1384	15330	AI639285	General		
1385	20026	AI639354	g		
1386	25971	AI639365	r		
1388	19152	AI639387	u,General		
1390	18338	AI639422	y		
1392	20082	AI639488	l,m		
1394	20056	AI639504	a,bb,General		
1395	4713	AI639518	q		
1396	14332	AJ001044	bb		
1397	7602	AJ001929	k		
1398	9867	AJ005424	u		
1400	16351	AJ011811	General		
1401	20116	AJ011969	l,General		
1402	17638	AJ223355	v,w		
1403	18686	D00729		Fatty acid metabolism	
1404	5049	D10655	n,w		
1405	25257	D13623	j		
1405	15281	D13623	h		
1406	11434	D14014	cc		
1407	1613	D14076	x		
1408	1728	D16479	q	Bile acid biosynthesis,Fatty acid biosynthesis (path 2),Fatty acid metabolism,Phenylalanine metabolism,Valine, leucine and isoleucine degradation	
1409	3015	D18554	c,s,v,z		
1410	472	D26111	d,s,bb		
1412	16233	D29960	j,l		
1413	9029	D30804	n		
1414	1485	D38222	y,z		
1415	9135	D45247	s	Proteasome	
1416	16354	D50564	u	Cysteine metabolism	
1417	1884	D50695	l,m,bb		
1418	21147	D63772	General		
1419	826	D82928	f	Glycerolipid metabolism	
1420	25306	D84485	u		
1421	18867	D88250	t		
1423	22543	H31117	r,v,General		
1424	12360	H31456	w		
1425	20514	H31489	h,j		
1426	11358	H31610	h		
1427	4360	H31813	bb,General		
1428	9343	H32169	l		
1429	4386	H33093	h,w		
1430	4415	H33636	h		
1431	15374	H34186	l		
1432	17159	J00797	u,General		
1433	16260	J01878	f		
1434	17284	J02827	bb	Valine, leucine and isoleucine degradation	
1435	15017	J03752	n		
1436	44	J03819	p,s		
1437	21014	J03914	e,f,General	Glutathione metabolism	
1438	20429	J05035	f	Androgen and estrogen metabolism,Bile acid biosynthesis	

TABLE 2: PATHWAYS				Atty. Docket No. 24927-5089 WO Doc. No. 1793397.1
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Pathways
1439	1247	J05181	j,l,m,s,y,z	Glutamate metabolism, Glutathione metabolism
1440	10464	J05510	n,u,General	
1441	20149	K03243	q	
1442	17756	K03249	q	
1443	381	L00124	w	
1444	2048	L00382	k,x	
1445	10500	L04619	s	
1447	108	L14002	p	
1448	25366	L14003	f	
1449	109	L14004	c,p	
1450	20414	L14323	General	
1451	25369	L14937	y	
1452	16119	L16532	k	
1453	25377	L25387	h	
1453	12058	L25387	h	
1455	21146	L35558	General	Glutamate metabolism, Glutathione metabolism
1456	106	L37203	w	
1458	13682	L38482	f,j,k,m,z	
1459	6405	L38615	p	
1461	15189	M11794	n,v	
1462	17086	M13011	j	
1464	21053	M15481	o	
1465	25405	M18330	j,l	
1466	25415	M19648	a	
1468	14967	M22366	w	
1469	20481	M22631	bb	
1471	15048	M24542	q	Oxidative phosphorylation
1472	20921	M29653	m	
1473	1224	M31931	u	
1474	15579	M33648	q	
1474	15580	M33648	q	
1475	17211	M34331	g,n,q,v	
1476	20699	M35601	b,x,bb	
1476	20700	M35601	b,l,bb	
1477	9223	M36151	o	
1479	1565	M57728	j,m,y	
1480	24844	M58040	c	
1481	25057	M58495	h	
1482	457	M60666	d,General	
1483	1223	M75281	f	
1484	5733	M81855	i,k,aa	
1485	4198	M83143	m	
1485	4199	M83143	m	
1486	24651	M83678	k,x,z	Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism
1487	1430	M8468	General	
1488	25467	M93297	c	
1489	729	M95762	a,y	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
1490	23698	NM_012489	q	
1490	23699	NM_012489	q	Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Phenylalanine metabolism, Valine, leucine and isoleucine degradation
1490	23699	NM_012489	q	Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Phenylalanine metabolism, Valine, leucine and isoleucine degradation

TABLE 2: PATHWAYS				Am. Doc. No. 44981-3089W Doc. No. 179397-1
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Metabolic Code	Pathways
1491	7062	NM_012495	q	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Inositol metabolism, Pentose phosphate cycle
1492	15511	NM_012498	u	Fructose and mannose metabolism, Galactose metabolism, Glycolipid metabolism, Pentose and glucuronate interconversions, Pyruvate metabolism
1494	7427	NM_012515	General	
1495	24433	NM_012527	i	
1496	4467	NM_012529	d	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
1497	16520	NM_012532	General	Porphyrin and chlorophyll metabolism
1498	225	NM_012544	x,z	
1499	1431	NM_012545	General	Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism
1500	23868	NM_012551	i,m,v,General	
1500	23872	NM_012551	i,v,cc,General	
1500	23869	NM_012551	v,General	
1501	19407	NM_012554	z	Glycolysis / Gluconeogenesis, Phenylalanine, tyrosine and tryptophan biosynthesis
1501	19408	NM_012554	n,s,y,z	Glycolysis / Gluconeogenesis, Phenylalanine, tyrosine and tryptophan biosynthesis
1502	21836	NM_012555	k	
1503	16895	NM_012558	g,s	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate cycle
1504	25317	NM_012559	bb	
1504	6477	NM_012559	b,bb	
1504	6478	NM_012559	bb	
1505	11731	NM_012561	k	
1507	4254	NM_012564	a	
1508	16026	NM_012578	r	
1508	16024	NM_012578	r	
1508	16025	NM_012578	r	
1509	16080	NM_012580	g,m	Porphyrin and chlorophyll metabolism
1510	15098	NM_012588	bb	
1511	4450	NM_012592	bb	Valine, leucine and isoleucine degradation
1511	4451	NM_012592	i,bb	Valine, leucine and isoleucine degradation
1511	4452	NM_012592	bb	Valine, leucine and isoleucine degradation
1512	17198	NM_012593	a,x	
1512	17197	NM_012593	x	
1513	18749	NM_012600	a,h	Carbon fixation, Pyruvate metabolism
1514	2628	NM_012603	General	
1514	2629	NM_012603	x,General	
1515	16849	NM_012608	n,a,q	
1517	15540	NM_012620	General	
1518	24568	NM_012630	General	
1518	24568	NM_012630	General	
1519	18553	NM_012631	k	
1520	1844	NM_012637	General	
1521	24668	NM_012642	f	
1522	18632	NM_012645	a	
1523	25435	NM_012647	g	
1524	9423	NM_012649	b,cc	
1525	24496	NM_012654	n	
1526	7101	NM_012679	x,bb,General	
1527	24707	NM_012693	i	Fatty acid metabolism, Tryptophan metabolism

TABLE 2: PATHWAYS				Aty, DocId:34509390
				Doc. No. 079397.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways
1528	1850	NM 012896	t	
1528	1854	NM 012896	t	
1529	1803	NM 012897	General	
1530	1372	NM 012734	u	Aminosugars metabolism, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism
1531	1478	NM 012744	bb, General	Alanine and aspartate metabolism, Citrate cycle (TCA cycle), Pyruvate metabolism
1532	343	NM 012747	h, l	
1533	8829	NM 012749	General	
1534	20828	NM 012752	General	
1534	20829	NM 012752	l, General	
1534	20830	NM 012752	l, General	
1535	15174	NM 012756	b	
1536	21685	NM 012760	j, m, n	
1537	18068	NM 012762	t	
1538	1246	NM 012770	a, General	Purine metabolism
1539	1348	NM 012776	f	
1540	18135	NM 012791	w	
1541	18947	NM 012793	p, bb	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups
1542	960	NM 012796	u	Glutathione metabolism
1543	260	NM 012798	f, u	
1544	556	NM 012803	d	
1545	21729	NM 012804	q	
1546	15032	NM 012816	General	
1547	24895	NM 012817	General	
1548	18109	NM 012823	u, General	
1549	373	NM 012833	h, l, q, General	
1550	2855	NM 012838	e	
1551	11136	NM 012839	s	
1552	20885	NM 012842	a	egl
1552	20884	NM 012842	a, bb	egl
1553	18770	NM 012857	e	
1554	20674	NM 012861	i	
1555	13151	NM 012862	a, r, General	
1556	24617	NM 012870	General	
1557	20945	NM 012875	a, v	
1558	15872	NM 012879	o, r	
1559	495	NM 012880	z	
1559	494	NM 012880	c	
1560	23651	NM 012881	d, u, General	
1562	19477	NM 012891	q	
1563	18564	NM 012899	v, General	Porphyrin and chlorophyll metabolism
1564	7197	NM 012904	t, cc, General	
1564	7198	NM 012904	v, cc, General	
1565	20202	NM 012909	b, r	
1566	16581	NM 012911	c, j	
1566	16582	NM 012911	c	
1567	24431	NM 012912	General	
1568	18118	NM 012913	p	Oxidative phosphorylation
1569	6108	NM 012915	n	
1570	20757	NM 012923	c, j, aa	
1570	20755	NM 012923	i	
1571	2830	NM 012925	f	
1571	2831	NM 012925	f	
1572	1977	NM 012930	q	Fatty acid metabolism, Glycerolipid metabolism
1573	18694	NM 012931	j, l, m, z	
1574	13723	NM 012935	n	

TABLE 2: PATHWAYS					App. Docet No. 44924-5089WO
					Box No. 179847
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways	
1575	9109	NM 012939	j,y,z		
1575	19398	NM 012939	aa		
1576	223	NM 012945	b,cc		
1577	15058	NM 012950	cc		
1579	19111	NM 012963	g		
1580	19374	NM 012964	x		
1581	2554	NM 012967	t		
1581	2555	NM 012967	Loc.General		
1582	24526	NM 012973	c		
1583	986	NM 012976	c		
1584	16417	NM 012981	g		
1585	17393	NM 012992	d		
1586	23544	NM 013013	s		
1587	1588	NM 013026	k		
1588	17894	NM 013027	m		
1589	18300	NM 013030	s,v,General		
1589	18076	NM 013030	g,s,z		
1589	18078	NM 013030	s		
1589	18077	NM 013030	e,s,z		
1591	730	NM 013040	w		
1592	17401	NM 013043	i,o,General		
1593	16684	NM 013052	General		
1594	14421	NM 013053	u		
1595	15254	NM 013058	k		
1596	14997	NM 013059	s,z	Folate biosynthesis, Glycerolipid metabolism	
1596	14996	NM 013059	General	Folate biosynthesis, Glycerolipid metabolism	
1597	25676	NM 013069	aa		
1597	16924	NM 013069	o		
1596	24748	NM 013070	h,q		
1599	1529	NM 013082	d,General		
1600	1521	NM 013091	j,l,z,General		
1601	1685	NM 013096	c,aa		
1601	26150	NM 013096	c,j		
1601	1688	NM 013096	p		
1601	1689	NM 013096	c,p		
1601	1684	NM 013096	c,s,aa		
1602	20686	NM 013097	u,x,bb		
1602	20687	NM 013097	u,x,bb		
				Galactose metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism	
1603	1321	NM 013098	c		
1604	15296	NM 013102	i,m		
1606	23709	NM 013113	o,s,z,aa		
1606	23711	NM 013113	p		
1606	23710	NM 013113	s		
1607	1976	NM 013118	u		
1609	870	NM 013130	h		
1610	16650	NM 013132	u,General		
1611	650	NM 013134	h	Sterol biosynthesis	
1611	651	NM 013134	h,j,j	Sterol biosynthesis	
1612	1712	NM 013138	General		
1613	16982	NM 013144	o,v,General		
1614	21683	NM 013154	l,cc,General		
1614	21682	NM 013154	cc		
1615	3431	NM 013156	b,g,n		
1615	25567	NM 013156	v,General		
1615	3430	NM 013156	General		
1616	1309	NM 013159	w		
1616	1310	NM 013159	w		
1617	21723	NM 013174	w		
1618	1314	NM 013181	m		
1619	17357	NM 013183	p,bb,General		

TABLE 2: PATHWAYS				Atty. Docket No. 44921-5089WG
				Doc. No. 1193337
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Pathway
1620	1300	NM_013190	y	Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate cycle
1621	16448	NM_013197	c	Glycine, serine and threonine metabolism
1622	20656	NM_013200	b	Fatty acid metabolism, Glycerolipid metabolism
1623	397	NM_013214	f	
1624	20664	NM_013215	g,n,y	
1625	20728	NM_013217	v	
1626	1396	NM_013222	j	
1627	815	NM_013224	w	
1628	18305	NM_013226	v	
1629	21078	NM_016986	d	Fatty acid metabolism, Propanoate metabolism, Valine, leucine and Isoleucine degradation, beta-Alanine metabolism
1630	24649	NM_016988	v	Riboflavin metabolism
1631	15239	NM_016989	q,w	
1632	46	NM_016996	General	
1633	20714	NM_016999	t	Fatty acid metabolism, Tryptophan metabolism
1633	20713	NM_016999	t	Fatty acid metabolism, Tryptophan metabolism
1633	20711	NM_016999	q,t	Fatty acid metabolism, Tryptophan metabolism
1633	20715	NM_016999	q,t	Fatty acid metabolism, Tryptophan metabolism
1634	1698	NM_017000	e,n,p,General	Steroid biosynthesis
1635	1399	NM_017006	h,n,General	Glutathione metabolism, Pentose phosphate cycle
1637	18989	NM_017013	n	Glutathione metabolism
1638	21013	NM_017014	e,f	Glutathione metabolism
1638	21015	NM_017014	e,General	Glutathione metabolism
1639	11836	NM_017023	b	
1639	5475	NM_017023	b	
1639	25546	NM_017023	b,bb	
1640	17807	NM_017025	i,General	Cysteine metabolism, Glycolysis / Gluconeogenesis, Propanoate metabolism, Pyruvate metabolism
1641	24597	NM_017040	u	
1642	24696	NM_017048	f,j,z	
1643	24695	NM_017049	u	
1644	20876	NM_017050	j,n,z	
1645	910	NM_017059	f,j,m	
1645	912	NM_017059	i	
1646	1946	NM_017061	h	
1646	1942	NM_017061	t,General	
1646	1943	NM_017061	t	
1647	8062	NM_017066	d	
1648	6654	NM_017068	w	
1649	11153	NM_017073	s	Glutamate metabolism, Nitrogen metabolism
1650	923	NM_017076	General	
1651	1523	NM_017079	s	
1652	23660	NM_017080	s	Androgen and estrogen metabolism, C21-Steroid hormone metabolism
1653	275	NM_017081	b,d,General	Androgen and estrogen metabolism, C21-Steroid hormone metabolism
1654	16211	NM_017082	j,s,z	
1655	1552	NM_017084	j	Glycine, serine and threonine metabolism
1655	1550	NM_017084	y	Glycine, serine and threonine metabolism
1656	22552	NM_017087	a,k,x	
1657	8888	NM_017090	m	Purine metabolism
1658	10887	NM_017094	s,General	

TABLE 2: PATHWAYS				Atty. Docket No. 44921-508910 Doc. No. 1793397.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathway
1659	4393	NM_017101	a,y	
1660	24770	NM_017111	d	
1661	20745	NM_017113	e	
1661	20746	NM_017113	a	
1662	1375	NM_017122	w	
1663	12903	NM_017124	k	
1664	24885	NM_017138	r	
1664	24886	NM_017138	d,q	
1665	15363	NM_017147	q,u	
1666	13392	NM_017148	u,General	
1667	5351	NM_017150	q	
1668	16954	NM_017151	a,n	
1669	21643	NM_017152	g	
1670	1694	NM_017153	a,q	
1671	17104	NM_017160	bb,General	
1671	17106	NM_017160	u	
1671	17107	NM_017160	d,e	
1672	17686	NM_017165	n,q	Glutathione metabolism
1673	20702	NM_017166	c	
1674	3513	NM_017177	r	Glycerolipid metabolism
1675	19031	NM_017180	v,General	
1676	15437	NM_017187	x,z	
1676	15433	NM_017187	y	
1676	15434	NM_017187	x,z	
1677	24437	NM_017190	p	
1678	1542	NM_017193	j,l,m,z	
1679	14695	NM_017202	q,s	Oxidative phosphorylation
1679	14694	NM_017202	s,z	Oxidative phosphorylation
1680	1428	NM_017213	m	
1681	1622	NM_017216	g,j,s,z	
1682	13642	NM_017220	v	
1682	19976	NM_017220	w	
1683	1510	NM_017224	General	
1684	1811	NM_017228	j,l,m,z	
1686	17563	NM_017245	a,c,e,q	
1687	17502	NM_017248	r	
1687	17501	NM_017248	x	
1688	19	NM_017258	v,General	
1689	15300	NM_017259	i,v,cc,General	
			l,m,v,aa,cc,	
1689	15301	NM_017259	General	
1689	15299	NM_017259	i,y,cc,General	
1690	15224	NM_017264	d	
1691	3987	NM_017280	bb	Proteasome
1692	1447	NM_017281	l	Proteasome
1693	15535	NM_017283	s,bb	Proteasome
1694	12349	NM_017290	General	Oxidative phosphorylation
1695	15819	NM_017298	p	
1696	23826	NM_017299	v	
1696	23826	NM_017299	v	
1697	14003	NM_017305	j,l,m,y,z	Glutamate metabolism, Glutathione metabolism
1698	26109	NM_017306	q,s	
1698	18687	NM_017306	q,t	Fatty acid metabolism
1699	18142	NM_017314	q,s,aa	
1700	1894	NM_017320	t	
1701	20809	NM_017326	u	
1702	355	NM_017334	cc	
1703	16148	NM_017340	q,s	Fatty acid metabolism
1703	16150	NM_017340	a	Fatty acid metabolism
1704	20849	NM_017343	r,u,General	
1704	20848	NM_017343	b,General	
1705	606	NM_017350	b	

TABLE 2: PATHWAYS				Atty. Pocket No. 44921-5089W0 Doc. No. 1790817.1
Sequence ID No.	Identifier	GenBank Acc/Ref. Seq. ID No.	Metab. Code	Pathways
1706	1581	NM_013765	General	
1707	455	NM_019131	x	
1707	456	NM_019131	y,z	
1708	4532	NM_019134	b	
1709	1608	NM_019166	j,y,z	
1710	7489	NM_019169	c,General	
1711	17066	NM_019170	p	Prostaglandin and leukotriene metabolism
1712	23924	NM_019174	bb	Nitrogen metabolism
1713	24019	NM_019186	t	
1714	22063	NM_019195	d	
1715	2079	NM_019220	j,k,z	
1716	16284	NM_019229	i,m	
1717	985	NM_019233	b,cc	
1718	15503	NM_019237	k,x	
1718	15504	NM_019237	k,x	
1719	17908	NM_019242	i,v,cc,General	
1720	11218	NM_019247	c	
1721	15259	NM_019259	d,f	
1722	21443	NM_019262	aa,General	
1722	21444	NM_019262	i,General	
1723	117	NM_019266	o,bb	
1724	1145	NM_019280	w	
1725	22220	NM_019286	c	Bile acid biosynthesis,Fatty acid metabolism,Glycerolipid metabolism,Glycolysis / Gluconeogenesis,Tyrosine metabolism
1726	10015	NM_019289	i,m,t,x,General	
1726	10016	NM_019289	bb,General	
1727	21651	NM_019296	c,f,x	
1728	20751	NM_019301	s	
1729	645	NM_019345	bb	
1730	1301	NM_019349	c	
1731	3776	NM_019354	a,u	
1732	4592	NM_019356	General	
1733	1324	NM_019371	w	
1734	19577	NM_019377	e	
1735	24626	NM_019381	s	
1736	744	NM_019622	p	
1737	20716	NM_019623	c	Fatty acid metabolism,Tryptophan metabolism
1738	20709	NM_019904	x	
1739	574	NM_019905	u,General	Glyoxylate and dicarboxylate metabolism
1740	9096	NM_019908	j	
1741	20457	NM_020073	i,General	
1741	20458	NM_020073	General	
1741	20460	NM_020073	General	
1742	18713	NM_020075	r	
1742	18715	NM_020075	r	
1743	20493	NM_020076	p	Tryptophan metabolism
1744	16375	NM_020976	g	
1745	20818	NM_021261	k,General	
1746	15335	NM_021264	a	
1747	18729	NM_021578	k,z	
1748	19060	NM_021587	cc	
1749	17324	NM_021593	o,General	
1750	19679	NM_021653	General	
1750	19678	NM_021653	a,v,General	
1751	19665	NM_021688	u,General	
1752	19667	NM_021690	rm	
1754	22916	NM_021740	a	
1755	19710	NM_021744	t	
1755	19711	NM_021744	t	
1756	19712	NM_021745	t	

TABLE 2: PATHWAYS				Atty. Pocket No. 44924-5089W6 Doc. No. 1793357.1
Sequence ID No.	Identifier	GenBank Acc/Ref. Seq. ID No.	Model Code	Pathways
1757	1962	NM_021750	j,k,y,z	
1757	19824	NM_021750	a,bb	Taurine and hypotaurine metabolism
1758	25198	NM_021754	h	
1758	20035	NM_021754	b,n,s,v,General	
1759	20090	NM_021757	m	
1760	17885	NM_021765	aa	
1762	20161	NM_021838	cc,General	
1764	1203	NM_021997	k,z	
1765	23151	NM_022005	b	
				Aminosugars metabolism,Fructose and mannose metabolism,Galactose metabolism,Glycolysis / Gluconeogenesis,Starch and sucrose metabolism
1767	17101	NM_022179	bb	
				Aminosugars metabolism,Fructose and mannose metabolism,Galactose metabolism,Glycolysis / Gluconeogenesis,Starch and sucrose metabolism
1767	17100	NM_022179	bb	
1768	20257	NM_022180	w,General	
1768	25699	NM_022180	i	
1768	10860	NM_022180	p	
1769	23780	NM_022183	k,x	
1770	20312	NM_022224	o	
1771	6585	NM_022266	d,p,cc	
1772	17161	NM_022298	l,v,cc,General	
1772	17162	NM_022298	u	
1772	17160	NM_022298	u	
1772	17158	NM_022298	q	
1773	11454	NM_022381	l,aa,General	
1773	11455	NM_022381	l,General	
1774	13480	NM_022390	s	Folate biosynthesis
1775	15184	NM_022391	z	
1776	22413	NM_022392	h	
1776	22414	NM_022392	n	
1777	22499	NM_022393	t	
1779	24537	NM_022399	e	
1779	24539	NM_022399	y	
1780	1141	NM_022401	o,General	
1781	1069	NM_022402	g	
1782	8211	NM_022500	j,n,s	
1782	8212	NM_022500	n,s	
1783	6815	NM_022503	s	Oxidative phosphorylation
1784	4259	NM_022504	q,w	
1785	1611	NM_022509	j	
				Butanoate metabolism,Fatty acid metabolism,Valine, leucine and isoleucine degradation
1786	2236	NM_022512	y,z	
1787	3026	NM_022514	a	
1787	3027	NM_022514	a,g,r,aa	
1788	2696	NM_022515	a,d	
1788	2697	NM_022515	n,w,aa	
1789	3900	NM_022516	h	
1790	4151	NM_022518	o	
				Arginine and proline metabolism,Urea cycle and metabolism of amino groups
1791	4242	NM_022521	c	
1792	4412	NM_022523	o	
1793	6641	NM_022533	General	
1794	8097	NM_022536	a	
1795	8597	NM_022538	c,r,u	
1795	8598	NM_022538	u	
1796	9296	NM_022541	o	
1797	21063	NM_022585	h	

TABLE 2: PATHWAYS				Atty. Docket No. 44924-5039WO Doc. No. 1798397.4	
Sequente ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Modal Code	Pathways	
1799	20781	NM_022591	z		
1800	20803	NM_022592	n	Carbon fixation, Penlose phosphate cycle	
1801	20925	NM_022594	q		
1802	20944	NM_022597	aa		
1803	21024	NM_022599	o, General		
1804	2250	NM_022643	General		
1805	17567	NM_022672	a, y		
1806	17661	NM_022674	bo		
1807	24563	NM_022676	b		
1807	24564	NM_022676	b, x		
1808	20506	NM_022686	l		
1809	20508	NM_022688	g		
1810	17586	NM_022694	k		
1811	17730	NM_022697	a		
1811	17729	NM_022697	q		
1812	154	NM_022849	t		
1813	127	NM_022855	h		
1814	152	NM_022856	j		
1816	18101	NM_022948	z		
1816	18103	NM_022948	u		
1817	21491	NM_022951	w		
1818	15742	NM_022958	y		
1819	9286	NM_023027	t, w		
1820	23215	NM_023102	z		
1821	21238	NM_024125	cc, General	i16, interact5-1	
1821	21239	NM_024125	cc, General	i16, interact5-1	
1822	353	NM_024127	i, n, General		
1822	354	NM_024127	i, n, General		
1822	352	NM_024127	h, General		
1823	17227	NM_024131	x		
1824	1598	NM_024134	l		
1825	1162	NM_024153	d	Porphyrin and chlorophyll metabolism	
1826	7863	NM_024156	c	Oxidative phosphorylation, Type III protein secretion system	
1827	22079	NM_024157	x		
1828	16476	NM_024162	General		
1829	17765	NM_024351	b, s, v		
1830	8879	NM_024360	h		
1831	20772	NM_024363	x		
1832	2812	NM_024386	c	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation	
1833	335	NM_024387	i, y	Porphyrin and chlorophyll metabolism	
1834	21	NM_024388	cc		
1834	22	NM_024388	cc		
1836	9929	NM_024392	f	Androgen and estrogen metabolism	
1837	3582	NM_024396	aa		
1838	19993	NM_024398	a, p, s, aa		
1839	10789	NM_024399	o		
1840	22626	NM_024400	cc, General		
1841	13633	NM_024403	g, General		
1841	13634	NM_024403	g, General		
1842	23387	NM_024404	b, General		
1843	21038	NM_024484	h	Glycine, serine and threonine metabolism	
1844	1853	NM_030826	s	Glutathione metabolism	
1845	15111	NM_030827	e, General		
1845	15112	NM_030827	y, z		
1845	15110	NM_030827	General		
1846	808	NM_030837	k, m		
1847	4057	NM_030844	k		
1848	1221	NM_030845	l		
1849	21509	NM_030847	x		
1850	1928	NM_030872	v		

TABLE 2: PATHWAYS				Atty. Docket No. 44924-6089WO
				Doc. No. 1738897.1
Sequence ID No.	Identifier	GenBank Acc/Ref. Seq. ID No.	Metabolic Code	Pathway
1851	17342	NM_030873	u	
1852	24648	NM_030985	u	
1852	25453	NM_030985	General	
1853	21802	NM_030987	h	
1854	23109	NM_031000	f,s,z	Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Pentose and glucuronate interconversions
1855	134	NM_031003	a,u	
1856	25461	NM_031009	o	
1857	1845	NM_031010	t	Prostaglandin and leukotriene metabolism
1857	25517	NM_031010	c,t	Prostaglandin and leukotriene metabolism
1858	16562	NM_031020	f	
1859	1480	NM_031021	f	
1860	1719	NM_031024	n	
1861	1350	NM_031030	h	
1862	16775	NM_031031	General	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups
1863	691	NM_031034	w	
1864	15886	NM_031035	z	
1866	3608	NM_031044	k, General	Histidine metabolism
1866	3610	NM_031044	d, General	Histidine metabolism
1867	15137	NM_031051	s	
1868	514	NM_031056	General	
1869	17269	NM_031057	General	Inositol metabolism, Propanoate metabolism, Valine, leucine and isoleucine degradation
1870	11849	NM_031065	a	
1871	1855	NM_031074	h	
1872	4683	NM_031083	d	
1873	15202	NM_031093	a	
1873	15201	NM_031093	a,n	
1874	12639	NM_031099	aa	
1875	20812	NM_031100	a	
1876	16938	NM_031103	w	
1877	19268	NM_031104	q	
1878	16929	NM_031108	q	
1879	10878	NM_031110	q,bb	
1880	19162	NM_031111	aa	
1880	19161	NM_031111	a,bb	
1881	24615	NM_031112	a,y	
1882	20639	NM_031113	a,q	
1883	19040	NM_031114	l,m, General	
1884	16349	NM_031115	u	
1885	14970	NM_031127	General	
1886	1814	NM_031134	n,q	
1887	13359	NM_031135	General	
1888	15062	NM_031136	a	
1888	18359	NM_031136	a	
1889	15185	NM_031140	General	
1890	21625	NM_031144	a,e	
1891	238	NM_031152	bb	
1891	240	NM_031152	bb	
1892	15277	NM_031237	g	
1893	18083	NM_031315	q	
1893	1858	NM_031315	q	
1894	15663	NM_031318	General	
1895	1422	NM_031324	bb, General	
1896	18597	NM_031325	g,bb	Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism
1897	11259	NM_031327	i, cc, General	
1898	4235	NM_031330	General	

TABLE 2: PATHWAYS				Atty. Docket No. 44921-5039WO Doc. No. 1743337.1	
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Metabolic Code	Pathway	
1899	18375	NM 031331	l,m		
1900	3519	NM 031334	cc		
1901	20698	NM 031357	b		
1903	634	NM 031509	n	Glutathione metabolism	
1903	25525	NM 031509	n	Glutathione metabolism	
1903	25069	NM 031509	b,n,w		
1903	635	NM 031509	z	Glutathione metabolism	
1904	848	NM 031517	t		
1905	1672	NM 031523	a		
1905	16245	NM 031523	a,d,u		
1905	16244	NM 031523	a		
1906	9370	NM 031527	w		
1907	20448	NM 031530	General		
1907	20449	NM 031530	General		
1908	14633	NM 031533	u	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	
1909	16048	NM 031541	f		
1910	4011	NM 031543	c,q	Fatty acid metabolism, Tryptophan metabolism	
1910	4010	NM 031543	c,q	Fatty acid metabolism, Tryptophan metabolism	
1910	4012	NM 031543	q	Fatty acid metabolism, Tryptophan metabolism	
1911	28	NM 031546	General		
1912	24640	NM 031548	h,cc		
1913	17149	NM 031549	x		
1913	17151	NM 031549	x		
1914	13105	NM 031552	w		
1915	15411	NM 031559	d,r	Fatty acid metabolism, Glycerolipid metabolism	
1916	16164	NM 031563	a,y		
1917	9621	NM 031570	bb		
1917	9620	NM 031570	w,bb		
1918	546	NM 031573	f		
1919	1921	NM 031576	f		
1919	1920	NM 031576	r		
1920	24219	NM 031579	l,General		
1921	770	NM 031584	k,x		
1922	18008	NM 031588	cc		
1922	18005	NM 031588	h		
1922	18011	NM 031588	cc,General		
1923	1584	NM 031595	k		
1924	24235	NM 031614	v	Pyrimidine metabolism	
1924	24234	NM 031614	General	Pyrimidine metabolism	
1925	1639	NM 031627	l,l,v		
1926	1727	NM 031642	m,General		
1927	20766	NM 031643	y		
1929	1993	NM 031655	k,l,m,General		
1930	2057	NM 031660	e		
1931	15039	NM 031672	k,General		
1932	15175	NM 031682	bb	Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Tryptophan metabolism, Valine, leucine and isoleucine degradation	
1933	1004	NM 031685	v		
1934	19727	NM 031687	a,q,s		
1935	20404	NM 031700	l,r,y		
1935	20405	NM 031700	o,r		

TABLE 2: PATHWAYS				Att. Doc. No. 44981-5089W
				Doc. No. 179337.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways
1936	811	NM_031705	General	Pantothenate and CoA biosynthesis, Pyrimidine metabolism, beta-Alanine metabolism
1936	812	NM_031705	o,v,bb,General	Pantothenate and CoA biosynthesis, Pyrimidine metabolism, beta-Alanine metabolism
1937	16204	NM_031706	g,bb	
1937	16205	NM_031706	a,y	
1938	24081	NM_031708	m	
1939	16918	NM_031709	a,q	
1940	1081	NM_031712	General	
1941	1340	NM_031715	b,n,u,cc, General	Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate cycle
1942	23884	NM_031731	j,s	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tyrophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
1943	10241	NM_031740	d	
1944	1214	NM_031741	r	
1944	1215	NM_031741	r	
1945	20724	NM_031753	h	
1946	20753	NM_031763	h	
1946	20752	NM_031763	y	
1947	14953	NM_031774	p	
1948	14184	NM_031776	t,General	Purine metabolism
1948	14185	NM_031776	d,o,t,General	Purine metabolism
1949	1189	NM_031789	c	
1950	16155	NM_031810	d,z	
1950	16156	NM_031810	d	
1951	17194	NM_031814	z	
1952	17535	NM_031816	bb	
1953	2655	NM_031821	i,l,m,aa	
1954	10167	NM_031830	i	
1955	22321	NM_031832	o,t,u,General	
1956	4748	NM_031834	e,t	
1956	4749	NM_031834	e,t	
1957	7914	NM_031835	e	Alanine and aspartate metabolism, Glycine, serine and threonine metabolism
1958	8385	NM_031836	h	
1958	8384	NM_031836	h	
1959	10268	NM_031838	a	
1959	10269	NM_031838	aa	
1959	10267	NM_031838	n,aa	
1960	15077	NM_031841	b	
1961	16726	NM_031855	x	Fructose and mannose metabolism
1962	25802	NM_031969	a	
1962	19191	NM_031969	c	
1962	19195	NM_031969	r	
1962	19190	NM_031969	p	
1963	17734	NM_031970	v,General	
1964	1475	NM_031971	v	
1965	15470	NM_031978	f	
1966	18502	NM_031984	c	
1967	19768	NM_031986	v,aa,General	
1968	723	NM_032084	n	

TABLE 2: PATHWAYS				App. Booklet No. 44921-5039 WO
				Doc. No. 1793897.1
Sequence ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Pathways
1969	17935	NM_032615	a	
1970	16831	NM_033095	n	
1971	25468	NM_033234	c,z	
1971	25469	NM_033234	c	
1971	17832	NM_033234	c,p	
1971	17829	NM_033234	c,z	
1972	4723	NM_033235	z	
1973	1409	NM_033349	p, General	Pyruvate metabolism
1974	19998	NM_033352	General	
1975	1410	NM_052798	d	
1976	15028	NM_052809	f	Cysteine metabolism, Taurine and hypotaurine metabolism
1977	5176	NM_053297	u	
1978	7660	NM_053299	i	
1979	5117	NM_053310	p	
1981	17473	NM_053319	a,v	
1982	25480	NM_053329	g	
1982	21977	NM_053329	y	
1983	14926	NM_053330	f	
1983	14929	NM_053330	e, General	
1984	16407	NM_053332	c,e	
1985	15790	NM_053341	j,x	
1986	6154	NM_053356	p	
1987	9215	NM_053374	i	
1988	6416	NM_053380	General	
1989	19113	NM_053395	a	
1990	2242	NM_053433	n, General	
1991	5561	NM_053438	y	
1992	14670	NM_053439	n, General	
1993	17102	NM_053440	w	
1994	24762	NM_053442	General	
1995	8085	NM_053453	General	
1996	4822	NM_053463	d	
1997	21866	NM_053472	p	
1998	9573	NM_053475	h	
1999	18137	NM_053480	k	
2000	15556	NM_053483	y	
2001	16394	NM_053485	General	
2002	4290	NM_053487	j,y	
2004	18826	NM_053523	d	
2005	7764	NM_053525	aa	
2006	14199	NM_053538	c	
2007	1058	NM_053539	c,d	
2008	4327	NM_053563	General	
2009	1342	NM_053573	h	
2010	19254	NM_053576	h,s	Methane metabolism, Phenylalanine metabolism
2010	19253	NM_053576	h	Methane metabolism, Phenylalanine metabolism
2011	3049	NM_053582	p, cc, General	
2011	3050	NM_053582	o, General	
2012	21423	NM_053586	s,y	Oxidative phosphorylation
2013	21445	NM_053587	lv	
2014	20871	NM_053591	j,l	
2014	20870	NM_053591	i	
2015	21044	NM_053594	d	
2016	21709	NM_053596	k	
2016	21708	NM_053596	z	
2017	1597	NM_053611	t	
2018	5565	NM_053618	General	
2019	13004	NM_053623	t	Fatty acid metabolism

TABLE 2: PATHWAYS					Atty. Docket No. 44924-1609/WO Doc. No. 179397.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways	
2020	1127	NM_053626	g	Arginine and proline metabolism, D-Arginine and D-ornithine metabolism, Glycine, serine and threonine metabolism	
2021	18644	NM_053648	n		
2022	21637	NM_053653	p		
2023	3454	NM_053662	cc		
2024	16121	NM_053698	h,j,z		
2024	16122	NM_053698	h,j,z		
2025	25379	NM_053713	General		
2025	13622	NM_053713	General		
2026	15376	NM_053747	h		
2027	1218	NM_053748	b		
2028	1137	NM_053763	y		
2029	15996	NM_053769	cc		
2030	8652	NM_053774	g		
2031	14664	NM_053806	General		
2032	4361	NM_053812	k		
2034	15002	NM_053819	b,x,bb,General		
2034	15003	NM_053819	b,l,x,bb,General		
2035	16173	NM_053822	t		
2036	17154	NM_053835	z		
2037	20868	NM_053843	t		
2037	20869	NM_053843	t		
2040	714	NM_053863	y		
2041	19781	NM_053883	b		
2041	19780	NM_053883	b		
2042	1454	NM_053887	General		
2043	1660	NM_053891	g		
2044	712	NM_053896	k		
2045	753	NM_053897	k		
2046	794	NM_053902	General	Tryptophan metabolism	
2047	17937	NM_053911	t		
2048	8188	NM_053927	General		
2050	1628	NM_053936	h		
2051	13954	NM_053955	General		
2052	408	NM_053961	General		
2052	19691	NM_053961	a		
2052	16190	NM_053961	q		
2052	21355	NM_053961	j,l,y,z		
2055	15136	NM_053971	aa		
2055	15135	NM_053971	d		
2056	1764	NM_053974	h		
2057	1292	NM_053980	l		
2058	15468	NM_053982	q		
2059	15642	NM_053985	General		
2060	21056	NM_054001	t		
2061	17326	NM_054008	o		
2061	17327	NM_054008	cc		
2061	17329	NM_054008	g,o,cc		
2062	25253	NM_057099	j,l,m,p,z		
2062	22849	NM_057099	j,l		
2063	19657	NM_057103	b,cc		
2064	5492	NM_057105	w	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	
2064	15126	NM_057105	tr	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	

TABLE 22: PATHWAYS				Atty. Docket No. 44924-5089WO
				Doc. No. 1793397.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways
2064	15125	NM_057105	s	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
2066	15391	NM_057114	n	
2067	727	NM_057123	m	
2068	915	NM_057124	s	
2069	15151	NM_057131	k	
2070	1892	NM_057144	b	
2071	12333	NM_057155	f	
2071	12331	NM_057155	v, General	
2071	12332	NM_057155	f, General	
2072	17477	NM_057194	a, General	
2073	15408	NM_057197	p, t	
2073	15409	NM_057197	t	
2074	7866	NM_057198	h	Glutamate metabolism, Purine metabolism
2075	14125	NM_057208	h, j, y, z	
2076	1743	NM_057210	k, s	
2077	10498	NM_076617	a	
2078	8820	NM_080399	n	
2079	15701	NM_080581	j, m, y, z	
2079	20105	NM_080581	aa	
2080	16109	NM_080585	c	
2081	1757	NM_080766	d	
2082	7108	NM_080778	y	
2083	132	NM_080782	k	
2083	133	NM_080782	l	
2084	20122	NM_080867	General	
2085	6143	NM_080882	e	
2086	9952	NM_080902	h	
2087	17546	NM_130401	b	
2088	21695	NM_130411	c, x	
2089	21391	NM_130416	x, General	
2090	20694	NM_130430	General	
2090	19818	NM_130430	cc	
2090	18810	NM_130430	e, s	
2091	18293	NM_130433	q	Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Phenylalanine metabolism, Valine, leucine and isoleucine degradation
2092	25064	S45392	a, n	
2093	3244	S63519	u	
2094	25501	S63521	q	
2095	16248	S68135	h	
2096	18647	S69316	q	
2097	24351	S74257	v	
2098	25066	S75280	d	
2099	1460	S76054	j, l, m, x, y,	
2100	25539	S76742	General	
2101	15400	S76779	c	
2102	24469	S77858	n	
2103	25545	S77900	k, s	
2103	21583	S77900	k	
2104	10260	S81497	s	
2105	3609	S82579	k	Histidine metabolism
2106	111	U02506	u	
2107	14959	U03390	a, q, General	
2109	2010	U05675	b, x, bb	
2110	15462	U06230	d	
2112	1563	U07201	s, General	
2113	627	U09229	h	

TABLE 2: PATHWAYS				Atty. Record No. 44024-5049W6 Rec. No. 1793897.1
Sequence ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Pathways
2114	809	U17035	General	
2115	16675	U17565	k,x,bb	
2116	25587	U20110	r	
2117	96	U20795	r	
2118	25589	U21718	h,aa	
2119	22196	U21719	h	
2120	17118	U25746	s	
2121	1537	U27518	g,h,n	
2122	1558	U28504	bb	
2123	16193	U30831	n	
2124	17480	U31598	z	
2125	18302	U33500	General	
2126	25599	U34897	y	
2127	1394	U37099	h	
2128	244	U38376	n	
2129	1623	U41164	h	
2130	15851	U42719	t,t,x,General	
2131	17585	U47315	s,z	
2132	21654	U53184	t,t,General	
2133	1439	U57391	w	
2134	725	U62316	bb	
2137	2153	U75404	b,cc,General	
2139	4956	U76714	j,y	
2140	4477	U77829	l,m	
2141	21703	U82591	z	
2142	977	U89744	s	
2143	23282	U90725	h	
2144	22005	U96490	m	
2146	819	X02264	j,z	Carbon fixation,Fructose and mannose metabolism,Glycolysis / Gluconeogenesis,Inositol metabolism,Pentose phosphate cycle
2147	818	X02291	e,j,z	Carbon fixation,Fructose and mannose metabolism,Glycolysis / Gluconeogenesis,Inositol metabolism,Pentose phosphate cycle
2148	20618	X02904	n,q	Glutathione metabolism
2149	16401	X04979	c	
2150	20513	X05684	o,r	Carbon fixation,Glycolysis / Gluconeogenesis,Purine metabolism,Pyruvate metabolism
2151	25084	X06769	cc	
2152	672	X13722	h	
2153	25675	X14181	n	
2153	20810	X14181	n,q,w	
2154	18541	X14671	y	
2155	25679	X15013	q	
2155	19244	X15013	c,q,w	
2158	15626	X17665	a	
2157	1893	X15129	t	Glycerolipid metabolism,Phospholipid degradation,Prostaglandin and leukotriene metabolism
2158	25666	X15136	bb	
2158	10619	X15136	aa,bb	
2159	18250	X15706	a,q,w	
2160	20872	X15707	a	
2161	516	X52711	c	
2162	25689	X52815	g	
2163	20427	X53378	w	
2164	18606	X53504	General	
2165	1463	X54467	d,u,General	
2166	24577	X55153	s,v	
2167	10344	X57405	l,m	

TABLE 2: PATHWAYS			Atty. Docket No. 44924-5083WO Doc. No. 1798397	
Sequence ID No.	Identifier	GenBank Acc/Ref. Seq. ID No.	Metabol Code	Pathways
2166	15106	X57529	g,n,q	
2169	5667	X56200	e,bb	
2169	18611	X56200	a,v	
2170	17175	X58389	w	
2171	25702	X58465	w	
2171	10109	X58465	c,q	
2172	25705	X59375	c,aa,General	
2173	25709	X59737	u	
2174	18354	X59859	General	
2174	18355	X59859	t	
2175	21657	X61381	General	
2176	25718	X62145	bb,General	
2176	15875	X62145	a,q,v	
2177	13646	X62166	bb	
2178	25721	X62325	p	
2179	16012	X62875	m,s,z	
2180	25730	X63369	cc	
2181	25089	X63594	General	
2181	25090	X63594	cc,General	
2182	20844	X65226	n,w	
2183	20879	X65296	j,y	
2184	25736	X68782	c	
2185	16426	X70369	c	
2186	16300	X70706	u	
2187	24232	X75207	c	
2188	16272	X76456	n,p	
2189	25741	X76489	u	
2190	23302	X76949	h	
2191	25747	X81448	General	
2192	24115	X81449	u	
2193	25754	X89696	g	
2194	25097	X90642	y,z	
2195	12978	X96437	cc,General	
2197	4594	Y07704	c	
2198	25777	Y08355	g,p,General	
2199	15986	Y09945	bb,General	
2200	20890	Y13275	k	
2201	21914	Y13336	d	
2202	406	Z11995	c,General	
2203	18352	Z12298	t	
2204	17481	Z49761	k	
2205	8664	Z75029	r,v	
2206	2459	AA964755	cc	
2207	23830	AA956638	aa	
2208	6100	X73524	k	
2209	439	Z22607	w	
2210	8665	AI071965	v	
2211	155	U32681	t	
2212	19252	AA892041	s	Methane metabolism,Phenylalanine metabolism
2213	15582	AI232320	q	
2214	17541	M26125	n	
2215	18609	M30689	i	
2216	6282	AI177125	g	
2217	23859	AI072161	f	
2218	21011	H52169	e	Glutathione metabolism
2220	2572	AI177143	b	
2221	25419	M22922	a	

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4-924-5083WC Doc. No. 162837v.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1	6949	AA012785	q		
2	25098	AA108277	h,v		
3	17312	AA108308	r		EST, Moderately similar to A Chain A, Mdm2 Bound To The Transactivation Domain Of P53 [SUB 17-125 [H.sapiens], mouse double minute 2, human homolog of, p53-binding protein
4	16882	AA684537	o		NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SODH)
5	6049	AA685178	y		EST, Weakly similar to T30827 nascent polypeptide-associated complex alpha chain, non-muscle splice form - mouse [M.musculus], FKSG17, Homo sapiens alpha-NAC gene for nascent polypeptide-associated complex component, KIAA0363 protein, expressed sequence AL022831, nascent-polypeptide-associated complex alpha polypeptide
6	4426	AA685974	i,m		
7	21815	AA686423	g		EST, Weakly similar to T46390 hypothetical protein DKFZp434C1920.1 [H.sapiens], hepatocellular carcinoma-associated antigen 59
8	1600	AA686470	i	DNA-damage inducible transcript 3, DNA-damage-inducible transcript 3	DNA-damage Inducible transcript 3, EST, Moderately similar to GA15_HUMAN GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 [H.sapiens], myozenin
8	1599	AA686470	i	DNA-damage inducible transcript 3, DNA-damage-inducible transcript 3	DNA-damage inducible transcript 3, EST, Moderately similar to GA15_HUMAN GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 [H.sapiens], myozenin
9	21997	AA799325	u		
10	18396	AA799330	v		
11	6561	AA799412	f,j		ESTs, Highly similar to ERR3_HUMAN ESTROGEN-RELATED RECEPTOR GAMMA [H.sapiens], Untitled, estrogen related receptor, alpha, estrogen related receptor, beta, estrogen-related receptor beta
12	16538	AA799449	k		ESTs, Moderately similar to NPL4_HUMAN NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 4 [H.sapiens], ESTs, Weakly similar to NPL4_HUMAN NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 4 [H.sapiens], SET translocation, nucleosome assembly protein 1-like 1, nucleosome assembly protein 1-like 4
13	23294	AA799472	u		
14	18290	AA799497	r		CGI-116 protein

TABLE 5: HUMAN HOMOLOGUE ANNOTATIONS					Atiy, DocId:344394-3383W0 Doc. No. 1193337-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
15	18981	AA799523	e		DAZ associated protein 1, ESTs, Highly similar to ROA1 RAT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 [R.norvegicus], ESTs, Moderately similar to Up1, The Two Rna-Recognition Motif Domain Of Hnmp A1 (SUB 3-184 [H.sapiens], ESTs, Weakly similar to ROA1 RAT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 [R.norvegicus], ESTs, Weakly similar to ROA2 MOUSE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 [M.musculus], RIKEN cDNA 3010025E17 gene, Ras-GTPase activating protein SH3 domain-binding protein 2, Ras-GTPase-activating protein SH3-domain binding protein, cell death regulator avien, heterogeneous nuclear ribonucleoprotein A1, heterogeneous nuclear ribonucleoprotein A2/B1
16	20843	AA799545	h		EST, Moderately similar to A38983 TCP1 ring complex protein TRICS [H.sapiens], T-complex 1, chaperonin containing TCP1, subunit 3 (gamma), expressed sequence A1528772, t-complex 1, t-complex protein 1
17	16993	AA799560	b		
18	16576	AA799570	d		
19	18361	AA799591	i		EST, Moderately similar to I38369 beta tubulin [H.sapiens], ESTs, Highly similar to I38370 beta-tubulin [H.sapiens], ESTs, Highly similar to T08726 tubulin beta chain [H.sapiens], ESTs, Highly similar to TB1 RAT TUBULIN BETA CHAIN [R.norvegicus], ESTs, Moderately similar to I38370 beta-tubulin [H.sapiens], RIKEN cDNA 2410129E14 gene, RIKEN cDNA 4930447K03 gene, RIKEN cDNA 4930542G03 gene, Rat mRNA for beta tubulin T beta15, beta tubulin 1, class VI, tubulin, beta 3, tubulin, beta, 2
20	17712	AA799598	z		
22	18346	AA799718	l		
23	8768	AA799726	l		
24	11687	AA799732	w		DiGeorge syndrome chromosome region 6, DiGeorge syndrome critical region gene 6, DiGeorge syndrome critical region gene 6 like
25	18349	AA799744	u		
26	17494	AA799751	n		
27	18360	AA799771	General		
28	18880	AA799801	w		
29	20998	AA799803	z		EST, Moderately similar to MAS2, HUMAN MANNAN-BINDING LECTIN SERINE PROTEASE 2 PRECURSOR [H.sapiens], Rattus norvegicus mRNA for serine protease, complete cds, complement C1r-like proteinase precursor, complement component 1, r subcomponent, complement component 1, s subcomponent, protein C

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44924-50830WG Reg. No. 9728397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Interpretive Cluster Name
30	21006	AA799861	c		interferon regulatory factor 7 ESTs, Moderately similar to Up1, The Two Rna-Recognition Motif Domain Of Hnmp A1 [SUS 3-184 [H.sapiens], ESTs, Weakly similar to ROA1 RAT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 [R.norvegicus], ESTs, Weakly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], Human DNA sequence from clone RP11-51N22 on chromosome 13 Contains ESTs, STSs and GSSs, Contains an HNRPA1 (heterogeneous nuclear ribonucleoprotein A1) pseudogene, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear ribonucleoprotein A1
31	15011	AA799893	General		
32	20811	AA799899	a		EST, Moderately similar to RL1X_HUMAN 60S RIBOSOMAL PROTEIN L18A [H.sapiens], EST, Weakly similar to RL1X_HUMAN 60S RIBOSOMAL PROTEIN L18A [H.sapiens], EST, Weakly similar to S47353 ribosomal protein L18a, cytosolic [H.sapiens], ESTs, Highly similar to RL1X_HUMAN 60S RIBOSOMAL PROTEIN L18A [H.sapiens], RIKEN cDNA 2510019J09 gene, ribosomal protein L18a
33	23202	AA799971	General		
34	4832	AA800190	b		ESTs, Moderately similar to 1701409A glycogen phosphorylase [H.sapiens], ESTs, Weakly similar to 1701409A glycogen phosphorylase [H.sapiens], phosphorylase, glycogen; brain
35	21656	AA800202	d		
36	18433	AA800218	j,y,z		
37	6386	AA800235	u		
38	18442	AA800258	h,k		
39	21092	AA800380	y		DNA segment, Chr 14, University of California at Los Angeles 2, Hydroxysteroid dehydrogenase, 11 beta type 1, expressed sequence C79874, hydroxysteroid (11-beta) dehydrogenase 1, hydroxysteroid 11-beta dehydrogenase 1, hydroxysteroid 17-beta dehydrogenase 11, retinal short-chain dehydrogenase/reductase retSDR2
40	17325	AA800587	General		ESTs, Highly similar to GSHG_MOUSE GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (GSHPX-GI) [M.musculus], Glutathione peroxidase 1, glutathione peroxidase 1, glutathione peroxidase 2 (gastrointestinal)
41	13930	AA800613	cc, General		zinc finger protein 36, zinc finger protein homologous to Zfp-36 in mouse
42	21372	AA800693	v		
42	21373	AA800693	s		
43	18161	AA800701	k		
44	6595	AA800753	w		
45	13348	AA800928	General		

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44924-308W3 Doc. No. 1728397.1
Seq. ID No.	Accession	GenBank Acc./Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
46	23115	AA801165	o,y		EST, Weakly similar to H2AL_HUMAN HISTONE H2A.L (H2A.L) [H.sapiens], H2A histone family, member L, similar to H2A histone family, member A (H.sapiens)
47	12399	AA801307	General		
48	7543	AA801395	General		
49	24237	AA817726	l,General		
50	11215	AA817921	o		
51	5985	AA818005	g		
52	11336	AA818016	x		EST, Weakly similar to RB6K MOUSE RABKINESIN-6 [M.musculus], RAB6 interacting, kinesin-like (rabkinesin 6), RIKEN cDNA 3110001D19 gene, Rab6, kinesin-like
53	2845	AA818026	k,General		COP9 (constitutive photomorphogenic), subunit 6 (Arabidopsis), Homo sapiens cDNA FLJ14833 fls, clone OVARC1001171, moderately similar to Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, IFP36, RIKEN cDNA 0610037M02 gene, eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD), hypothetical protein MGC13045, proteasome (prosome, macropain) 26S subunit, non-ATPase, 7
54	16756	AA818089	l,k,General		glycyl-HRNA synthetase
55	17771	AA818224	e,g,p,General		EST, Weakly similar to S45140 tubulin beta chain [H.sapiens], RIKEN cDNA 2410129E14 gene, RIKEN cDNA 4930542G03 gene, tubulin, beta 2, tubulin, beta 5, tubulin, beta polypeptide, tubulin, beta, 2
56	6522	AA818261	g,m		
57	5924	AA818359	y		
58	7806	AA818421	b,aa		
59	8237	AA818512	v		
60	17434	AA818574	h		
61	8728	AA818615	General		
62	6054	AA818658	b,v,cc,General	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), heparin binding epidermal growth factor-like growth factor	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), expressed sequence AW047313, heparin binding epidermal growth factor-like growth factor
63	11590	AA818721	d		
64	4291	AA818741	q,General		
65	4330	AA818747	o,General		
66	19723	AA818761	v,General		
67	13684	AA818770	h,l,m		
68	6322	AA818801	k		
69	7690	AA818875	General		expressed sequence AV066530, guanylate cyclase activator 2B (uroguanylin), guanylate cyclase activator 2b (retina)
70	4952	AA818907	q,General		
71	6094	AA818911	l		
72	10985	AA818998	o,General		
73	6120	AA819008	t		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4:924-500W0 Ex. No. 179337-1	
Seq. ID No.	Identifier	GenBank Acc# Ref. Seq. ID No.	Model Code	Homologues Gene Name	Homologues Cluster Name	
					CocoaCrisp, ESTs, Weakly similar to JC5308 testis-specific, vespid, and pathogenesis-related protein 1 precursor [H.sapiens], Homo sapiens. Similar to RIKEN cDNA 1700011E04 gene, clone MGC:26856 IMAGE:4822995, mRNA, complete cds, RIKEN cDNA 1200009H11 gene, RIKEN cDNA 1700011E04 gene, RIKEN cDNA 4921508O11 gene, acidic epididymal glycoprotein-like 1, glioma pathogenesis-related protein, specific granule protein (28 kDa), testis specific gene 1, testis specific protein 1, testis specific protein 1 (probe H4-1 p3-1)	
74	2586	AA819081	c			
76	6438	AA819269	o			
77	24721	AA819306	d,w			
78	6250	AA819376	o,y		ESTs, Weakly similar to T17246 hypothetical protein DKFZp586M0617.1 [H.sapiens], KIAA0263 gene product, mammalian inositol hexakisphosphate kinase 2 HYA22 protein, conserved gene amplified in osteosarcoma, nuclear LIM interactor-interacting factor	
80	6281	AA819517	j			
81	10141	AA819526	j			
82	6551	AA819558	t			
83	6723	AA819653	r			
84	14958	AA819744	aa			
85	19433	AA819776	v		ESTs, Highly similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus], expressed sequence A1024080, expressed sequence C81438, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1	
86	6204	AA819889	aa			
87	22820	AA848315	General		GMPR2 for guanosine monophosphate reductase isolog, IMP (inosine monophosphate) dehydrogenase 2, RIKEN cDNA Z31000AP21 gene, RIKEN cDNA 5730544D12 gene, expressed sequence AA959850, guanosine monophosphate reductase, inosine 5'-phosphate dehydrogenase 2	
88	6614	AA848389	bb			
89	21125	AA848437	General			
90	23504	AA849496	q		ESTs, Moderately similar to IF4B_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 4B [H.sapiens], eukaryotic translation initiation factor 4B	
91	18532	AA848675	g		ESTs, Highly similar to FMO2_HUMAN DIMETHYLANILINE MONOOXYGENASE [H.sapiens], Flavin-containing monooxygenase 1, flavin containing monooxygenase 1, flavin containing monooxygenase 2, flavin containing monooxygenase 3, hypothetical protein PRO1257	
92	21140	AA848738	c			
93	16128	AA848807	o			
94	22923	AA848929	g			
95	17339	AA849497	General			
96	11727	AA849518				
97	21275	AA849796	U,m,General			

TABLE 8: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44924-4083WO	Doc. No. 0782837.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Accession No.	Homologous Gene Name	Homologous Cluster Name	
98	16678	AA849827	aa			
99	8515	AA849817	e			
100	18447	AA849839	General			
101	12130	AA850037	p			
						RIKEN cDNA 2610452G09 gene, adenyl cyclase-associated CAP protein homolog 1 (S. cerevisiae, S. pombe), adenyl cyclase-associated protein
102	23981	AA850040	x,aa			
103	13815	AA850364	i			
105	2637	AA850693	x			DKFZP434O125 protein
106	22093	AA850909	d			
107	21766	AA850916	ic			
						ESTs, Highly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE [H.sapiens], ESTs, Weakly similar to FAS RAT FATTY ACID SYNTHASE [R.norvegicus], ESTs, Weakly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE [H.sapiens], crystallin, zeta, fatty acid synthase
108	2847	AA850919	w			
109	12162	AA850975	h			
110	9514	AA850978	General			
111	3924	AA851017	e,q			
111	3925	AA851017	o,General			
112	4490	AA851184	a,k			cathepsin Z
113	19187	AA851230	General			
114	19189	AA851237	c			RIKEN cDNA 1110058H21 gene, ubiquitin specific protease 18
115	15386	AA851241	m			breast cancer metastasis-suppressor 1, hypothetical protein MGC11295
116	21462	AA851261	g,l,General			ART-4 protein
117	21471	AA851343	General			
						NADH dehydrogenase (ubiquinone) Fe S protein 8 (23kD) (NADH-coenzyme Q reductase)
118	18902	AA851379	p			
119	23378	AA851392	i,x			kinesin-like 4
119	23377	AA851392	x			kinesin-like 4
120	13349	AA851417	General			
121	21527	AA851733	r,u			
						EST, Moderately similar to PM17 MOUSE MELANOCYTE PROTEIN PMEL 17 PRECURSOR [M.musculus], Homo sapiens, Similar to glycoprotein (transmembrane) rmb, clone MCC-1696 IMAGE3345861, mRNA, complete cds, glycoprotein (transmembrane) rmb, silver
122	4048	AA851814	i,o,u,General			signal sequence receptor, alpha (translocon-associated protein alpha)
123	10561	AA851871	bb			ESTs, Weakly similar to A60021 tropomyosin-related protein, neuronal - rat [R.norvegicus], RIKEN cDNA 0710005K15 gene, expressed sequence R75279, reticulon 1, reticulon 3
124	17411	AA858821	i,y			
						expressed sequence A1747533, mini chromosome maintenance deficient 7 (S. cerevisiae), minichromosome maintenance deficient (S. cerevisiae) 7
125	1801	AA858636	k,s,x,bb			
126	18350	AA858674	p			
127	19484	AA858693	e			
128	8360	AA858696	d			

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS				Atty. Doc. No. 4:EPH 6183WO
				Doc. No. 1793897.1
Seq. ID No.	Identifier	GenBank Acc./Ref. Seq. ID No.	Model Code	Homologous Gene Name
129	17334	AA858704	p	
130	6380	AA858756	g	
131	13219	AA858759	a	
132	6384	AA858788	l,m,General	
				exotoxins (multiple) 1, exotoxins (multiple)-like 1, expressed sequence AA409028
134	13412	AA858830	p	
135	7279	AA858892	f	
136	18217	AA858930	t	
137	5867	AA858953	v,General	
				LanC (bacterial lantibiotic synthetase component C)-like, LanC (bacterial lantibiotic synthetase component C)-like 1, RIKEN cDNA 170003F10 gene
				asparaginyl-tRNA synthetase, hypothetical protein FLJ23441
138	14479	AA858969	r	
139	6431	AA859085	t	
140	17361	AA859114	o,General	
				Interleukin 1 receptor accessory protein, Mus musculus IL-1Rrp2 mRNA, complete cds, interleukin 1 receptor accessory protein-like 2, Interleukin 1 receptor, type 1, Interleukin 18 receptor 1
141	21025	AA859241	General	
142	10076	AA859271	c	
				EST, Highly similar to OM25_RAT MITOCHONDRIAL OUTER MEMBRANE PROTEIN 25 (NPW16) [R.norvegicus], EST, Weakly similar to OM25_RAT MITOCHONDRIAL OUTER MEMBRANE PROTEIN 25 (NPW16) [R.norvegicus], ErbB2 interacting protein, discs, large homolog 4 (Drosophila), expressed sequence A1115201, hypothetical protein FLJ11271, synaptojanin 2 binding protein
				EST, Moderately similar to CYSR RAT CYSTEINE-RICH PROTEIN 1 [R.norvegicus], ESTs, Weakly similar to S12658 cysteine-rich protein [H.sapiens], cysteine and glycine-rich protein 1, cysteine and glycine-rich protein 3 (cardiac LIM protein), cysteine rich protein, cysteine-rich protein 2, cysteine-rich protein 3, thymus LIM protein
143	21791	AA859333	k	
144	16314	AA859348	cc,General	
145	16882	AA859520	f	
146	15059	AA859545	r	
				EST, Highly similar to SPERM-COATING GLYCOPROTEIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to JC4131 glioma pathogenesis-related protein [H.sapiens], Human DNA sequence from clone RP5-881L22 on chromosome 20 Contains ESTs, GSSs, STSs and CpG islands. Contains a gene for a novel protein similar to a trypsin inhibitor and four other genes for novel proteins, RIKEN cDNA 1810049K24 gene, RIKEN cDNA 2410114O14 gene, RIKEN cDNA 9230112K08 gene, acidic epididymal glycoprotein 1, acidic epididymal glycoprotein 2, epididymal glycoprotein, glioma pathogenesis-related protein
147	19884	AA859581	s	

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Ally. DocId: No. 44921-5083WC Doc. No. 1798877
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Match Score	Homologous Gene Name	Homologous Cluster Name
148	14353	AA859585	h		DnaJ (Hsp40) homolog, subfamily B, member 1, DnaJ (Hsp40) homolog, subfamily B, member 5, DnaJ (Hsp40) homolog, subfamily B, member 6, DnaJ (Hsp40) homolog, subfamily B, member 8, ESTs, Weakly similar to DnaJ-like protein [M.musculus], ESTs, Weakly similar to HS44 MOUSE HEAT SHOCK 40 KDA PROTEIN 4 [R.norvegicus], Homo sapiens cDNA FLJ13992 fls, clone Y79AA1002139, weakly similar to DNAJ PROTEIN HOMOLOG 1, RIKEN cDNA 1700029A20 gene, RIKEN cDNA 2010306G19 gene
149	16318	AA859648	h		
150	17316	AA859652	General		
151	19067	AA859663	n,q		
152	22406	AA859680	n		
153	20599	AA859690	x		
154	14261	AA859693	u		
155	14138	AA859700	v		protoporphyrinogen oxidase
155	14139	AA859700	v		protoporphyrinogen oxidase
157	22374	AA859804	l		
					ESTs, Weakly similar to PROTEIN-LYSINE 6-OXIDASE PRECURSOR [R.norvegicus], Lysyl oxidase, lysyl oxidase, lysyl oxidase-like, lysyl oxidase-like 1, lysyl oxidase-like 2
158	22385	AA859805	b,k		
159	22773	AA859885	n		
160	22816	AA859898	k,x,z		
161	11891	AA859926	x		
					EST, Weakly similar to JC1343 glycopeptide N-tetradecanoyltransferase [H.sapiens], N-mristoyltransferase 1
162	23070	AA859942	k		
163	23121	AA859948	k		
164	23166	AA859954	cc,General		
					Homo sapiens cDNA FLJ14666 fls, clone NT2RP2003000, weakly similar to TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, Homo sapiens polymerase delta-interacting protein 1 mRNA, complete cds, MSTP028 protein, tumor necrosis factor, alpha-induced protein 1 (endothelial)
165	18468	AA859966	aa		
					ESTs, Moderately similar to A Chain A, inositol Monophosphatase [H.sapiens], inositol (myo)-1(or 4)-monophosphatase 1, RIKEN cDNA 2900059K10 gene, bisphosphate 3'-nucleotidase 1, inositol (myo)-1(or 4)-monophosphatase 1, inositol (myo)-1(or 4)-monophosphatase 2, inositol(myo)-1(or 4)-monophosphatase 1, inositol(myo)-1(or 4)-monophosphatase 2
166	23336	AA859981	q		
					EST, Moderately similar to EF1G, HUMAN ELONGATION FACTOR 1-GAMMA [H.sapiens], ESTs, Highly similar to EF1G, HUMAN ELONGATION FACTOR 1-GAMMA [H.sapiens], Homo sapiens cDNA FLJ11216 fls, clone PLACE1008002, eukaryotic translation elongation factor 1 gamma
167	4222	AA860024	a,bb		

TABLE 2: HUMAN TO MICE GENE ANNOTATIONS					FIG. 1: Bacter No. 4322-2000/02 Doc. No. 179837/1
Seq. ID ID	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
166	13974	AA860030	u,x,General		EST, Moderately similar to I38369 beta tubulin [H.sapiens], EST, Weakly similar to I36369 beta-tubulin [H.sapiens], EST, Weakly similar to TUBULIN BETA-5 CHAIN [M.musculus], ESTs, Highly similar to A25113 tubulin beta chain 15 - rat [R.norvegicus], FK506-binding protein 1A (12kD), RIKEN cDNA 2310061K05 gene, RIKEN cDNA 2410129E14 gene, tubulin, beta 2, tubulin, beta 5, tubulin, beta polypeptide
169	7090	AA860039	x	hyaluronan mediated motility receptor (RHAMM), hyaluronan-mediated motility receptor (RHAMM)	Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:5720466F14, full insert sequence, RIKEN cDNA 0810027D24 gene, TRAF4 associated factor 1, hyaluronan mediated motility receptor (RHAMM), hyaluronan-mediated motility receptor (RHAMM)
170	23769	AA860055	k,x		DKFZP547E2110 protein, hypothetical protein FLJ10604
171	18323	AA866240	w		
172	4462	AA866264	General		EST, Weakly similar to PE2R RAT 20-ALPHA-HYDROXYSTERIOD DEHYDROGENASE [R.norvegicus], Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610526B18, full insert sequence, RIKEN cDNA 9430025F20 gene, Rattus norvegicus mRNA for 20-alpha-hydroxysteroid dehydrogenase (20-alpha-HSD), complete cds, aldo-keto reductase family 1, member C1, aldo-keto reductase family 1, member C4 (chlorocone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4), expressed sequence A1315367, expressed sequence A1503553, hydroxysteroid (17-beta) dehydrogenase 5
173	15884	AA866276	k		ESTs, Highly similar to A54602 microtubule-associated serine/threonine protein kinase MAST205 - mouse [M.musculus], ESTs, Moderately similar to A54602 microtubule-associated serine/threonine protein kinase MAST205 - mouse [M.musculus], Homo sapiens cDNA, FLJ21699 f5, clone COL09629, KIAA0303 protein, KIAA0807 protein, Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130026D18, full insert sequence, microtubule associated testis specific serine/threonine protein kinase, syntrophin associated serine/threonine kinase

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 44921-568WO Doc. No. 1733327.1
Seq. ID No.	Identifier	SeqBank Acct/ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Clus. Name
174	17742	AA866302	c,y	4-hydroxyphenylpyruvate dioxygenase, 4-hydroxyphenylpyruvic acid dioxygenase	4-hydroxyphenylpyruvate dioxygenase, 4-hydroxyphenylpyruvic acid dioxygenase, ESTs, Weakly similar to HPPD MOUSE 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE [M.musculus], ESTs, Weakly similar to S32820 alloantigen F - rat [R.norvegicus], hypothetical protein M5C15668
175	16333	AA866414	a,h	solute carrier family 4 (anion exchanger), member 1, solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	ESTs, Highly similar to BAND 3 ANION EXCHANGE PROTEIN [M.musculus], ESTs, Weakly similar to B3HU band 3 anion transport protein, erythrocyte [H.sapiens], solute carrier family 4 (anion exchanger), member 1, solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)
176	18918	AA866444	p,g		
177	18853	AA866454	j,l,m,y,z		
178	18995	AA866459	h,m		
179	18013	AA866482	s		ESTs, Highly similar to FGD1_HUMAN PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [H.sapiens], ESTs, Weakly similar to FGD1 MOUSE PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [M.musculus], ESTs, Weakly similar to FGD1_HUMAN PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [H.sapiens], [FGD1 family, member 3, RIKEN cDNA 5830461L01 gene, faciogenital dysplasia (Aarskog-Scott syndrome), faciogenital dysplasia homolog, faciogenital dysplasia homolog 2 (human)]
180	26036	AA874849	r		
181	16059	AA874857	h		
182	16069	AA874873	r		
183	21633	AA874951	f		ESTs, Weakly similar to RNA binding protein [H.sapiens]
184	16192	AA874995	w		
185	16254	AA875025	j		cellular retinoic acid-binding protein 1
186	16312	AA875032	cc,General		
187	20701	AA875097	b	fibrinogen, A alpha polypeptide	Homo sapiens clone HQ0582, expressed sequence A1303526, fibrinogen, A alpha polypeptide, fibrinogen, gamma polypeptide
188	16416	AA875098	bb		ADP-ribosylation factor 3, RIKEN cDNA 5430400P17 gene, Rattus norvegicus ADP-ribosylation factor 3 mRNA, complete cds, expressed sequence AA08731
189	16419	AA875102	bb		expressed sequence A1022645, expressed sequence C78690, small nuclear ribonucleoprotein E, small nuclear ribonucleoprotein polypeptide E
190	15313	AA875126	l,m,General		
191	10936	AA875146	w		
192	18084	AA875186	h		
193	15371	AA875205	u		ESTs, Weakly similar to IF38_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 [H.sapiens]

TABLE 5: HUMAN HOMOLOGUE ANNOTATIONS					Pub. No. 4:921-300WG Doc. No. 170247-1
Seq. ID No.	Identifier	GenBank Acc# Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
194	15401	AA875257	x,z		NADH dehydrogenase (ubiquinone) Fe S protein 7 (20kD) (NADH-coenzyme Q reductase)
195	15410	AA875268	p,s		
196	15420	AA875286	f		
197	15446	AA875327	s,w		
198	7936	AA875495	b,General		
199	17314	AA875509	l,l,m		EST, Moderately similar to A Chain A, Mdm2 Bound To The Transactivation Domain Of P53 (SUB 17-125 [H.sapiens], mouse double minute 2, human homolog of, p53-binding protein
200	24472	AA875523	k		EST, Weakly similar to MOH6N myosin alkali light chain 6, nonmuscle form [H.sapiens], myosin light chain, alkali, nonmuscle, myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
201	15587	AA875577	l		
202	15617	AA875620	General		
202	15618	AA875620	General		
203	5384	AA891041	f,cc,General		Jun-B oncogene, jun B proto-oncogene
204	24814	AA891209	f,p		
205	21930	AA891322	d		EST, Moderately similar to JH0148 nucleolin - rat [R.norvegicus], EST, Weakly similar to NUCL_HUMAN NUCLEOLIN [H.sapiens], ESTs, Highly similar to FUS_HUMAN RNA-BINDING PROTEIN FUS [H.sapiens], ESTs, Weakly similar to T17210 hypothetical protein DkFp454N04.1 [H.sapiens], RIKEN cDNA 2700022N2.1 gene, fusion, derived from (12;16) malignant liposarcoma, poly(A) binding protein, nuclear 1, small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen)
206	17225	AA891553	h		EST, Weakly similar to IF37 MOUSE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 7 [M.musculus], eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67 kDa), eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD)
207	7522	AA891571	l,m		
208	9071	AA891578	b		
209	19321	AA891666	u	melanoma antigen, family D, 1	Homo sapiens, Similar to neurofilament, heavy polypeptide (200kD), clone MGC:20701 IMAGE:4634024, mRNA, complete cds, MAGE-E1 protein, MAGEF1 protein, Neurofilament, heavy polypeptide, RIKEN cDNA 2010107K23 gene, RIKEN cDNA 3830417A13 gene, general transcription factor IIH, polypeptide 1 (62kD subunit), melanoma antigen, family D, 1, melanoma antigen, family D, 2, necdin, neurofilament, heavy polypeptide, neurofilament, heavy polypeptide (200kD)
210	17853	AA891737	l,l,m,u,y,z		
211	17256	AA891739	General		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Alt. Desc. No. 44891-50870
					Ref. No. 178387-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
213	18269	AA891769	General		ESTs, Highly similar to S03917 fibronectin ED-A [H.sapiens], ESTs, Moderately similar to Fourth And Fifth Fibronectin Type I Module Pair [SUB 183-275 [H.sapiens], Fibronectin 1, fibronectin 1
214	9905	AA891774	s.bb.General		
215	17061	AA891812	d		
216	7050	AA891824	h		ESTs, Highly similar to 2013348A Ser kinase SRPK1 [H.sapiens], Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110005M20, full insert sequence, Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200011B22, full insert sequence, SFRS protein kinase 1, SFRS protein kinase 2, serine/arginine-rich protein specific kinase 2, serine/threonine kinase 23
217	4463	AA891831	General		EST, Weakly similar to PE2R RAT 20-ALPHA-HYDROXYSTEROID DEHYDROGENASE [R.norvegicus], Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610528B18, full insert sequence, RIKEN cDNA 9430025F20 gene, Rattus norvegicus mRNA for 20-alpha-hydroxysteroid dehydrogenase (20-alpha-HSD), complete cds, aldo-keto reductase family 1, member C1, aldo-keto reductase family 1, member C4 (chlorocone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4), expressed sequence A1315367, expressed sequence A1503553, hydroxysteroid (17-beta) dehydrogenase 5
218	14289	AA891838	i		
219	20523	AA891842	r.cc		
220	17779	AA891914	g.s.z		EST, Weakly similar to ACY1_HUMAN AMINOACYLASE-1 [H.sapiens], aminocyclase 1
221	17438	AA891943	General		
222	22862	AA891944	p		
223	1159	AA891949	e.z		
224	4473	AA891965	General		
225	6362	AA892053	f.i.j.m		
226	9037	AA892066	y		
227	19469	AA892112	General		EST, Weakly similar to PROD_HUMAN PROLINE OXIDASE, MITOCHONDRIAL PRECURSOR [H.sapiens], Homo sapiens mRNA for KIAA1653 protein, partial cds, proline dehydrogenase, proline dehydrogenase (proline oxidase), proline oxidase 1, proline oxidase homolog
228	14595	AA892128	o.lv		
229	16527	AA892154	cc		
230	4482	AA892173	bb		
231	20917	AA892236	h		Met proto-oncogene, RYK receptor-like tyrosine kinase, macrophage stimulating 1 receptor (c-met-related tyrosine kinase), met proto-oncogene
232	2357	AA892268	d		

TABLE 8: HUMAN HOMOLOGUE ANNOTATIONS					Ally, DocRef No. 449215689W0 Doc. No. 1192897-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Accession Name	Homologues Cluster Name
233	18183	AA892271	h		
234	8523	AA892299	d		
					EST, Weakly similar to 60S RIBOSOMAL PROTEIN L3 [R.norvegicus], EST, Weakly similar to 184501 ribosomal protein L3 [H.sapiens], ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L3 [R.norvegicus], ESTs, Moderately similar to 184501 ribosomal protein L3 [H.sapiens], ESTs, Weakly similar to RL3 MOUSE 60S RIBOSOMAL PROTEIN L3 [M.musculus], RIKEN cDNA 1110057H16 gene, ribosomal protein L3, ribosomal protein L3-like
236	13647	AA892367	a		
237	3473	AA892378	v		
					ESTs, Weakly similar to T44342 hypothetical protein TSC501 [H.sapiens], kidney- and liver-specific gene, putative N-acetyltransferase Camello 2
238	17682	AA892382	j,p,s,x,General		
				aldolase 2, B isoform, aldolase B, fructose-bisphosphate	
239	820	AA892395	q,s		
240	14754	AA892414	u		
241	17439	AA892448	f		
242	16469	AA892462	p		
					ubiquinol-cytochrome c reductase (6.4kD) subunit
					EST, Weakly similar to MAST CELL PROTEASE 7 PRECURSOR [M.musculus], ESTs, Weakly similar to MCT7 RAT MAST CELL PROTEASE 7 PRECURSOR [R.norvegicus], RIKEN cDNA 2410039E18 gene, RIKEN cDNA 4933401F05 gene, marapsin, mast cell protease 7, protease, serine, 21 (testisin), protease, serine, 22, protease, serine, 8 (prostatin), tryptase delta 1, tryptase, alpha
243	13609	AA892466	i,General		
					EST, Weakly similar to MAST CELL PROTEASE 7 PRECURSOR [M.musculus], ESTs, Weakly similar to MCT7 RAT MAST CELL PROTEASE 7 PRECURSOR [R.norvegicus], RIKEN cDNA 2410039E18 gene, RIKEN cDNA 4933401F05 gene, marapsin, mast cell protease 7, protease, serine, 21 (testisin), protease, serine, 22, protease, serine, 8 (prostatin), tryptase delta 1, tryptase, alpha
243	13610	AA892466	n,v,General		
					EST, Weakly similar to histone H2A.F/Z variant [H.sapiens], H2A histone family, member Z, RIKEN cDNA C530002L11 gene, histone H2A.F/Z variant
244	9254	AA892470	n,u		
245	11991	AA892483	s		
					EST, Weakly similar to A32609 alpha-glucosidase [H.sapiens], ESTs, Weakly similar to LYAG MOUSE LYOSOMAL ALPHA-GLUCOSIDASE PRECURSOR [M.musculus], alpha glucosidase 2, alpha neutral subunit, glucosidase, alpha, acid
246	1522	AA892486	f		
					ESTs, Highly similar to DS1_HUMAN DS-1 PROTEIN [H.sapiens], immature colon carcinoma transcript 1
247	11994	AA892507	aa		
248	23888	AA892520	w		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Ally, DocId: No. 44924-5008V0 Rec. No. 1193837.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
248	23889	AA892520	h		
249	8599	AA892522	p		
					expressed sequence A987846, expressed sequence AL023058, expressed sequence C77895, hypothetical protein MGC3178, protein disulfide isomerase-related protein, quiescin Q6
250	15154	AA892532	p		
251	17468	AA892545	r		
252	11203	AA892554	f,h		
253	18906	AA892561	a,bb,General		
					ESTs, Moderately similar to DKC1 RAT DYSKERIN [R.norvegicus], ESTs, Weakly similar to DKC1_HUMAN DYSKERIN [H.sapiens], RIKEN cDNA 9030425C13 gene, dyskeratosis congenita 1, dyskerin, hypothetical protein, MGC:7014, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1
254	19327	AA892562	f,j,y,z		
255	18274	AA892572	p		
256	4512	AA892578	cc		
					EST, Highly similar to 60S RIBOSOMAL PROTEIN L8 [R.norvegicus], EST, Moderately similar to 60S RIBOSOMAL PROTEIN L8 [R.norvegicus], EST, Weakly similar to JN0923 ribosomal protein L8, cytosolic [H.sapiens], ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L8 [R.norvegicus], ESTs, Highly similar to RLB_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus], ESTs, Moderately similar to RLB_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus], expressed sequence AL024098, ribosomal protein L8
257	15876	AA892582	w		
258	19085	AA892598	General		
258	19085	AA892598	General		
					EST, Highly similar to HISTONE H4 [R.norvegicus], ESTs, Highly similar to HISTONE H4 [R.norvegicus], H4 histone family, member D, H4 histone family, member H, H4 histone family, member I, H4 histone family, member K, Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810029H14, full insert sequence, Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610027B07, full insert sequence, Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493055A/J22, full insert sequence, Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310067E17, full insert sequence, histone 4 protein
259	20065	AA892647	i		
260	20088	AA892666	a,n		
261	23783	AA892773	n		

TABLE 8: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 449291-0033/WG Doc. No. 4733397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
262	17549	AA892776	fz		Mus musculus, Similar to solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3, clone MGC:7631, mRNA, complete cds, expressed sequence W51672, solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3
263	13542	AA892798	ib		
264	22537	AA892799	General		3-phosphoglycerate dehydrogenase, EST, Weakly similar to SERA RAT D-3-PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus], ESTs, Moderately similar to SERA_HUMAN D-3-PHOSPHOGLYCERATE DEHYDROGENASE [H.sapiens], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930404C15, full insert sequence, RIKEN cDNA 1110059D05 gene, RIKEN cDNA 6430629L09 gene, glyoxylate reductase/hydroxypyruvate reductase, phosphoglycerate dehydrogenase
264	22539	AA892799	v		3-phosphoglycerate dehydrogenase, EST, Weakly similar to SERA RAT D-3-PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus], ESTs, Moderately similar to SERA_HUMAN D-3-PHOSPHOGLYCERATE DEHYDROGENASE [H.sapiens], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930404C15, full insert sequence, RIKEN cDNA 1110059D05 gene, RIKEN cDNA 6430629L09 gene, glyoxylate reductase/hydroxypyruvate reductase, phosphoglycerate dehydrogenase
264	22538	AA892799	General		3-phosphoglycerate dehydrogenase, EST, Weakly similar to SERA RAT D-3-PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus], ESTs, Moderately similar to SERA_HUMAN D-3-PHOSPHOGLYCERATE DEHYDROGENASE [H.sapiens], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930404C15, full insert sequence, RIKEN cDNA 1110059D05 gene, RIKEN cDNA 6430629L09 gene, glyoxylate reductase/hydroxypyruvate reductase, phosphoglycerate dehydrogenase
265	6951	AA892820	h		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 4397-5009WO Doc. No. 193847-1
Seq. ID No.	Identifier	SeqBank/ Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
266	23322	AA892821	j,z		ESTs, Highly similar to AR72_HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE 1 (AFB1-AR 1) (ALDOKETOREDUCTASE 7) [H.sapiens], ESTs, Moderately similar to AFAR RAT AFLATOXIN B1 ALDEHYDE REDUCTASE [R.norvegicus], RIKEN cDNA 0610025K21 gene, aflatoxin B1 aldehyde reductase, aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase), aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)
267	17923	AA892843	i		
268	22871	AA892859	m		RIKEN cDNA 2410042F05 gene, procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2, procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI), procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1
269	9053	AA892861	p,v,General		
270	16482	AA892940	w		EST, Weakly similar to EFH2 translation elongation factor eEF-2 [H.sapiens], ESTs, Highly similar to ELONGATION FACTOR 2 [R.norvegicus], U5 snRNP-specific protein, 116 kD, eukaryotic translation elongation factor 2, expressed sequence A1451340, hypothetical protein FLJ21661
271	12020	AA893035	j,y		
272	3863	AA893060	General		
273	13332	AA893060	i,General		
274	21305	AA893062	General		
275	16591	AA893191	j,z		
276	17447	AA893192	General		
277	3876	AA893205	n		
278	3878	AA893230	General		
					Calmodulin 1 (phosphorylase kinase, delta), Calmodulin iii, ESTs, Highly similar to A Chain A, Calmodulin Complexed With Calmodulin-Binding Peptide From Smooth Muscle Myosin Light Chain Kinase (SUB 2-148) [H.sapiens], RIKEN cDNA 231006B022 gene, calmodulin, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3

TABLE 8: HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 4926-5680W6 Doc. No. 179397.1
Seq. ID No.	Identifier	SeqBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
279	20986	AA893242	q	fatty acid Coenzyme A ligase, long chain 2, fatty acid-Coenzyme A ligase, long-chain 2	ESTs, Weakly similar to LCB8 MOUSE LONG-CHAIN-FATTY-ACID-COA LIGASE 2 [M.musculus], Mus musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Rattus norvegicus gonadotropin-regulated long chain acyl-CoA synthetase (GR-LACS) mRNA, complete cds, fatty acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 1, fatty-acid-Coenzyme A ligase, long-chain 2, lipidosis
280	16168	AA893280	i,z.General		RIKEN cDNA 130012C15 gene, adipose differentiation related protein, adipose differentiation-related protein
281	3886	AA893289	j,m,y		
282	15209	AA893327	y		
283	17800	AA893436	cc		
284	17836	AA893626	h		Guanine nucleotide-binding protein beta 1, Homo sapiens mRNA for FLJ00083 protein, partial cds, Mus musculus, clone MGC:7934 IMAGE:3583848, mRNA, complete cds, RIKEN cDNA 5930415H02 gene, WD repeat domain 5, guanine nucleotide binding protein (G protein), beta polypeptide 1, guanine nucleotide binding protein beta subunit 4, guanine nucleotide binding protein, beta 1, guanine nucleotide binding protein, beta 4, hypothetical protein, recombination protein REC14
285	9084	AA893717	x		
286	22731	AA893743	d		
287	12031	AA893860	v		ESTs, Highly similar to YSHUT threonine-tRNA ligase [H.sapiens], ESTs, Moderately similar to YSHUT threonine-tRNA ligase [H.sapiens], hypothetical protein FLJ12528, threonyl-tRNA synthetase
288	17897	AA893905	k		
289	3447	AA893982	d		
290	22583	AA894009	n		
291	10540	AA894027	j		
292	4569	AA894059	x		

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					ATU: Pocket No. 44921-5089WG Doc No. 4793897-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
					Amyloid protein precursor-like protein 2, EST, Weakly similar to AMYLOID-LIKE PROTEIN 2 PRECURSOR [R.norvegicus], Human DNA sequence from clone RP3-461P17 on chromosome 20q12-13.2. Contains two novel genes, gene HE4 for Major Epididymis-specific protein E4 precursor (Epididymis Secretory protein E4), RPL5 (60S Ribosomal Protein L5), COX6C (Cytochrome C Oxidase subunit VIC) and HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL, HUCHA60) pseudogenes, the SPINT3 gene for Kunitz type serine protease inhibitor 3 (HKIB9), two genes for novel Kunitz/Bovine pancreatic trypsin inhibitor and WAP-type (Whey Acidic Protein) four-disulfide core' domains containing proteins and the gene for Eppin-1, -2 and -3. Contains ESTs, STSs, GSSs and a CpG island, RIKEN cDNA 1700024E17 gene, amyloid beta (A4) precursor-like protein 2, serine protease inhibitor, Kunitz type 2, tissue factor pathway inhibitor, tissue factor pathway inhibitor 2
293	18419	AA894130	d		
294	17336	AA894297	j		
295	19120	AA894318	j		
296	19762	AA899113	i		
					EST, Weakly similar to S45140 tubulin beta chain [H.sapiens], ESTs, Highly similar to T08726 tubulin beta chain [H.sapiens], ESTs, Highly similar to TBB1 RAT TUBULIN BETA CHAIN [R.norvegicus], ESTs, Moderately similar to I38370 beta-tubulin [H.sapiens], ESTs, Moderately similar to TBB1 RAT TUBULIN BETA CHAIN [R.norvegicus], RIKEN cDNA 2410129E14 gene, RIKEN cDNA 493047K03 gene, RIKEN cDNA 4930542G03 gene, tubulin, beta 3, tubulin, beta polypeptide
297	18286	AA899219	u		
298	22051	AA899498	w		
299	22052	AA899498	q		
299	21628	AA899563	aa		
300	4262	AA899590	i		
301	4661	AA899709	L.General	receptor (calcitonin) activity modifying protein 3	receptor (calcitonin) activity modifying protein 3
302	21354	AA899721	q		
					EST, Moderately similar to EGFR_HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR [H.sapiens], Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (ErbB1), avian erythroblastosis oncogene B 3, epidermal growth factor receptor, epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erbB) oncogene homolog)
303	17905	AA899762	General		
304	15231	AA899840	r		

TABLE 6: HUMAN HOMOLOGUE ANNOTATIONS					ATM Doc# WO 02/095000 Doc. No. 1723297A
Seq. ID No.	Identifier	GenBank Acc. Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
				topoisomerase (DNA) II alpha, topoisomerase (DNA) II alpha (170kD)	ESTs, Moderately similar to A40493 DNA topoisomerase [H.sapiens], ESTs, Moderately similar to TP2A MOUSE DNA TOPOISOMERASE II, ALPHA [M.musculus], topoisomerase (DNA) II alpha, topoisomerase (DNA) II beta, topoisomerase (DNA) II beta (180kD)
305	23778	AA899854	c,k,x		
306	22060	AA899858	b		
307	9114	AA899851	v,General		
308	8988	AA900148	f		
309	11841	AA800247	v		ESTs, Highly similar to IEFS_HUMAN TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H.sapiens], hypothetical protein FLJ12788
310	4725	AA900290	cc		Alpha-2-macroglobulin, ESTs, Moderately similar to A2M2 MOUSE MURINOGLOBULIN 2 PRECURSOR [M.musculus], RIKEN cDNA 2610307121 gene, alpha-2-macroglobulin, carbon catabolite repression 4 homolog (S. cerevisiae), expressed sequence AW456442, pregnancy-zone protein
311	4747	AA900465	General		
312	20998	AA900562	e		
313	3822	AA900863	b,g,General		DNA segment, Chr 17, human D6S81E 1, ESTs, Highly similar to S33681 translation initiation factor eIF-4A.I [H.sapiens], HLA-B associated transcript 1, Human clone 23933 mRNA sequence, eukaryotic translation initiation factor 4A, isoform 1, mitochondrial DEAD-box polypeptide 28, nuclear RNA helicase, DECD variant of DEAD box family
315	12420	AA901017	b		Mus musculus, Similar to aspartyl-tRNA synthetase, clone MGC:6719 IMAGE:3586278, mRNA, complete cds, esparaginy-tRNA synthetase, aspartyl-tRNA synthetase, hypothetical protein FLJ10514, hypothetical protein FLJ23441
316	4849	AA901155	s		
317	3959	AA901338	General		
318	22846	AA923982	a,d		succinate-CoA ligase, ADP-forming, beta subunit
319	4895	AA923999	k		
320	21546	AA924188	cc,General		
321	24192	AA924210	n,General		
322	4933	AA924301	g,l,General		
323	4944	AA924405	l,General		ESTs, Weakly similar to NEUROFILAMENT TRIPLET H PROTEIN [M.musculus], RIKEN cDNA 0610009L18 gene, RIKEN cDNA 1300003A17 gene, RIKEN cDNA 2410142G14 gene, nucleolar protein (RKE/D repeat)
324	4948	AA924428	r		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Ally, Patent No. 4,924,568 WO 98/01,738 P. 1
Seq. ID No.	Identifier	GenBank Acc. Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
325	4949	AA924432	General		ESTs, Weakly similar to NP72_HUMAN RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [H.sapiens], Homo sapiens, Similar to solute carrier family 34 (sodium phosphate), member 1, clone MGC:18179 IMAGE:4155326, mRNA, complete cds, Rattus norvegicus mRNA for NaPi-2 alpha, complete cds, Solute carrier family 17 (sodium/hydrogen exchanger), member 2, expressed sequence A1649385, solute carrier family 34 (sodium phosphate), member 1, solute carrier family 34 (sodium phosphate), member 2
326	18861	AA924598	e		3-phosphoglycerate dehydrogenase, EST, Weakly similar to SERA RAT D-3 PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus], ESTs, Moderately similar to SERA_HUMAN D-3-PHOSPHOGLYCERATE DEHYDROGENASE [H.sapiens], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930404C15, full insert sequence, RIKEN cDNA 1110059D05 gene, RIKEN cDNA 6430629L09 gene, glyoxylate reductase/hydroxypyruvate reductase, phosphoglycerate dehydrogenase
327	22540	AA924630	v.General		3-phosphoglycerate dehydrogenase, EST, Weakly similar to SERA RAT D-3 PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus], ESTs, Moderately similar to SERA_HUMAN D-3-PHOSPHOGLYCERATE DEHYDROGENASE [H.sapiens], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930404C15, full insert sequence, RIKEN cDNA 1110059D05 gene, RIKEN cDNA 6430629L09 gene, glyoxylate reductase/hydroxypyruvate reductase, phosphoglycerate dehydrogenase
327	22541	AA924630	General		3-phosphoglycerate dehydrogenase, EST, Weakly similar to SERA RAT D-3 PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus], ESTs, Moderately similar to SERA_HUMAN D-3-PHOSPHOGLYCERATE DEHYDROGENASE [H.sapiens], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930404C15, full insert sequence, RIKEN cDNA 1110059D05 gene, RIKEN cDNA 6430629L09 gene, glyoxylate reductase/hydroxypyruvate reductase, phosphoglycerate dehydrogenase
328	14759	AA924766	k		
329	23123	AA924794	x		
330	4067	AA924813	g.p		
331	2888	AA924902	r.General		
332	18130	AA924964	d		
333	23141	AA925019	r		
334	23195	AA925026	General		ESTs, Weakly similar to A35863 trypsin [H.sapiens], ESTs, Weakly similar to MCT7 RAT MAST CELL PROTEASE 7 PRECURSOR [R.norvegicus], RIKEN cDNA 4733401N09 gene, mast cell protease 7, trypsin delta 1, trypsin gamma 1, trypsin, alpha
335	21458	AA925049	f,aa.General		
336	5073	AA925061	m		
337	14790	AA925087	o.General		

TABLE 1: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4924-8800W
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
338	5089	AA925126	g		Homo sapiens, clone IMAGE-3940519, mRNA, partial cds, hypothetical protein DKFZp762006
339	23261	AA925145	k, General		Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930572N12, full insert sequence, betaine-homocysteine methyltransferase, betaine-homocysteine methyltransferase 2
340	17363	AA925150	a		KIAA0438 gene product, Rattus norvegicus mRNA for neurodegeneration associated protein 1, complete cds, expressed sequence AL022700, g1-related zinc finger protein, hypothetical protein, hypothetical protein FLJ11830 similar to Praja1, hypothetical protein, similar to (U06944) PRAJA1, prja1
341	23448	AA925167	l		
342	23159	AA925318	e		EST, Weakly similar to TR19_HUMAN THYROID RECEPTOR INTERACTING PROTEIN 9 [H.sapiens], ESTs, Highly similar to A44437 regenerating liver inhibitory factor RLIP-1 - rat [R.norvegicus], ESTs, Weakly similar to I-kappa B alpha chain [M.musculus], nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha, nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon
343	21500	AA925353	k		
344	22479	AA925418	l		
345	21151	AA925539	b		
346	16944	AA925541	f	heterogeneous nuclear ribonucleoprotein L	EST, Moderately similar to 1604358A nuclear RNP protein L [H.sapiens], ESTs, Highly similar to 1604358A nuclear RNP protein L [H.sapiens], ESTs, Moderately similar to 1604358A nuclear RNP protein L [H.sapiens], heterogeneous nuclear ribonucleoprotein L
346	16945	AA925541	t	heterogeneous nuclear ribonucleoprotein L	EST, Moderately similar to 1604358A nuclear RNP protein L [H.sapiens], ESTs, Highly similar to 1604358A nuclear RNP protein L [H.sapiens], ESTs, Moderately similar to 1604358A nuclear RNP protein L [H.sapiens], heterogeneous nuclear ribonucleoprotein L
347	17514	AA925554	bb		ESTs, Moderately similar to JX0336 succinate dehydrogenase [H.sapiens], succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
348	5183	AA925662	i, General		
349	23189	AA925844	r		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 4924-588 WO Orig. No. 178337.1
Seq. ID No.	Identifier	SortRank Acc/ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Gene Name
350	23190	AA925863	aa		EST, Weakly similar to IMB3, HUMAN IMPORTIN BETA-3 SUBUNIT [H.sapiens], Homo sapiens cDNA FLJ12978 fis, clone NTZRP2006321, RAN binding protein 6, karyopherin (importin) beta 3
351	5252	AA926051	General		
352	22967	AA926080	n,cc		
353	17157	AA926129	b		
354	13411	AA926196	u,General		
355	5295	AA926247	General		potassium channel, subfamily K, member 1 (TWIK-1), potassium channel, subfamily K, member 3 (TASK-1), potassium channel, subfamily K, member 6 (TWIK-2), potassium channel, subfamily K, member 7
356	22928	AA926262	General		DNA segment, human D4S114, P311 protein
357	8948	AA926316	r		
358	21798	AA926365	aa		CGI-69 protein, EST, Moderately similar to T43493 hypothetical protein DKFZp434C119.1 [H.sapiens], mitochondrial carrier family protein, mitochondrial solute carrier
359	9942	AA942697	s		
360	6039	AA942716	x,General		DNA segment, Chr 17, ERATO D01 441, expressed, hematological and neurological expressed 1
361	11174	AA942745	g,o,w		
362	23005	AA942770	g		
363	21318	AA942774	General		
364	6615	AA942889	v		
365	6691	AA943028	c		RAT MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR PRECURSOR [R.norvegicus], colony stimulating factor 1 receptor, colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog
366	22142	AA943066	p		DEAD (aspartate-glutamate-alanine- aspartate) box polypeptide 5, DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD), KIAA0801 gene product, RIKEN cDNA 261007K22 gene, RIKEN cDNA 4921506D17 gene, RIKEN cDNA 9130430L19 gene, RNA helicase, Rattus norvegicus RNA helicase with arginine-serine-rich domain mRNA, complete cds, expressed sequence A1325430, hypothetical protein, prp28, U5 snRNP 100 kd protein
367	21993	AA943149	v,General		ALEX1 protein, ALEX3 protein, armadillo repeat protein ALEX2, hypothetical protein MGC3195
368	9051	AA943508	General		TUSA protein, hypothetical protein MGC11034
369	24390	AA943531	b,j,n,y		ESTs, Weakly similar to VIL1 MOUSE VILLIN [M.musculus], actin binding LIM protein 1, advillin, erythrocyte membrane protein band 4.9 (dema1n), erythrocyte protein band 4.9, villin

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any. Ident. No. 4-92450000	Doc. No. 179397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
					EST, Moderately similar to I38369 beta tubulin [H.sapiens], EST, Weakly similar to I38369 beta-tubulin [H.sapiens], EST, Weakly similar to TUBULIN BETA-5 CHAIN [M.musculus], ESTs, Highly similar to A25113 tubulin beta chain 15 - rat [R.norvegicus], FK506-binding protein 1A (12kD), RIKEN cDNA 2310061K05 gene, RIKEN cDNA 2410129E14 gene, tubulin, beta 2, tubulin, beta 5, tubulin, beta polypeptide	
370	13976	AA943532	f,s,x			
371	22248	AA943537	cc,General		ajuba, expressed sequence A1481106, expressed sequence R75157, zyxin	
372	22257	AA943558	m		TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD	
373	12673	AA943773	u,cc,General			
374	13641	AA944154	u			
375	2658	AA944155	f			
376	12770	AA944161	d			
377	20903	AA944190	i,x		CDC28 protein kinase 2, RIKEN cDNA 1110038L14 gene, expressed sequence A1047807	
378	13507	AA944244	v			
379	15596	AA944353	General			
380	22681	AA944413	i,v,cc,General			
381	6711	AA944439	General			
382	14763	AA944481	i,g,General		ESTs, Highly similar to AGP2_RAT ANGIOPOIETIN-2 (ANG-2) [R.norvegicus], angiopeptin 1, angiopeptin 2, angiopeptin-like 3, angiopeptin-like 4, angiopeptin-like factor	
383	22466	AA944605	h			
384	12301	AA944727	b		B-cell CLL/lymphoma 3, B-cell leukemia/lymphoma 3, ESTs, Highly similar to A44437 regenerating liver inhibitory factor RLIF-1 - rat [R.norvegicus], ESTs, Weakly similar to kappa B alpha chain [M.musculus], molecule possessing ankyrin repeats induced by lipopolysaccharide (MAIL), homolog of mouse, nuclear factor of kappa light chain gene enhancer in B-cells 1, p105, nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha, nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon, testis-specific ankyrin motif containing protein	
385	7023	AA944792	d,m,aa			
386	22536	AA944803	bb			
387	22501	AA944811	g,l		CGI-89 protein, hypothetical protein DKFZp667O2416, hypothetical protein FLJ20984, leukocyte receptor cluster (LRC) member 4	
388	23907	AA944831	s			
389	28084	AA944922	i			
390	11974	AA944958	General			
391	22547	AA944970	aa			

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 44824-118W0
					Doc. No. 1798397-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
392	22554	AA945076	z.General		
393	14352	AA945181	General		
395	1798	AA945569	General		
396	22050	AA945604	aa		
397	19731	AA945615	d.o		
					Diaphorase (NADH/NADPH), NAD(P)H menadiene oxidoreductase 2, dioxin inducible, NAD(P)H menadiene oxidoreductase 2, dioxin-inducible, diaphorase (NADH/NADPH) (cytochrome b-5 reductase), diaphorase 4 (NADH/NADPH)
398	22612	AA945624	aa.General		
399	22618	AA945656	aa		
400	11871	AA945679	v		
401	22656	AA945818	General		
402	6720	AA945828	p		
403	22351	AA945867	m		
404	22665	AA945877	f		
405	24243	AA945950	b		
406	22689	AA945962	General		
407	22692	AA945986	d		
408	22696	AA945996	c.General		
408	22697	AA945996	c.o		
409	22658	AA945998	w		
					ESTs, Weakly similar to COXG MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE VIB [M.musculus], Human DNA sequence from clone RP4-591N18 on chromosome 22q13.1-13.2 Contains a COX8B (Cytochrome C Oxidase subunit VIB (EC 1.9.3.1)) pseudogene, ESTs, GSSs and two putative CpG islands, RIKEN cDNA 201000G05 gene, cytochrome c oxidase subunit VIB
410	20832	AA946040	s		
411	18337	AA946046	General		
					EST, Highly similar to LMA3_HUMAN LAMININ ALPHA-3 CHAIN PRECURSOR [H.sapiens], ESTs, Highly similar to LMA3_HUMAN LAMININ ALPHA-3 CHAIN PRECURSOR [H.sapiens], Homo sapiens cDNA: FLJ21236 fls, clone COL01111, expressed sequence A1853660, laminin, alpha 3 (lncin (150kD), kalinin (165kD), BM600 (150kD), spilegrin)
412	825	AA946108	General		
413	8639	AA946221	e.cc.General		
414	23237	AA946224	f		
415	15600	AA946250	o,aa		
416	19387	AA946275	t		
					actin related protein 2/3 complex, subunit 3 (21 kD)
					EST, Weakly similar to JC5111 cyclin-dependent kinase-related protein 1b - rat [R.norvegicus], EST, Weakly similar to S10889 proline-rich protein [H.sapiens], ESTs, Highly similar to JC5111 cyclin-dependent kinase-related protein 1b - rat [R.norvegicus], Homo sapiens ALS2CR7 mRNA, complete cds, PCTAIRE protein kinase 1, PCTAIRE-motif protein kinase 1, PFTAIRE protein kinase 1
417	6351	AA946344	d		
418	22057	AA946348	e		
419	22069	AA946349	aa		
420	13962	AA946351	General		

TABLE 1: HUMAN HOMOLOGUE ANNOTATIONS					Affy Decklet No. 44924-5089W (Doc. No. 179399)
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
421	18280	AA946361	g		EST, Moderately similar to 1923401A protein CBP [M.musculus], EST, Weakly similar to 1923401A protein CBP [M.musculus], ESTs, Highly similar to 1923401A protein CBP [M.musculus], ESTs, Weakly similar to 1923401A protein CBP [M.musculus], bromodomain, testis-specific, bromodomain-containing 2
422	18944	AA946391	v		
424	21410	AA946408	t		
425	643	AA946439	c,y		EST, Highly similar to HISTONE H4 [R.norvegicus], H4 histone family, member D, H4 histone family, member H, H4 histone family, member K, Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810029H14, full insert sequence, Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610027B07, full insert sequence, Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930558J22, full insert sequence, Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310067E17, full insert sequence, germinal histone H4 gene, histone 4 protein
426	20736	AA946443	x		EST, Weakly similar to NPD1_HUMAN NEURAL PROLIFERATION DIFFERENTIATION AND CONTROL PROTEIN-1 PRECURSOR (NPC-1 PROTEIN) [H.sapiens], expressed sequence A1314472, neural proliferation, differentiation and control gene 1, neural proliferation, differentiation and control, 1
427	21878	AA946448	r		
428	21947	AA946451	bb		EST, Highly similar to AF151863.1 CG105 protein [H.sapiens]
429	17499	AA946467	General		
430	1809	AA946503	x,General		
431	23360	AA955104	f		
432	23471	AA955162	General		
433	9452	AA955206	b,General		
434	23512	AA955282	General		
435	22596	AA955298	General		
436	23283	AA955391	h		
437	23546	AA955393	General		
438	12404	AA955408	b		ESTs, Weakly similar to SX10 RAT TRANSCRIPTION FACTOR SOX-10 [R.norvegicus], SRY (sex determining region Y)-box 10, SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex reversal), SRY-box containing gene 10, expressed sequence AV220920
439	23626	AA955540	aa		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS				Atty. Doc. No. 4492-3689WO	Doc. No. 1798897-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
441	17540	AA955914	bb		EST, Highly similar to FBRL MOUSE FIBRILLARIN [M.musculus], EST, Weakly similar to A38712 fibrillarlin [H.sapiens], ESTs, Highly similar to A38712 fibrillarlin [H.sapiens], ESTs, Weakly similar to FBRL MOUSE FIBRILLARIN [M.musculus], expressed sequence AL022665, fibrillarlin
442	24277	AA955962	General		
443	19639	AA955980	General		
444	24000	AA956005	i		ESTs, Weakly similar to PCB3_MOUSE POLY(RC)-BINDING PROTEIN 3 (ALPHA-CP3) [M.musculus], ESTs, Weakly similar to ROK_HUMAN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K [R.norvegicus], IGF-II mRNA-binding protein 3, RIKEN cDNA 2610101N11 gene, coding region determinant-binding protein, heterogeneous nuclear ribonucleoprotein K, poly(rC)-binding protein 3, poly(rC)-binding protein 4
445	11050	AA956164	s,v		EST, Weakly similar to T-COMPLEX PROTEIN 1, EPSILON SUBUNIT [M.musculus], ESTs, Moderately similar to T-COMPLEX PROTEIN 1, EPSILON SUBUNIT [M.musculus], T-complex 1, chaperonin containing TCP1, subunit 5 (epsilon), chaperonin subunit 5 (epsilon), expressed sequence AJ526772, t-complex 1, t-complex protein 1
446	458	AA956278	s,General		
447	23409	AA956294	q		
449	23773	AA956476	f,x		
450	23799	AA956530	d		
451	23800	AA956534	aa		ESTs, Weakly similar to RING1_HUMAN RING1 PROTEIN [H.sapiens], ring finger protein 1, ring finger protein 2
452	23834	AA956659	cc,General		
453	16425	AA956688	f,x		gene rich cluster, C8 gene, hypothetical protein MGC2577
454	23847	AA956723	s		
455	23852	AA956746	j,j,m,z		ESTs, Weakly similar to CHD4_HUMAN CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 [H.sapiens], KIAA1416 protein, KIAA1696 protein, chromodomain helicase DNA binding protein 4
456	5989	AA956907	g,s		DnaJ (Hsp40) homolog, subfamily C, member 8, Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone DKFZp434C2016), eukaryotic translation initiation factor 3, eukaryotic translation initiation factor 3, subunit 10 (theta, 150/170kD), expressed sequence C85189, guanylate kinase membrane-associated inverted 1, hypothetical protein DKFZp434B227, nasopharyngeal epithelium specific protein 1

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any DocId: No. 44921-88806 Doc. No. 199897.1
Seq. ID No.	Identifier	GeneBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
456	5990	AA956907	General		DnaJ (Hep40) homolog, subfamily C, member 8, Homo sapiens mRNA; cDNA DKFp434C2016 (from clone DKFp434C2016), eukaryotic translation initiation factor 3, eukaryotic translation initiation factor 3, subunit 10 (theta, 150/170kD), expressed sequence C85189, guanylate kinase membrane-associated inverted 1, hypothetical protein DKFp434B227, nasopharyngeal epithelium specific protein 1
457	23957	AA957123	u,General		X-linked protein, brain expressed, X-linked 1, hypothetical protein FLJ10097, nerve growth factor receptor (TNFRSF16) associated protein 1
458	22357	AA957264	General		EST, Weakly similar to T12456 hypothetical protein DKFp564M2423.1 [H.sapiens], ESTs. Highly similar to T12456 hypothetical protein DKFp564M2423.1 [H.sapiens], PAI-1 mRNA-binding protein, intracellular hyaluronan-binding protein
459	23314	AA957270	g.l.m.p.v.cc.Gene	ral	
460	23956	AA957292	a,b		
461	2702	AA957307	General		EST, Moderately similar to G01026 serine-IRNA ligase [H.sapiens], hypothetical protein FLJ20450, seryl-IRNA synthetase, uncharacterized gastric protein YC12P
462	24040	AA957422	c		CD3 antigen, zeta polypeptide, CD32 antigen, zeta polypeptide (T1T3 complex), Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide, Fc receptor, IgE, high affinity I, gamma polypeptide, expressed sequence A1573376
463	12478	AA957554	m		EST, Weakly similar to 501696 gene P3 protein [H.sapiens], ESTs, Highly similar to P3 PROTEIN [M.musculus], Protein P3
464	21306	AA957811	v		
465	24183	AA957889	t		
466	24178	AA957905	d		
467	17034	AA963071	e		EST, Moderately similar to COPE, HUMAN COATOMER EPSILON SUBUNIT [H.sapiens], ESTs, Highly similar to COPE, HUMAN COATOMER EPSILON SUBUNIT [H.sapiens], coatomer protein complex, subunit epsilon, hypothetical protein FLJ13241
468	24053	AA963092	General		X-linked protein, brain expressed, X-linked 1, hypothetical protein FLJ10097, nerve growth factor receptor (TNFRSF16) associated protein 1
469	2767	AA963201	o		
470	2022	AA963259	ig		
471	2126	AA963488	d		
472	24246	AA963703	b		
473	2195	AA963746	General		
474	19370	AA963797	i		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 43991-303W Doc. No. 1193887.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
475	2262	AA964147	e			
476	2284	AA964152	x			
478	2350	AA964368	g.General		ubiquitin specific protease 14 (RNA-guanine transglycosylase)	
479	18830	AA964496	aa		ESTs, Weakly similar to A29861 actin gamma [H.sapiens], ESTs, Weakly similar to I39393 alpha-actin [H.sapiens], ESTs, Weakly similar to S38782 actin beta' chain [H.sapiens], Homo sapiens mRNA, cDNA DKFZp434B2115 (from clone DKFZp434B2115), RIKEN cDNA 1700052K15 gene, RIKEN cDNA 1700061J02 gene, actin-like 7a, expressed sequence AV259599, melanoma X-actin, uncharacterized hypothalamus protein HARF11	
480	2302	AA964541	b			
481	2395	AA964554	General			
482	2410	AA964589	ja			
483	19145	AA964613	t			
484	2424	AA964617	g			
485	3107	AA964687	General			
486	2457	AA964752	g,l			
487	6778	AA964763	b			
489	2468	AA964807	t			
490	2469	AA964814	w	glutamate-cysteine ligase, modifier subunit, glutamate-cysteine ligase, modifier subunit	ESTs, Highly similar to GSHO_HUMAN GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT [H.sapiens], glutamate-cysteine ligase, modifier subunit, glutamate-cysteine ligase, modifier subunit	
491	12561	AA964815	General			
492	2326	AA964862	aa		EST, Weakly similar to PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR [M.musculus], collagen, type IV, alpha 1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 3, procollagen, type IV, alpha 5	
493	21339	AA964962	General		ATP-binding cassette, sub-family A (ABC1), member 1, ATP-binding cassette, sub-family A (ABC1), member 12, ATP-binding cassette, sub-family A (ABC1), member 7, EST, Moderately similar to ABC1_HUMAN ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 1 [H.sapiens], EST, Weakly similar to ABC1_MOUSE ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 1 [M.musculus], RIKEN cDNA 1810036E22 gene	
494	21390	AA964988	General			
495	12569	AA965023	g			
496	2583	AA965166	bb		Homo sapiens, clone MGC-8857 (IMAGE:3866266, mRNA, complete cds, inorganic pyrophosphatase, pyrophosphatase (inorganic)	
497	15885	AA965207	r		EST, Highly similar to T14795 hypothetical protein DKFZp434E171.1 [H.sapiens]	
499	2905	AA96727	b,l,m,u.General			
500	2915	AA96782	u,bb		ESTs, Moderately similar to LAMIN B3 [M.musculus], hypothetical protein MGC2721, lamin B1, lamin B2	
501	2920	AA96813	d			
502	19525	AA96856	aa.General			

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					ALY10044100 44924-6030 V03 Doc No. 17A382 4
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Group Name	Homologous Cluster Name
503	2984	AA997015	c		
504	2986	AA997028	General		
505	3145	AA997237	General		
506	19249	AA997342	m		
507	16883	AA997345	General		
508	12598	AA997362	s		methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase, protease, serine, 15 EST, Weakly similar to LIS1 MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus], ESTs, Weakly similar to LIS1 MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus], WD repeat domain 3, 1-box and WD-40 domain protein 2, hypothetical protein MGC2655, platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta), platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit, platelet-activating factor acetylhydrolase, isoform 1b, elphe subunit (45kD)
509	3470	AA997374	p		
510	3180	AA997425	t		
511	3245	AA997608	General		EST, Weakly similar to PLASMINOGEN ACTIVATOR INHIBITOR-2, TYPE A [R.norvegicus], expressed sequence A1876477, expressed sequence C76171, plasminogen activator inhibitor 2 type A, serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2, serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6, serine protease inhibitor 12
512	3020	AA997656	l		
513	3269	AA997800	x, ee		Homo sapiens, clone IMAGE:4810400, mRNA, antigen identified by monoclonal antibody Ki 67
514	3288	AA997877	f		
515	23992	AA998164	k, x		DNA segment, Chr 4, ERATO Doi 639, expressed, EST, Moderately similar to CGB2 MOUSE G2/MITOTIC-SPECIFIC CYCLIN B2 [M.musculus], ESTs, Weakly similar to CGB1 HUMAN G2/MITOTIC-SPECIFIC CYCLIN B [H.sapiens], cyclin B1
516	17470	AA998264	b		biliverdin reductase B (flavin reductase (NADPH))
517	3773	AA998356	General		B-cell CLL/lymphoma 3, molecule possessing ankrytin repeats induced by lipopolysaccharide (MAIL), homolog of mouse, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon
518	19623	AA998422	General		
519	3572	AA998516	x		ESTs, Weakly similar to G2/MITOTIC-SPECIFIC CYCLIN B1 [R.norvegicus], cyclin A2, cyclin B1, cyclin B1, related sequence 1, cyclin B2
520	2782	AA998565	c		cyclin-dependent kinase inhibitor 1C (p57), cyclin-dependent kinase inhibitor 1C (p57, Kip2)

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any DocId No. 43921-363970 Doc. No. 1793997
Seq. ID No.	Unifrac	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
521	26119	AA998576	l,r,w.General		
522	22737	AA998660	aa		
523	3696	AA999030	e		
524	3079	AA999169	k,x.General		
				signal transducer and activator of transcription 1, signal transducer and activator of transcription 1, 91kD	Signal transducer and activator of transcription 3, expressed sequence AA408197, signal transducer and activator of transcription 1, signal transducer and activator of transcription 1, 91kD, signal transducer and activator of transcription 2, signal transducer and activator of transcription 3, signal transducer and activator of transcription 3 (acute-phase response factor), signal transducer and activator of transcription 4
525	3081	AA999171	e,p,r		ESTs, Moderately similar to A54847 GMP synthase [H.sapiens], guanine monophosphate synthetase
526	3082	AA999172	General		
527	17337	AB000717	k		
528	1535	AB000778	a		phospholipase D1, phosphatidylcholine-specific, phospholipase D2
				RuvB (E coli homolog)-like 1, RuvB-like protein 1	Homer, neuronal immediate early gene, 1B, Homer, neuronal immediate early gene, 2, homer, neuronal immediate early gene, 1, homer, neuronal immediate early gene, 2
529	1382	AB002406	k		
530	20184	AB003753	d		
					EST, Weakly similar to JC5408 carboxylesterase [H.sapiens], ESTs, Moderately similar to ES22 MOUSE LIVER CARBOXYLESTERASE 22 PRECURSOR [M.musculus], ESTs, Weakly similar to A48809 carboxylesterase [H.sapiens], ESTs, Weakly similar to JC5408 carboxylesterase [H.sapiens], T-complex expressed gene 5, carboxylesterase 1, carboxylesterase 2 (intestine, liver), carboxylesterase 3, carboxylesterase 3 (brain), hypothetical protein FLJ21736
531	4312	AB010635	c,j,k,y,z		
					DNA (cytosine-5)-methyltransferase 1, DNA (cytosine-5)-methyltransferase 2, DNA methyltransferase (cytosine-5) 1, EST, Weakly similar to JE0378 DNA [R.nonvegicus], Mus musculus DNA-cytosine methyltransferase mRNA, f-box and leucine-rich repeat protein 11, protein containing CXXC domain 2
532	21666	AB012214	k		
					Mus musculus mouse-thyrotropin-releasing hormone receptor 2 (TRH-R2) mRNA, complete cds, thyrotropin-releasing hormone receptor, thyrotropin-releasing hormone receptor
533	15772	AB015645	g		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Allyl Docx No. 4:101-403W0 (Doc. No. 1726897)
Seq. ID No.	Ident/Var	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
534	1183	AF013144	h		ESTs, Weakly similar to DUS8, HUMAN DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 [H.sapiens], Human DNA sequence from clone RP11-243J16 on chromosome 20 Contains parts of 2 isoforms of the BCL2L1 (BCL2-like 1) gene, the gene for a novel protein (FLS35S), the gene for a protein similar to MYLK (myosin, light polypeptide kinase), the FKHL18 (forkhead (Drosophila)-like 18) gene, part of three novel genes, ESTs, STSs, GSSs and CpG islands, KIAA1725 protein, dual specificity phosphatase 13, dual specificity phosphatase 14, dual specificity phosphatase 6, expressed sequence BB104621, expressed sequence C79103, protein tyrosine phosphatase, non-receptor type 16
					B-cell CLL/lymphoma 6, member B (zinc finger protein), ESTs, Moderately similar to zinc finger protein [H.sapiens], Homo sapiens, Similar to RIKEN cDNA OS1002002 gene, clone MGC:23427 IMAGE:4654320, mRNA, complete cds
535	1582	AF015911	h,z		
536	11483	AF020618	u,cc,General		
537	20295	AF024712	aa		HLA-G histocompatibility antigen, class I, G
					hypothetical protein, clone 1-53, small inducible cytokine subfamily D (Cys-X3 Cys), member 1 (fractalkine, neurotactin), small inducible cytokine subfamily D, 1
538	19077	AF030358	y,z		RIKEN cDNA 4632428M18 gene, hyaluronidase 1, hyaluronidase 2, hyaluronoglucosaminidase 1, hyaluronoglucosaminidase 2, hyaluronoglucosaminidase 3, sperm adhesion molecule
539	23044	AF034218	General		
540	25178	AF035955	d		
541	1564	AF035953	x,bb,General		ESTs, Moderately similar to hepatitis A virus cellular receptor 1 [H.sapiens], ESTs, Moderately similar to kidney injury molecule-1 [R.norvegicus], ESTs, Weakly similar to kidney injury molecule-1 [R.norvegicus]
					ESTs, Moderately similar to NR54, HUMAN 54 KDA NUCLEAR RNA-BINDING PROTEIN [H.sapiens], ESTs, Moderately similar to p54nrb [H.sapiens], ESTs, Weakly similar to A54691 octamer-binding protein NonO - mouse [M.musculus], ESTs, Weakly similar to PSF, HUMAN PTB-ASSOCIATED SPLICING FACTOR [H.sapiens], RIKEN cDNA 5730470C09 gene, RIKEN cDNA 9030402K04 gene, non-POU-domain-containing, octamer-binding protein
542	18426	AF036335	f		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any. Def. No. 4494-628105 (Orig. No. 179887-1)
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Grade	Homologous Gene Name	Homologous Cluster Name
543	21817	AF038537	k		ESTs, Highly similar to A55318 serine/threonine protein kinase [M.musculus], ESTs, Weakly similar to RIP MOUSE SERINE/THREONINE PROTEIN KINASE RIP [M.musculus], Human DNA sequence from clone RP5-1182A14 on chromosome 1 Contains part of a gene similar to rat Espin, a pseudogene similar to KIAA0454, a gene similar to MST1 (macrophage stimulating 1 (hepatocyte growth factor-like)), a pseudogene similar to KIAA0445, two isoforms of a novel gene (isoform 2 is the gene for KIAA1245 protein), ESTs, STSs, GSSs and CpG islands, ankyrin repeat domain 3, cerebral cavernous malformations 1, mitogen activated protein kinase kinase kinase 12, mitogen-activated protein kinase kinase kinase 12, receptor (TNFRSF)-interacting serine-threonine kinase 1, receptor interacting protein 3, receptor-interacting serine-threonine kinase 2
544	21145	AF038571	General	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1, solute carrier family 1, member 1	
545	22802	AF044574	General		2,4-dienoyl CoA reductase 1, mitochondrial, 2,4-dienoyl-CoA reductase 2, peroxisomal, 2,4-dienoyl-Coenzyme A reductase 2, peroxisomal, ESTs, Weakly similar to S11021 2,4-dienoyl-CoA reductase [R.norvegicus], Homo sapiens AS10 protein mRNA, partial cds, RIKEN cDNA 1200012F07 gene, RIKEN cDNA 2400003B18 gene, hydroxyprostaglandin dehydrogenase 15 (NAD), hydroxysteroid (17-beta) dehydrogenase 10, peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase
546	13464	AF047707	h		UDP-glucose ceramide glucosyltransferase
547	24024	AF052695	x		
548	12259	AF061266	h		EST, Highly similar to JC5807 trp3 protein - rat [R.norvegicus], EST, Weakly similar to TRP1 MOUSE TRANSIENT RECEPTOR POTENTIAL CHANNEL 1 (TRANSIENT RECEPTOR PROTEIN 1) (MTRP1) (TRP-RELATED PROTEIN 1) [M.musculus], transient receptor potential channel 1, transient receptor protein 1, transient receptor protein 3, transient receptor protein 4, transient receptor protein 5

TABLE 1. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc# No. 4191-508W0 Doc. No. 179337/1
Seq. ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
549	4589	AF062389	y,z		EST, Highly similar to A61209 hypertension-associated protein SA - rat [R.norvegicus], ESTs, Highly similar to A61209 hypertension-associated protein SA - rat [R.norvegicus], ESTs, Weakly similar to I54401 hypertension-associated protein SA [H.sapiens], KIAA1504 protein, SA (rat hypertension-associated) homolog, SA rat hypertension-associated homolog, expressed sequence A178878, hypothetical protein FLJ20581, medium-chain acyl-CoA synthetase, solute carrier family 27 (fatty acid transporter), member 1, solute carrier family 27 (fatty acid transporter), member 4
550	16007	AF062594	t	nucleosome assembly protein 1-like 1	ESTs, Highly similar to 2008108A set gene [R.norvegicus], ESTs, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], SET translocation, SET (translocation (myeloid leukemia-associated), nucleosome assembly protein 1-like 1, nucleosome assembly protein 1-like 2, nucleosome assembly protein 1-like 4
551	15761	AF062741	u		KIAA1348 protein, protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
552	17426	AF073839	p		
553	18615	AF074608	s		
554	15797	AF084205	f		ESTs, Moderately similar to T17365 serine/threonine protein kinase TAO1 - rat [R.norvegicus], ESTs, Weakly similar to ST25_MOUSE SERINE/THREONINE PROTEIN KINASE 25 (STERILE 20/OXIDANT STRESS-RESPONSE KINASE 1) (STE20/OXIDANT STRESS RESPONSE KINASE-1) (SOK-1) (STE20-LIKE KINASE) [M.musculus], KIAA1361 protein, STE20-like kinase, expressed sequence AU020252, prostate derived STE20-like kinase PSK, serine/threonine kinase 10, thousand and one amino acid protein kinase
555	12932	AF102552	s		ESTs, Moderately similar to A55575 ankyrin 3, long splice form [H.sapiens], RIKEN cDNA 231008G15 gene, RIKEN cDNA 2410004E01 gene, RIKEN cDNA 2410197A17 gene, RIKEN cDNA 4933400N19 gene, RIKEN cDNA 8430401K06 gene, RIKEN cDNA C430011H06 gene, ankyrin 3, node of Ranvier (ankyrin G), hypothetical protein FLJ20189, phospholipase A2, group VI, phospholipase A2, group VI (cytosolic, calcium-independent), proteasome (prosome, macropain) 26S subunit, non-ATPase, 10

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					App. Doc. No. 4127-368W
					Doc. No. 178387.1
Seq. ID No.	Identifier	GenBank Acc. Rel. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
					EST, Moderately similar to A49013 tumor cell suppression protein HTS1 (H.sapiens), KIA1227 protein, hypothetical protein FLJ22457, suppression of tumorigenicity 5
556	18603	AI007649	x		
557	22733	AI007668	r		
558	22746	AI007672	r		
559	24109	AI007725	General		
					EST, Highly similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA (R.norvegicus), EST, Weakly similar to HHMS84 heat shock protein 84 - mouse [M.musculus], ESTs, Highly similar to T46243 hypothetical protein DKFZp761K0511.1 (H.sapiens), expressed sequence AL022974, expressed sequence CB1438, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1
560	15848	AI007820	n,v		
					HGF-regulated tyrosine kinase substrate, Homo sapiens cDNA FLJ13428 fls, clone PLACE1002493, highly similar to Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, Mouse 31-kDa proline-rich salivary protein, complete cds of clone PLMP125, Mus musculus, Similar to proline-rich protein BstII subfamily 2, clone MGC:18611 (IMAGE:4165240, mRNA, complete cds, RIKEN cDNA 1700120F24 gene, RIKEN cDNA 4930406E12 gene, Rattus norvegicus proline-rich proteoglycan (PRPG2) mRNA, complete cds, proline-rich protein HaeII subfamily 2, signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
561	10108	AI007857	f		
562	6804	AI007877	General		
563	20099	AI007893	f,u		
564	11368	AI007948	d		
					EST, Highly similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA (R.norvegicus), EST, Weakly similar to HHMS84 heat shock protein 84 - mouse [M.musculus], ESTs, Highly similar to T46243 hypothetical protein DKFZp761K0511.1 (H.sapiens), expressed sequence AL022974, expressed sequence CB1438, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1
565	15849	AI008074	h		
566	3121	AI008160	General		CGI-83 protein

TABLE 91. HUMAN HOMOLOGUE ANNOTATIONS					Any. Doc. No. 4:092-508WO
Seq. ID No.	Identifying	Gap/Cont. Acc./ Ref. Seq. ID No.	Modal Code	Homologous Gene Name	Homologous Cluster Name
567	16646	AI008190	t		EST, Highly similar to JC7290 guanine nucleotide binding protein G gamma 2 chain [H.sapiens], EST, Weakly similar to GBG9 RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)G(S)G(O) GAMMA-9 SUBUNIT [M.musculus], EST, Weakly similar to JC7290 guanine nucleotide binding protein G gamma 2 chain [H.sapiens], RIKEN cDNA 111003P13 gene, guanine nucleotide binding protein (G protein), gamma t2, guanine nucleotide binding protein (G protein), gamma 2, guanine nucleotide binding protein (G protein), gamma 2 subunit, guanine nucleotide binding protein (G protein), gamma 3 subunit, guanine nucleotide binding protein (G protein), gamma 4 subunit, guanine nucleotide binding protein 4
568	12683	AI008203	x		EST, Moderately similar to CGB2 MOUSE G2/MITOTIC-SPECIFIC CYCLIN B2 [M.musculus], ESTs, Weakly similar to G2/MITOTIC-SPECIFIC CYCLIN B1 [R.norvegicus], Homo sapiens cDNA FLJ13342 fs, clone OVARC1001950, cyclin A1, cyclin B1, cyclin B1, related sequence 1, cyclin B2
569	22018	AI008309	b		ESTs, Highly similar to PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE PIM-1 [M.musculus], ESTs, Highly similar to S55333 protein kinase pim-2 [M.musculus], ESTs, Moderately similar to S55333 protein kinase pim-2 [M.musculus], Pim-1 oncogene, pim-1 oncogene, pim-2 oncogene, proviral integration site 1, serine threonine kinase pim3
570	23917	AI008441	n		phosphoglucosyle dehydrogenase
571	22599	AI008458	General		
572	22698	AI008578	p,General		
573	14405	AI008579	r,x		
574	4086	AI008629	x		EST, Weakly similar to JH0446 75K autoantigen [H.sapiens], polymyositis/scleroderma autoantigen 1 (75KD) DnaJ (Hsp40) homolog, subfamily B, member 1, DnaJ (Hsp40) homolog, subfamily B, member 12, DnaJ (Hsp40) homolog, subfamily B, member 4, DnaJ (Hsp40) homolog, subfamily B, member 5, ESTs, Weakly similar to H54L HUMAN HEAT SHOCK 40 KDA PROTEIN 1 HOMOLOG [H.sapiens], RIKEN cDNA 1700029A20 gene, RIKEN cDNA 2010306G19 gene
575	3808	AI008643	l,v,General		
576	3931	AI008697	l		

TABLE OF HUMAN HOMOLOGUE ANNOTATIONS					Ally: Depol No: 4091-5088 WO Doc No: 179397.1
Seq. ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
577	7785	AI008758	aa	dipeptidylpeptidase 4, dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)	ESTs, Weakly similar to DPP4 MOUSE DIPEPTIDYL PEPTIDASE IV [M.musculus], ESTs, Weakly similar to DPP4 RAT DIPEPTIDYL PEPTIDASE IV [R.norvegicus], Homo sapiens chromosome 19, cosmid R26894, Homo sapiens, clone IMAGE3447394, mRNA, partial cds, RIKEN cDNA 4932434F09 gene, dipeptidylpeptidase 4, dipeptidylpeptidase 6, dipeptidylpeptidase 8, fibroblast activation protein, fibroblast activation protein, alpha
578	16701	AI008638	q		
579	21789	AI008930	k		EST, Moderately similar to CYSR RAT CYSTEINE-RICH PROTEIN 1 [R.norvegicus], ESTs, Weakly similar to S12658 cysteine-rich protein [H.sapiens], cysteine and glycine-rich protein 1, cysteine and glycine-rich protein 3 (cardiac LIM protein), cysteine rich protein, cysteine-rich protein 2, cysteine-rich protein 3, thymus LIM protein
580	21885	AI008971	General		
581	410	AI008974	Laa,General		
582	21632	AI009167	General		BCL2-associated athanogene 2, ESTs, highly similar to T08764 hypothetical protein DKFZp586C021.1 [H.sapiens]
583	21596	AI009168	General		
584	22801	AI009197	General		
585	11876	AI009321	cc,General		
586	2506	AI009341	General		
587	6382	AI009362	General		
588	14370	AI009427	k		EST, Weakly similar to PRCF_HUMAN PROTEASOME COMPONENT MECL-1 PRECURSOR [H.sapiens], ESTs, Weakly similar to PRCF_HUMAN PROTEASOME COMPONENT MECL-1 PRECURSOR [H.sapiens], proteasome (prosome, macropain) subunit, beta type 10, proteasome (prosome, macropain) subunit, beta type 7, proteasome (prosome, macropain) subunit, beta type, 10, proteasome (prosome, macropain) subunit, beta type, 7
589	19275	AI009460	x		EST, Moderately similar to ABP2_HUMAN ENDOTHELIAL ACTIN-BINDING PROTEIN [H.sapiens], ESTs, Moderately similar to ABP2_HUMAN ENDOTHELIAL ACTIN-BINDING PROTEIN [H.sapiens], flamin A, alpha (actin-binding protein-280), flamin B, beta (actin-binding protein-278)
590	4154	AI009467	g		
591	3464	AI009586	cc		
592	3926	AI009592	e		
593	19358	AI009675	c		
594	22545	AI009747	g		
595	15089	AI009752	cc,General		

Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
				programmed cell death 6 interacting protein, programmed cell death 6-interacting protein	EST, Moderately similar to T14756 hypothetical protein [XfZp564F0923.1 [H.sapiens], EST, Weakly similar to A26896 proline-rich protein M14 precursor - mouse [M.musculus], EST, Weakly similar to PRP4_HUMAN SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR [H.sapiens], expressed sequence AI462446, poly(A)-binding protein, nuclear 1, proline rich protein, proline rich protein 2, proline-rich protein BS21 subfamily 4, protein tyrosine phosphatase, non-receptor type 23
596	5458	AI009756	h		
597	6844	AI009770	e,r,cc		
598	15627	AI009810	aa		EST AI317031, EST, Weakly similar to R3HU16 ribosomal protein S16, cytosolic [H.sapiens], expressed sequence AA420385, ribosomal protein S16
599	22619	AI009825	d		
600	7857	AI009898	[I,m,z		
601	13259	AI009946	r		
602	21105	AI010067	General		
				testis enhanced gene transcript, testis enhanced gene transcript (BAX inhibitor 1)	CGI-119 protein, RIKEN cDNA 5031406P05 gene, testis enhanced gene transcript (BAX inhibitor 1) CGI-100 protein
603	24627	AI010102	aa		
604	12716	AI010178	General		
605	18757	AI010216	aa		
606	2912	AI010220	aa,General		RIKEN cDNA 672045616 gene, claudin 10, claudin 15, claudin 7
607	3316	AI010237	t		
608	15644	AI010256	General		ESTs, Highly similar to HISTONE H3.3 [R.norvegicus], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B [H3.3B] colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage), interleukin 4 receptor, interleukin 4 receptor, alpha
609	657	AI010262	b		
610	3271	AI010303	b		
611	11081	AI010407	bb		
				ceruloplasmin, ceruloplasmin (ferroxidase)	DNA segment, Chr 3, ERATO Doc 555, expressed, EST, Highly similar to 1012258A factor VIIIC [H.sapiens], ESTs, Weakly similar to CERU MOUSE CERULOPLASMIN PRECURSOR [M.musculus], ESTs, Weakly similar to CERU RAT CERULOPLASMIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to KIUHU ferroxidase [H.sapiens], Hermansky-Pudlak syndrome 3, ceruloplasmin, ceruloplasmin (ferroxidase), hephaestin
612	16521	AI010470	c,a,t,General		
613	6927	AI010542	General		
614	17524	AI010568	a,j,y,General	growth hormone receptor	
615	6946	AI010642	n		
616	23509	AI010662	aa		RIKEN cDNA 2510028H01 gene, sorting nexin 2, sorting nexin 3
617	6844	AI011285	t		
618	13855	AI011361	o		
619	21779	AI011380	cc		
621	12534	AI011460	cc		

TABLE 8: HUMAN HOMOLOGUE ANNOTATIONS					Any. Doc. No. 4987-5000W Doc. No. 0193897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
622	12629	AI011492	e,f		HYA22 protein, conserved gene amplified in osteosarcoma, nuclear LIM interactor-interacting factor
623	735	AI011560	f		Homo sapiens, Similar to RIKEN cDNA 2300002L21 gene, clone MGC:17528 IMAGE:3458906, mRNA, complete cds, RIKEN cDNA 2300002L21 gene, S100 calcium-binding protein A12 (calgranulin C), S100 calcium-binding protein, beta (neural), S100 protein, beta polypeptide, neural
624	3941	AI011598	General		ESTs, Moderately similar to 2113291A laminin:SUBUNIT, Usher syndrome 2A (autosomal recessive, mild) homolog (human), hypothetical protein, MGC:8159, laminin, alpha 5
625	17550	AI011607	j,General		butyrobetaine (gemina), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1, epsilon-trimethyllysine hydroxylase
626	10636	AI011634	a		
627	3995	AI011678	General		
628	16112	AI011706	h		EST, Weakly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 5 (R.norvegicus), Mus musculus, Similar to splicing factor, arginine/serine-rich 7 (35kD), clone MGC:5268 IMAGE:2646366, mRNA, complete cds, neural-salient serine/arginine-rich, splicing factor, arginine/serine-rich 3, splicing factor, arginine/serine-rich 3 (SRp20), splicing factor, arginine/serine-rich 5, splicing factor, arginine/serine-rich 5 (SRp40, HRS)
629	13354	AI011757	c		Fc fragment of IgG, high affinity Ia, receptor for (CD64), Fc fragment of IgG, low affinity IIIa, receptor for (CD16), Fc fragment of IgG, low affinity IIIb, receptor for (CD16), Fc receptor, IgG, low affinity III, expressed sequence BB219290
630	12745	AI011799	cc		
631	18684	AI011812	t		DKFZP564O123 protein, putative breast adenocarcinoma marker (32kD)
632	4205	AI011982	b		
633	6518	AI012114	General		chromosome 1 open reading frame 25, hypothetical protein FLJ20244
634	17407	AI012145	General		
635	13093	AI012177	r		FK506 binding protein 4 (59 kDa), FK506 binding protein 8 (38 kDa), FK506-binding protein 4 (59kD), FK506-binding protein 6 (36kD), FK506-binding protein like, RIKEN cDNA 2210019E14 gene
636	15395	AI012216	f		Fas-associated factor 1, ORF, RIKEN cDNA 2210404D11 gene, UBX domain containing 2, expressed sequence AA408698, expressed sequence AI196514, putative glioblastoma cell differentiation-related

TABLE 9: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4:924-300-000 Doc. No. 179347.1
Seq. ID No.	Identif.	GenBank/Accession Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
					EST X83352, ESTs, Highly similar to T17226 hypothetical protein DKFZp586G223.1 [H.sapiens], Homo sapiens, Similar to chloride intracellular channel 4, clone MGC:8612 IMAGE:3861372, mRNA, complete cds, RIKEN cDNA 5730531E12 gene, chloride intracellular channel 1, chloride intracellular channel 4, chloride intracellular channel 4 (mitochondrial), hypothetical protein DKFZp434N127, intracellular chloride ion channel protein p54H1
637	21796	AI012221	d,General		
638	3981	AI012235	i,General		
639	6606	AI012308	l,r		
					ESTs, Weakly similar to NHPX RAT NHP2656 FAMILY PROTEIN YEL026W HOMOLOG [R.norvegicus], RIKEN cDNA 2410130M07 gene, non-histone chromosome protein 2 (S. cerevisiae)-like 1, nucleolar protein family A, member 2 (HACA small nucleolar RNPs), sperm specific antigen 1
640	3417	AI012337	w		
641	24200	AI012336	b,General		
642	7471	AI012379	cc		
643	7247	AI012438	g		
644	7127	AI012464	p,General		
645	3304	AI012471	b		
646	2311	AI012485	aa		
647	20817	AI012589	g,n,g		
648	3493	AI012590	v,General		
649	8975	AI012613	General		
650	11335	AI012619	j		
651	21409	AI012637	General		
652	8015	AI012638	aa		
					EST, Weakly similar to S33710 ribosomal protein S20, cytosolic [H.sapiens], Mus musculus, Similar to ribosomal protein S20, clone MGC:5876 IMAGE:2651405, mRNA, complete cds, expressed sequence AL024076
653	8476	AI012647	w		
654	4232	AI012958	e,p,General		
655	23128	AI013011	General		
656	20086	AI013260	General		
					ESTs, Highly similar to A26061 glia-derived neurite promoting factor precursor [H.sapiens], ESTs, Highly similar to A27496 glia-derived nexin I alpha precursor [H.sapiens], ESTs, Weakly similar to GLIA DERIVED NEXIN PRECURSOR [R.norvegicus], serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2, serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1
657	11969	AI013273	k		
658	26147	AI013387	aa		
659	8815	AI013437	p		
660	19722	AI013508	k		
661	8674	AI013568	General		
662	23145	AI013647	o,i		
663	15130	AI013676	w		

TABLE 8: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4381-3038WG Doc. No. 1793877.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Grade	Homologous Gene Name	Homologous Cluster Name
664	7274	AI013715	aa		Bone morphogenetic protein 6, bone morphogenetic protein 5, bone morphogenetic protein 6, bone morphogenetic protein 7, bone morphogenetic protein 7 (osteogenic protein 1), growth differentiation factor 15
665	7276	AI013730	e		
666	7278	AI013738	y,z,aa		
667	22592	AI013740	s,x,bb,General		ESTs, Weakly similar to S32567 A4 protein [H.sapiens], Homo sapiens, Similar to RIKEN cDNA 2900052H21 gene, clone MGC:21625 IMAGE:4214683, mRNA, complete cds, Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds, proteolipid protein 2 (colonic epithelium-enriched) Mus musculus retinal cone arrestin 3 (Arr3) mRNA, complete cds, RIKEN cDNA 120006117 gene, arrestin, beta 2, expressed sequence A1326910, retinal S-antigen
668	16584	AI013765	w		
669	24143	AI013804	jj		
670	15528	AI013829	a,General		
671	21950	AI013861	j		3-Hydroxyisobutyrate dehydrogenase, ESTs, Highly similar to D3H1, HUMAN 3-HYDROXYISOBUTYRATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (HIBADH) [H.sapiens], cytokine-like nuclear factor n-pac
672	3260	AI013875	i		
673	2708	AI013882	d,q		
674	6565	AI013886	i		
675	7299	AI013911	p,r,i,General		H.sapiens PABII pseudogene, Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS, Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310074E15, full insert sequence, RNA binding motif protein 3, RNA binding motif protein, X chromosome, RNA binding motif protein, X chromosome retrogene, cold inducible RNA-binding protein, testes-specific heterogeneous nuclear ribonucleoprotein G-T
676	15904	AI013971	General		
677	12781	AI014023	w		EST, Moderately similar to Y124_HUMAN HYPOTHETICAL PROTEIN KIAA0124 [H.sapiens], block of proliferation 1
678	19372	AI014135	aa	beta-carotene 15, 15'-dioxygenase, beta-carotene 15, 15'-dioxygenase	EST, Moderately similar to 0806162D protein COH [M.musculus], EST, Weakly similar to 810024D cytochrome oxidase II [H.sapiens] DKFZP564A2416 protein, EST, Moderately similar to T14738 hypothetical protein DKFZp564A2416.1 [H.sapiens], Homo sapiens cDNA FLJ14138 fls, clone MAMMA1002765, hypothetical protein FLJ13117
679	4241	AI014140	w		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 4497-5089/0 Doc. No. 179387/1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
660	15247	AI014169	c,u		Homo sapiens cDNA: FLJ22783 fis, clone KIA1993, Homo sapiens mRNA: cDNA DKFZp434B102 (from clone DKFZp434B102), KIAA1376 protein, expressed sequence AV216361, upregulated by 1,25-dihydroxyvitamin D-3
661	7315	AI028831	n		ESTs, Highly similar to JE0363 mitogen-activated protein kinase kinase kinase [H.sapiens], mitogen activated protein kinase kinase kinase 5, mitogen-activated protein kinase kinase kinase 6
662	16631	AI028656	General		
663	23297	AI028953	x		ESTs, Moderately similar to RUXG_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN G [H.sapiens], small nuclear ribonucleoprotein polypeptide G
664	11326	AI029015	b		
665	2866	AI029058	n,y		
666	12612	AI029126	General		
667	17602	AI029156	p		
668	7392	AI029185	aa		
669	6517	AI029264	d,k,x		
670	7639	AI029282	b		
691	3874	AI029428	i,General		ESTs, Moderately similar to CB80_HUMAN 80 KDA NUCLEAR CAP BINDING PROTEIN [H.sapiens], Homo sapiens cDNA FLJ11599 fis, clone HEMBA1003879, nuclear cap binding protein subunit 1, 80kD
692	12619	AI029437	f		
693	7452	AI029466	r		
694	7493	AI029608	b		
696	7537	AI029629	o,General		
697	2310	AI029669	v		
698	7585	AI030023	x		
699	7586	AI030024	b,n		
700	14492	AI030091	cc		
701	10673	AI030134	f		EST, Weakly similar to 1605244A erythrocyte ankyrin [H.sapiens], ESTs, Weakly similar to S68418 protein phosphatase 1M chain M110 isoform - rat [R.norvegicus], Human DNA sequence from clone RP11-196N14 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains three novel genes, part of a gene for a novel protein similar to protein serine/threonine phosphatase 4 regulatory subunit 1 (PP4R1) and a gene for a novel protein with an ankyrin domain, RIKEN cDNA 1110058D09 gene, RIKEN cDNA 1600009D24 gene, RIKEN cDNA 4930539L19 gene, expressed sequence AA408090, hypothetical protein MGC5540, leukocyte receptor cluster (LRC) member 3, myosin phosphatase, target subunit 1, protein phosphatase 1, regulatory (inhibitor) subunit 12A, testis-specific ankyrin motif containing protein
702	7615	AI030163	o,z		
703	2370	AI030179	General		
704	7681	AI030449	n		

TABLE 9: HUMAN HOMOLOGUE ANNOTATIONS					Ally: DocRef No. 4194-50896 Doc. No. 179387.1
Seq. ID No.	Identifier	SanBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
705	11559	AI030472	General		ESTs, Highly similar to 2008109A set gene [R.norvegicus], ESTs, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], SET translocation, SET translocation (myeloid leukemia-associated), nucleosome assembly protein 1-like 1, nucleosome assembly protein 1-like 2, nucleosome assembly protein 1-like 4
706	7655	AI030668	lhb	nucleosome assembly protein 1-like 1	
707	24222	AI030704	k		
708	10740	AI030743	h		
709	10742	AI030773	e		
711	16169	AI030932	General		RIKEN cDNA 1300012C15 gene, RIKEN cDNA 2310076L09 gene, adipose differentiation related protein, adipose differentiation-related protein
712	19527	AI030991	f		
713	22614	AI031004	f		
714	3167	AI031012	e		CipP (caseinolytic protease, ATP-dependent, proteolytic subunit, E. coli) homolog, caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli)
715	5350	AI043611	a		
716	7858	AI043654	i		
717	10784	AI043678	d		
718	9180	AI043694	aa		
719	7867	AI043695	aa		ESTs, Highly similar to PUR1_HUMAN AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR [H.sapiens], ESTs, Moderately similar to PUR1_HUMAN AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR [H.sapiens], RIKEN cDNA 5730454C12 gene, expressed sequence AA675351, expressed sequence C79945, glutamine fructose-6-phosphate transaminase 2, glutamine-fructose-6-phosphate transaminase 2, phosphoribosyl pyrophosphate amidotransferase
720	7584	AI043724	General		
721	7895	AI043768	e		
722	7903	AI043805	General		
723	7913	AI043849	cc		ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR, ESTs, Highly similar to ELL2_HUMAN RNA POLYMERASE II ELONGATION FACTOR ELL2 [H.sapiens], ESTs, Weakly similar to ELL_MOUSE RNA POLYMERASE II ELONGATION FACTOR ELL [M.musculus], ESTs, Weakly similar to ELL2_HUMAN RNA POLYMERASE II ELONGATION FACTOR ELL2 [H.sapiens], Mus musculus, clone IMAGE:3563970, mRNA, partial cds, Mus musculus, clone MGC:11987 IMAGE:3601737, mRNA, complete cds, eleven-nineteen lysine-rich leukemia gene, hypothetical protein FLJ22637
724	3899	AI043904	l		
725	6765	AI043914	f		
726	10818	AI043990	g,l,m,General		
727	7956	AI044018	f		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44924-5081WO (Orig. No. 1796887, 1)
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
728	5393	AI044170	p		
729	5398	AI044177	q		
					EST, Weakly similar to S59856 collagen alpha 1(II) chain precursor - mouse [M.musculus], ESTs, Weakly similar to S59856 collagen alpha 1(III) chain precursor - mouse [M.musculus], Homo sapiens, Similar to hypothetical protein FLJ20783, clone MGC:1005 (IMAGE:3139876, mRNA, complete cds, expressed sequence AW122071, hypothetical protein FLJ10355, procollagen, type XX, alpha 1, sequence-specific single-stranded-DNA-binding protein, single-stranded-DNA-binding protein 2
730	5425	AI044237	a,d		
					2,4-dienoyl CoA reductase 1, mitochondrial, 2,4-dienoyl CoA reductase 2, peroxisomal, ESTs, Weakly similar to LUNG CARBOXYL REDUCTASE [M.musculus], ESTs, Weakly similar to S11021 2,4-dienoyl-CoA reductase [R.norvegicus], FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, E coli) like, Homo sapiens AS10 protein mRNA, partial cds, RIKEN cDNA 1200012F07 gene, RIKEN cDNA 1810027F18 gene, carbonyl reductase, carbonyl reductase 2, oxidoreductase UCPA
731	8692	AI044247	r		
732	5430	AI044253	i		
733	5461	AI044338	g,p,General		
734	5464	AI044345	i		
735	3359	AI044347	aa		
					EST, Moderately similar to IL6B_HUMAN INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR [H.sapiens], colony stimulating factor 3 receptor (granulocyte), cytokine receptor-like factor 1, interleukin 12 receptor, beta 2, interleukin 6 signal transducer, interleukin 6 signal transducer (gp130, oncostatin M receptor)
737	2695	AI044396	b		
738	5494	AI044425	General		
740	9882	AI044588	j,m		
741	5575	AI044688	g		
742	2348	AI044794	General		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44924-3087WG Sec. No. 129337-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Group	Homologous Gene Name	Homologous Gene Name
					EST, Moderately similar to JH0148 nucleolin - rat [R.norvegicus], EST, Moderately similar to RBM8_HUMAN PUTATIVE RNA-BINDING PROTEIN 8 [H.sapiens], EST, Weakly similar to NUCL_HUMAN NUCLEOLIN [H.sapiens], ESTs, Highly similar to FUS_HUMAN RNA-BINDING PROTEIN FUS [H.sapiens], ESTs, Highly similar to RBM8_HUMAN PUTATIVE RNA-BINDING PROTEIN 8 [H.sapiens], ESTs, Moderately similar to RBM8_HUMAN PUTATIVE RNA-BINDING PROTEIN 8 [H.sapiens], Mus musculus pippen protein mRNA, complete cds, RNA binding motif protein 8A, TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 58KD (RNA-binding protein 56), fusion, derived from (12;16) malignant liposarcoma
743	18205	AI044836	n		
744	5626	AI044864	u		
745	5630	AI044869	f		
746	5634	AI044883	General		
747	4047	AI044947	l,m		
748	5654	AI044976	w		
749	5654	AI045056	r		
					ESTs, Highly similar to BGAL MOUSE BETA-GALACTOSIDASE PRECURSOR [M.musculus], ESTs, Weakly similar to BGAL MOUSE BETA GALACTOSIDASE PRECURSOR [M.musculus], Homo sapiens, clone IMAGE:3502329, mRNA, partial cds, Homo sapiens, clone IMAGE:3936286, mRNA, partial cds, RIKEN cDNA 4833408P15 gene, galactosidase, beta 1
750	19235	AI045074	General		
751	5689	AI045075	i,aa,General		
					ESTs, Weakly similar to MCAT_HUMAN MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN [H.sapiens], expressed sequence AW108044, solute carrier family 25 (carnitine/acylcarnitine translocase), member 20, solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20, solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 10, solute carrier family 25 (mitochondrial carrier; ornithine transporter), member 15, uncoupling protein 2 (mitochondrial, proton carrier), uncoupling protein 2, mitochondrial
752	5711	AI045151	General		

TABLE 1: HUMAN HOMOLOGUE ANNOTATIONS					Allyl, DocId: No. 4497-6089W0 Doc. No. 9793897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
					ESTs, Moderately similar to K6B2, MOUSE RIBOSOMAL PROTEIN S6 KINASE BETA 2 (S6K-BETA 2) (70 KDA RIBOSOMAL PROTEIN S6 KINASE 2) (P70-S6KB) (P70 RIBOSOMAL S6 KINASE BETA) (P70 S6KBETA) (S6K2) [M.musculus], NIMA (never in mitosis gene a)-related expressed kinase 3, RIKEN cDNA 261031815 gene, expressed sequence A1256796, expressed sequence AW319595, ribosomal protein S6 kinase, 70kD, polypeptide 2, serine/threonine kinase 5
753	19237	AI045153	c		
754	9964	AI045161	f		
755	5735	AI045223	f		
756	5474	AI045477	a, General		
757	5811	AI045502	d, e		
758	5819	AI045537	General		
759	5839	AI045594	i		
760	5808	AI045600	s		TRAM-like protein, translocating chain-associating membrane protein
761	17785	AI045608	y		
763	10020	AI045632	a		
764	5855	AI045668	General		
765	5881	AI045789	i		B aggressive lymphoma gene, DKFZP434J214 protein, KIAA1268 protein
766	5897	AI045862	General		KIAA0138 gene product, hypothetical protein FLJ13213, scaffold attachment factor B
767	5900	AI045866	y, z		
					EST, Weakly similar to C29149 proline-rich protein - mouse [M.musculus], ESTs, Weakly similar to C29149 proline-rich protein - mouse [M.musculus], KIAA0999 protein, Mouse 31-kDa proline-rich salivary protein, complete cds of clone pLUMP125, Mus musculus, Similar to proline-rich protein BatH subfamily 2, clone MGC:18611 IMAGE:4165240, mRNA, complete cds, RIKEN cDNA 6030468B19 gene, Rattus norvegicus proline-rich proteoglycan (PRPG2) mRNA, complete cds, proline-rich protein HaeIII subfamily 2
768	7540	AI045882	a, i, General		
769	5329	AI045970	p		
770	15093	AI058285	d		
771	8002	AI058304	i		
772	8017	AI058341	c		
773	6826	AI058359	General		Cdc42 effector protein 2, Cdc42 effector protein 3
774	8177	AI058603	aa		
775	3090	AI058730	aa		
776	10093	AI058748	g		
777	8143	AI058759	General		
778	18659	AI058762	f		
779	8163	AI058837	aa		
780	4789	AI058889	General		
781	8221	AI059061	General		
782	10159	AI059147	d		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Ally, Doc. No. 4-925-508W3 Doc. No. 979897-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Gene Name
					EST, Weakly similar to GBLP_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 [H.sapiens], Homo sapiens mRNA for FLJ00083 protein, partial cds, IRA1 protein, Rattus norvegicus Sprague Dawley protein kinase C receptor mRNA, complete cds, WD repeat domain 5, expressed sequence AL033335, hypothetical protein, recombination protein REC14
783	8245	AI059154	b		
784	8283	AI059290	n		
785	8314	AI059386	g.General		
786	10200	AI059444	i		
					DKFZP566D213 protein, EST, Moderately similar to EPIDERMAL GROWTH FACTOR PRECURSOR [M.musculus], ESTs, Weakly similar to mel [M.musculus], Epidermal growth factor, epidermal growth factor, epidermal growth factor (beta-urogastrone), hypothetical protein MGCI1256, nel-like 2 homolog (chicken)
787	8347	AI059519	s		
					EST, Highly similar to TERA HUMAN [H.sapiens], EST, Weakly similar to T46437 hypothetical protein DKFZp434K0126.1 [H.sapiens], ESTs, Weakly similar to T46437 hypothetical protein DKFZp434K0126.1 [H.sapiens], ESTs, Weakly similar to TERA HUMAN [H.sapiens], ESTs, Weakly similar to TERA RAT TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE [R.norvegicus], RIKEN cDNA 4633413G10 gene, RIKEN cDNA 5430414H02 gene, spermatogenesis associated factor, valosin containing protein, valosin-containing protein
788	18359	AI059675	n		
789	10281	AI059947	b.i		
790	8494	AI059968	aa		
					Homo sapiens (clone NCD18) tumor necrosis factor receptor related protein mRNA, complete exon and repeat region, lymphotoxin B receptor, lymphotoxin beta receptor (TNFR superfamily, member 3), tumor necrosis factor receptor superfamily, member 8
791	8496	AI059971	General		
792	8496	AI059974	General		
793	10289	AI060053	i		KIAA1585 protein, KIAA1713 protein
794	8548	AI060176	k		CGI-142, RIKEN cDNA 3930401K13 gene
795	8565	AI060236	t		
796	18322	AI060279	y,z		
797	8745	AI060939	r		
					IK cytokine, down-regulator of HLA II, Mus musculus, Similar to IK cytokine, down-regulator of HLA II, clone MGC:25508 IMAGE:4920184, mRNA, complete cds
798	8785	AI070067	o		
					growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-inducible, alpha, growth arrest and DNA-damage-inducible, beta
799	17506	AI070068	cc		

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					Ally. Search No. 44924-Sub-WG
					Doc. No. 1763897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
800	9067	AI070087	General		ESTs, Highly similar to NUC1_HUMAN, NUCLEOLIN [H.sapiens], Nucleolin, RIKEN cDNA 0610010A22 gene, eukaryotic translation initiation factor 3, subunit 4 (delta, 44 kDa), eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD), nucleolin
801	3551	AI070122	a		CGI-97 protein, EST, Weakly similar to YC97_HUMAN HYPOTHETICAL PROTEIN CGI-97 [H.sapiens], RIKEN cDNA 4733401P19 gene
802	4967	AI070179	k		gla maturation factor, gamma
803	18	AI070195	General		CGI-20 protein
804	24197	AI070314	General		armadillo repeat gene deletes in velocardiofacial syndrome, catenin (cadherin-associated protein), delta 1, catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein), plakophilin 4
805	8869	AI070330	r		
806	8874	AI070336	b,cc		
807	10417	AI070410	m		
808	8901	AI070419	aa		toll-like receptor 1, toll-like receptor 10,
809	14424	AI070421	lp,General		toll-like receptor 2, toll-like receptor 8
810	10434	AI070497	General		
811	8927	AI070523	v		
812	8946	AI070611	q		
813	8950	AI070621	w		
814	8972	AI070673	General		
815	8981	AI070715	bb		
816	26184	AI070784	l,j		ESTs, Highly similar to I49636 DNA-binding protein - mouse [M.musculus], ESTs, Moderately similar to I49636 DNA-binding protein - mouse [M.musculus], ESTs, Weakly similar to B57785 zinc finger protein ZNF136 [H.sapiens], ESTs, Weakly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], Homo sapiens, Similar to zinc finger protein 136 (clone pH2-20), clone MCC-10647 IMAGE:4053041, mRNA, complete cds, RIKEN cDNA 2310011F05 gene, pancreas zinc finger protein, zinc finger protein 136 (clone pH2-20), zinc finger protein 260, zinc finger protein 63, zinc finger protein 97
817	3007	AI070824	w		DKFZP664F0522 protein, ESTs,
818	8999	AI070839	p		Weakly similar to T08675 hypothetical protein DKFZp564F0522.1 [H.sapiens]
819	10477	AI070858	e,f		ESTs, Highly similar to NRP2_RAT NEUROFILIN-2 PRECURSOR (VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165 RECEPTOR 2) [R.norvegicus], neuropilin 2, neuropilin-2, platelet derived growth factor C
820	24301	AI070911	k		
821	8721	AI071024	General		
822	9212	AI071098	x		
823	1831	AI071137	c		cell division cycle 25 homolog B (S. cerevisiae), cell division cycle 25 homolog C (S. cerevisiae), cell division cycle 25B, cell division cycle 25C, expressed sequence A1604853

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4:891-686W
					Doc. No. 1:98077.1
Seq. ID No.	Identifier	GenBank Acc. Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
824	11005	AI071139	r		ESTs, Highly similar to ROG_HUMAN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G [H.sapiens], Homo sapiens, Similar to RNA binding motif protein, X chromosome, clone MGC:9398 IMAGE:3875965, mRNA, complete cds, RIKEN cDNA 1700012H05 gene, RNA binding motif protein, X chromosome, RNA binding motif protein, X chromosome retrogene, RNA binding motif protein, Y chromosome, family 1, member A1, testes-specific heterogenous nuclear ribonucleoprotein G-T
825	9104	AI071173	l,m		
826	9583	AI071185	General		
827	9644	AI071410	c		
828	16058	AI071490	General		serine palmitoyltransferase, long chain base subunit 2
829	11057	AI071509	f,o		
831	5695	AI071566	bb		
832	9671	AI071568	w		
833	22929	AI071578	General		DNA segment, human D4S114, P311 protein
834	8673	AI071581	General		
835	9899	AI071646	General		
837	9799	AI072008	q,y,z		
838	9808	AI072050	d		
839	22796	AI072213	General		
840	9271	AI072405	v		
841	10869	AI072425	w		
842	21797	AI072439	General		EST X83352, ESTs, Highly similar to T17226 hypothetical protein DKFZp566G223.1 [H.sapiens], Homo sapiens, Similar to chloride intracellular channel 4, clone MGC:8812 IMAGE:3861372, mRNA, complete cds, RIKEN cDNA 5730531E12 gene, chloride intracellular channel 1, chloride intracellular channel 4, chloride intracellular channel 4 (mitochondrial), hypothetical protein DKFZp434N127, intracellular chloride ion channel protein p64H1
843	9306	AI072521	r		
844	9312	AI072550	j		
845	10893	AI072559	x		
846	1501	AI072634	cc,General		
847	6548	AI072658	General		
848	9363	AI072695	d		DnaJ (Hsp40) homolog, subfamily C, member 4, Homo sapiens, clone MGC:19482 IMAGE:4309314, mRNA, complete cds, hypothetical protein FLJ11506
850	9409	AI072841	n		
851	9410	AI072842	w		
852	9468	AI073021	General		
853	9518	AI073223	f		
854	11183	AI100768	i		EST, Moderately similar to CARBONIC ANHYDRASE II (R.norvegicus), carbonic anhydrase 2, carbonic anhydrase II, carbonic anhydrase VIII, carbonic anhydrase-like sequence 1
855	9190	AI100835	e		

TABLE 8. HUMAN HOMOLOGUE ANNOTATION				Any DocId No. 44924-5185W6 Doc. No. 11993817.1	
Seq. ID No.	Accession	GenBank Acc./ Ref. Seq. ID No.	Accession Code	Homologous Gene Name	Homologous Quarter Name
856	2029	AI100842	p		
857	5687	AI101006	e		
858	15192	AI101099	g,cc		ESTs, Moderately similar to AF078844.1 hsp376 protein [H.sapiens], expressed sequence AA409533
859	17399	AI101157	o		ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2, EST, Weakly similar to ATPK_HUMAN ATP SYNTHASE F CHAIN, MITOCHONDRIAL [H.sapiens], ESTs, highly similar to ATPK_HUMAN ATP SYNTHASE F CHAIN, MITOCHONDRIAL [H.sapiens]
860	9339	AI101160	l,m,o		
861	6321	AI101256	General		ESTs, Moderately similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C [R.norvegicus], Mus musculus high-glycyltyrosine protein type 1 E5 mRNA, complete cds, RNA binding protein p4SAUF1, expressed sequence C85084, heterogeneous nuclear ribonucleoprotein A/B, heterogeneous nuclear ribonucleoprotein D, heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1, 37kD), heterogeneous nuclear ribonucleoprotein D-like
862	5421	AI101270	c		Rho GDP dissociation inhibitor (GDI) beta, expressed sequence C87222, rho, GDP dissociation inhibitor (GDI) beta
863	11910	AI101323	General		ets variant gene 5 (ets-related molecule)
864	23140	AI101608	e		
865	4119	AI101901	General		
866	16324	AI102009	b		
867	18642	AI102023	o		brain-specific membrane-anchored protein, chromosome 1 open reading frame 8
868	19373	AI102044	a	beta-carotene 15, 15'-dioxygenase, beta-carotene 15, 15'-dioxygenase, frizzled (Drosophila) homolog 1, frizzled homolog 1, (Drosophila)	EST, Moderately similar to 0806162D protein COII [M.musculus], EST, Weakly similar to 810024D cytochrome oxidase II [H.sapiens]
869	7051	AI102055	h		ESTs, Highly similar to 2013348A Ser kinase SRPK1 [H.sapiens], Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110005M20, full insert sequence, Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200011B22, full insert sequence, SFRS protein kinase 1, SFRS protein kinase 2, serine/arginine-rich protein specific kinase 2, serine/threonine kinase 23
870	6544	AI102064	c		
871	10227	AI102248	w		
872	23849	AI102316	e,q		
873	11954	AI102505	g,l,s		
874	2125	AI102519	c,k		TYRO protein tyrosine kinase binding protein

TABLE OF HUMAN HOMOLOGUE ANNOTATIONS					Pub. Ref. No. 4498-0000	Doc. No. 1798397-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
875	5967	AI102520	y		ESTs, Weakly similar to GEF2_HUMAN GANGLIOSIDE EXPRESSION FACTOR 2 [R.norvegicus], GABA(A) receptor-associated protein-like 2, RIKEN cDNA 0610012F20 gene, ganglioside expression factor 2	
875	5969	AI102520	p,w		ESTs, Weakly similar to GEF2_HUMAN GANGLIOSIDE EXPRESSION FACTOR 2 [R.norvegicus], GABA(A) receptor-associated protein-like 2, RIKEN cDNA 0610012F20 gene, gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1, ganglioside expression factor 2	
876	11563	AI102560	General			
877	15190	AI102562	b,g,n,p,v		EST, Moderately similar to Cd-7 Metallothionein-2 [H.sapiens], EST, Moderately similar to SMHUIE metallothionein 1E [H.sapiens]	
878	19769	AI102570	bb			
879	22467	AI102576	General		EST, Highly similar to I49523 Mouse primary response gene B94 mRNA, S'end - mouse [M.musculus], Homo sapiens, clone MGC:16332 (IMAGE:3842543, mRNA, complete cds, RIKEN cDNA 1200009106 gene, RIKEN cDNA 1600013K19 gene, similar to S. cerevisiae Sec6p and R. norvegicus rsec6, tumor necrosis factor, alpha-induced protein 2	
880	19011	AI102616	General			
881	23637	AI102620	q,t			
882	23536	AI102727	g,General		solute carrier family 20 (phosphate transporter), member 1, solute carrier family 20 (phosphate transporter), member 2, solute carrier family 20, member 1, solute carrier family 20, member 2	
883	17234	AI102741	c	tissue inhibitor of metalloproteinase 3, tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	tissue inhibitor of metalloproteinase 3, tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	
884	5691	AI102745	k			
885	6796	AI102753	General			
886	6837	AI102849	o,p			
887	15661	AI102868	i		phosphoserine aminotransferase	
888	3533	AI102877	g			
889	13222	AI102977	General			
890	6806	AI103016	o,u			
891	10659	AI103059	w,cc,General			
892	17400	AI103097	e		ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit f, isoform 2, EST, Weakly similar to ATPK_HUMAN ATP SYNTHASE F CHAIN, MITOCHONDRIAL [H.sapiens], ESTs, Highly similar to ATPK_HUMAN ATP SYNTHASE F CHAIN, MITOCHONDRIAL [H.sapiens]	
893	3584	AI103106	x,aa			
894	13296	AI103143	r			

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Desk No. 4191-6038W0 Bnc No. 979887.1
Seq. ID No.	Identifier	SeqBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Group Name	Homologous Cluster Name
895	15981	AI103150	i,x		ESTs, Highly similar to S17516 hypothetical protein [H.sapiens], ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [R.norvegicus], RIKEN cDNA 1110015A16 gene, RIKEN cDNA 2610301N02 gene, expressed sequence AI327276, ubiquitin-conjugating enzyme, ubiquitin-conjugating enzyme E2A (RAD6 homolog), ubiquitin-conjugating enzyme E2B (RAD6 homolog), ubiquitin-conjugating enzyme E2B (RAD6 homolog), ubiquitin-conjugating enzyme E2C, ubiquitin-conjugating enzyme E2G 2
896	3475	AI103245	w		
898	23619	AI103314	p		
899	24181	AI103320	e		
901	4355	AI103410	General		
902	7622	AI103472	General		
903	20918	AI103552	n		
904	21579	AI103572	General		
905	2222	AI103631	o		
906	2752	AI103641	e		
907	4856	AI103708	i		
908	8990	AI103719	I,m,y,z		
909	15942	AI103738	r		
910	22885	AI103828	e,General		
911	15853	AI103841	x	complement component 4 (within H-2S), complement component 4B	EST, Weakly similar to complement component C4A [H.sapiens] EST, Moderately similar to UCRI RAT UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR [R.norvegicus], EST, Weakly similar to UCRI_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR [H.sapiens], ESTs, Moderately similar to UCRI_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR [H.sapiens], Human DNA sequence from clone RP1-228J4 on chromosome 6 Contains a pseudogene similar to UQCRCF1 (ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1), ESTs, an STS and GSSs, RIKEN cDNA 4430402G14 gene, expressed sequence AI875505, ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
912	15050	AI103911	j,y		
913	12376	AI103939	u		
914	22271	AI103947	o,y		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Aty. Doc. No. 4481-338WC Doc. No. 1798897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
915	20833	AI104035	f,q		ESTs, Weakly similar to COXG MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE VIB [M.musculus], Human DNA sequence from clone RP4-591N18 on chromosome 22q13.1-13.2 Contains a COX6B (Cytochrome C Oxidase subunit Vlb (EC 1.9.3.1)) pseudogene, ESTs, GSSs and two putative CpG islands, RIKEN cDNA 201000G05 gene, cytochrome c oxidase subunit Vlb
916	7010	AI104099	w		
917	22101	AI104251	General		DKFZP564O243 protein
918	22633	AI104258	General		
919	22211	AI104279	g,m		EST, Weakly similar to IF6_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 6 [H.sapiens], Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:8530402L05, full insert sequence, integrin beta 4 binding protein
920	10720	AI104296	l		
921	15416	AI104340	l		
922	10991	AI104342	a		
923	18831	AI104357	p		ESTs, Weakly similar to A29861 actin gamma [H.sapiens], ESTs, Weakly similar to I39393 alpha-actin [H.sapiens], ESTs, Weakly similar to S38782 actin beta' chain [H.sapiens], Homo sapiens mRNA; cDNA DKFZp434B2115 (from clone DKFZp434B2115), RIKEN cDNA 1700052K15 gene, RIKEN cDNA 1700061J02 gene, actin-like 7a, expressed sequence AL023024, expressed sequence AV259599, melanoma X-actin, uncharacterized hypothalamus protein HARP11
924	7223	AI104373	e		
925	23574	AI104520	e,g,s	cytochrome c oxidase subunit Vlb polypeptide 1, cytochrome c oxidase, subunit Vlb, polypeptide 1	
926	16509	AI104528	q		NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17)
927	11680	AI104605	v		
928	12342	AI104658	w		ESTs, Weakly similar to RENAL TRANSCRIPTION FACTOR KID-1 [R.norvegicus], ESTs, Weakly similar to T42682 hypothetical protein DKFZp434G1221.1 [H.sapiens], Homo sapiens, clone MGC:20975 IMAGE:4634585, mRNA, complete cds, expressed sequence AA415813, expressed sequence AI639920, expressed sequence AL024263, hypothetical protein FLJ20531, transcription factor 17, transcription factor 17-like 1, zinc finger protein 91, zinc finger protein homologous to Zfp91 in mouse
929	23689	AI104685	r		
930	15377	AI104821	o,cc		hypothetical protein MGC10947, leucine rich repeat (in FLII) interacting protein 2
931	22957	AI104897	General		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Pub. No. 4191-3089WO Doc. No. 1798897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
					ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit, EST, Moderately similar to ATPD_HUMAN ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR [H.sapiens], RIKEN cDNA 0610008F14 gene, expressed sequence AA960090, expressed sequence AI876556, expressed sequence C85518
932	18451	AI104953	o,s		
933	24375	AI104979	n,General		
934	18278	AI105080	bb		3-oxoacid CoA transferase, hypothetical protein FKSG25
935	2196	AI105243	g		
936	5199	AI105272	bb,General		
937	12901	AI105301	o,s		
938	7700	AI105383	cc,General		
939	13343	AI105398	u		
940	22931	AI105417	a,General		DNA segment, human D4S114, P311 protein
941	23596	AI105435	bb		expressed sequence D17825, glutaryl-Coenzyme A dehydrogenase
					ESTs, Highly similar to DHSD_HUMAN SUCCINATE DEHYDROGENASE [H.sapiens], ESTs, Moderately similar to DHSD_HUMAN SUCCINATE DEHYDROGENASE [H.sapiens], succinate dehydrogenase complex, subunit D, integral membrane protein
942	15893	AI105465	o		
943	12660	AI111492	c		
944	4479	AI111599	General		
					EST, Moderately similar to 0710252A histone H3 [H.sapiens], ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], ESTs, Weakly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], ESTs, Weakly similar to JQ1983 H3.3 like histone MH921 - mouse [M.musculus], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B)
945	24211	AI111853	k		
946	2539	AI111960	r		
					EGF-containing fibulin-like extracellular matrix protein 1, EGF-containing fibulin like extracellular matrix protein 2, EST, Weakly similar to FBL3_RAT EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (FIBULIN-3) (FIBL-3) (T16 PROTEIN) [R.norvegicus], ESTs, Highly similar to FBL3_RAT EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (FIBULIN-3) (FIBL-3) (T16 PROTEIN) [R.norvegicus], ESTs, Weakly similar to FBL3_RAT EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (FIBULIN-3) (FIBL-3) (T16 PROTEIN) [R.norvegicus], epidermal growth factor-containing fibulin-like extracellular matrix protein 1, epidermal growth factor-containing fibulin-like extracellular matrix protein 2
947	5729	AI111990	k		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 44921-608000
					Doc. No. 1793897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
948	4049	AI112012	i,q,u,General		EST, Moderately similar to PM17 MOUSE MELANOCYTE PROTEIN PMEL 17 PRECURSOR [M.musculus], Homo sapiens, Similar to glycoprotein (transmembrane) nmb, clone MGC:1696 IMAGE:3345861, mRNA, complete cds, glycoprotein (transmembrane) nmb, silver
949	12908	AI112043	i		
950	20041	AI112161	i		
951	12937	AI112462	General		
952	3713	AI112571	b		
953	12921	AI112636	General		Homo sapiens BAC clone RP11-335J18 from 2, RIKEN cDNA 1700124F02 gene, expressed sequence AI325217, uridine phosphorylase
954	12965	AI112928	General		
955	7499	AI112986	General		
956	4969	AI113008	r		
957	11617	AI136295	f		DKFZP564O123 protein, putative breast adenocarcinoma marker (32kd)
959	11165	AI136372	c		
960	4045	AI136460	cc		
961	12782	AI136493	k		
962	6850	AI136665	h		RIKEN cDNA 2010320H07 gene, ectonucleoside triphosphate diphosphohydrolase 1, ectonucleoside triphosphate diphosphohydrolase 2, ectonucleoside triphosphate diphosphohydrolase 3, ectonucleoside triphosphate diphosphohydrolase 6 (putative function)
963	20920	AI136891	p,v	butyrate response factor 1, zinc finger protein, C3H type, 36-like 1	ESTs, Moderately similar to TISB RAT TIS11B PROTEIN [R.norvegicus], ESTs, Weakly similar to TISB RAT TIS11B PROTEIN [R.norvegicus], butyrate response factor 1, butyrate response factor 1 (EGF-response factor 1), butyrate response factor 2, butyrate response factor 2 (EGF-response factor 2), expressed sequence AW742437
964	6552	AI137062	o		6.2 kd protein
965	22722	AI137211	i		
966	13111	AI137224	o,General		hypothetical protein FLJ20260, oxysterol binding protein 2
967	15969	AI137302	e		DNA segment, Chr 17, ERATO Doi 197, expressed, EST, Weakly similar to ZF37_RAT ZINC FINGER PROTEIN 37 (ZFP-37) [R.norvegicus], ESTs, Weakly similar to I38600 zinc finger protein ZNF135 [H.sapiens], ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-29 [M.musculus], Homo sapiens GIOT-1 mRNA for gonadotropin inducible transcription repressor-1, partial cds, expressed sequence AI449432, hypothetical protein FLJ14855, zinc finger protein 135 (clone pHZ-17), zinc finger protein 29, zinc finger protein 37, zinc finger protein homologous to Zfp37 in mouse
968	14349	AI137303	d		

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS				Atty. Docket No. 4:02A-500000
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name
969	9166	AI137406	General	Homologous Cluster Name
				protein C receptor, endothelial, protein C receptor, endothelial (EPCR)
				EST, Weakly similar to ZF37_RAT
				ZINC FINGER PROTEIN 37 (ZFP-37) [R.norvegicus], ESTs, Weakly similar to B32891 finger protein 2, placental [H.sapiens], ESTs, Weakly similar to ML24 MOUSE ZINC FINGER PROTEIN ML2-4 [M.musculus], Homo sapiens cDNA FLJ14967 fls, clone THYRO1000242, moderately similar to ZINC FINGER PROTEIN 84, expressed sequence A1854635, zinc finger protein 113, zinc finger protein 258, zinc finger protein 37, zinc finger protein 46, zinc finger protein 84 (HPP2), zinc finger protein homologous to Zfp37 in mouse
970	9525	AI137516	r	
971	6638	AI137579	General	
				EST, Weakly similar to IMB3_HUMAN IMPORTIN BETA-3 SUBUNIT [H.sapiens], Homo sapiens cDNA FLJ12978 fls, clone NT2RP2006321, RAN binding protein 6, karyopherin (importin) beta 3
972	7414	AI137586	General	
				EST, Highly similar to R5HU7 ribosomal protein L7, cytosolic [H.sapiens], EST, Weakly similar to RL7 MOUSE 60S RIBOSOMAL PROTEIN L7 [M.musculus], ESTs, Highly similar to R5HU7 ribosomal protein L7, cytosolic [H.sapiens], calponin like transmembrane domain protein, ribosomal protein L7
973	11321	AI137752	z	
974	23473	AI137932	l	
975	13158	AI138024	l	
976	13467	AI138034	cc	UDP-glucose ceramide glucosyltransferase
977	11377	AI138105	y	
978	6790	AI144801	d,h	
979	6506	AI144819	l,l,y	
980	8027	AI144958	l	
982	14458	AI145095	General	
983	7476	AI145202	g	
984	17545	AI145384	e	
985	17479	AI145385	r	
986	4194	AI145387	r	
987	8634	AI145722	g	
988	8339	AI145761	y,General	
989	2059	AI146005	h,General	RIKEN cDNA 2610020J05 gene, pseudouridine synthase 1, pseudouridylation synthase 1
990	23224	AI146033	o	translocase of inner mitochondrial membrane 10 homolog (yeast), translocase of inner mitochondrial membrane 9 (yeast) homolog
				branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease), branched chain ketoacid dehydrogenase E1, beta polypeptide
991	5232	AI168942	bb	
992	18472	AI168975	u	
992	18473	AI168975	u	
993	13235	AI169020	r	
994	11618	AI169115	o,y,General	

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Al17, Board No. 4492-6039 WO Doc. No. 4733367-1
Seq. ID No.	Identif.	Seq. Bank Acc./ Ref. Seq. ID No.	Modif. Code	Homologous Gene Name	Homologous Cluster Name
995	17386	AI169144	o		
996	10984	AI169156	o,u		
997	8205	AI169176	e		
998	12979	AI169177	e		immediate early response 3
					Homo sapiens clone 24468 mRNA sequence, Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone-4633401122, full insert sequence, heterogeneous nuclear ribonucleoprotein C, heterogeneous nuclear ribonucleoprotein C (C1/C2), hnRNP-associated with lethal yellow
999	2607	AI169211	c		ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1, EST, Weakly similar to I54197 hypothetical protein [H.sapiens], ESTs, Weakly similar to VAS1_RAT VACUOLAR ATP SYNTHASE SUBUNIT S1 PRECURSOR (V-ATPASE S1 SUBUNIT) (V-ATPASE S1 ACCESSORY PROTEIN) (V-ATPASE AC45 SUBUNIT) (C7-1 PROTEIN) [R.norvegicus], Homo sapiens cDNA FLJ12553 fls, clone NT2RM4000820, weakly similar to VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34)
1000	22661	AI169265	s,z		
1001	13239	AI169278	g,j,l,y,z		
1002	24162	AI169279	m		
1003	16879	AI169284	o		ADP-ribosylation factor-like 6 interacting protein
					EST, Moderately similar to 0710252A histone H3 [H.sapiens], ESTs, Highly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], ESTs, Weakly similar to H33_HUMAN HISTONE H3.3 [H.sapiens], ESTs, Weakly similar to JQ1983 H3.3 like histone MH921 - mouse [M.musculus], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B)
1004	24213	AI169289	p		
1005	13240	AI169311	cc		
1006	5931	AI169324	b		
1007	20891	AI169337	d		hypothetical protein
1008	11979	AI169365	cd		
					EST, Weakly similar to S13101 cytochrome P450 c17 - rat [R.norvegicus], RIKEN cDNA 2010301M18 gene, RIKEN cDNA 2010318C06 gene, RIKEN cDNA 2210009K14 gene, cytochrome P450, 2c29, cytochrome P450, subfamily 11C (mephenytoin 4-hydroxylase), polypeptide 19
1009	10947	AI169372	s		

TABLE 2. HUMAN HOMOLOGUE ANNOTATIONS				Atty. Order No. 44929-6981W0 Doc. No. 17282PT.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1010	20697	AI169494	o,u		ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump), 42 kDa, ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump), member D, ESTs, Moderately similar to VA00_HUMAN VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) (VACUOLAR PROTON PUMP D SUBUNIT) (V-ATPASE AC39 SUBUNIT) (V-ATPASE 40 KDA ACCESSORY PROTEIN) (P39) (H.sapiens)
1011	8234	AI169517	z		
1012	18343	AI169648	o		
1013	10639	AI169655	l,m		
1014	24146	AI169668	l,j		ATP-binding cassette, sub-family F (GICN20), member 1, ATP-binding cassette, sub-family F (GICN20), member 2, hypothetical protein FLJ11198
1015	22575	AI169728	r		EST, Highly similar to T47184 hypothetical protein DKFZp434F1526.1 (H.sapiens), ESTs, Weakly similar to T47184 hypothetical protein DKFZp434F1526.1 (H.sapiens), hypothetical protein FLJ10889
1016	804	AI169756	cc		Gene 33/Mig-6, RIKEN cDNA 1300002F13 gene
1017	8213	AI169883	p	ferritin light chain 1, ferritin, light polypeptide	ESTs, Highly similar to FRHL ferritin light chain (H.sapiens), ESTs, Moderately similar to FRHL ferritin light chain (H.sapiens), FRC0470 protein, RIKEN cDNA 4933416E14 gene, ferritin light chain 2, ferritin, light polypeptide
1018	3916	AI169947	l,bb		
1019	3733	AI170053	u,General		
1020	14179	AI170224	cc		
1021	11406	AI170263	r		Interleukin 20 receptor, alpha
1022	3547	AI170279	General		ESTs, Weakly similar to ZNT4_HUMAN ZINC TRANSPORTER 4 (H.sapiens), RIKEN cDNA 1810059J10 gene, hypothetical protein DKFZp547M236, hypothetical protein FLJ12496, solute carrier family 30 (zinc transporter), member 1, solute carrier family 30 (zinc transporter), member 4
1023	11524	AI170340	l,y,z		PDZ and LIM domain 1 (ellin), PDZ and LIM domain 3, PDZ-LIM protein myosin, RIKEN cDNA 1110003B01 gene, Rattus norvegicus LIM-domain protein LMP-1 mRNA, complete cds, Z-band alternatively spliced PDZ-motif, actinin alpha 2 associated LIM protein, reversion induced LIM gene
1024	2729	AI170363	e,j		
1025	18811	AI170525	i		
1026	22524	AI170542	h		
1027	24048	AI170570	a,g		CGI-10 protein

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					At1g60400 No. 4166-3089W
					Org. No. 1726897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1028	5968	AI170692	y,aa		GABA(A) receptor-associated protein-like 2, RIKEN cDNA 0610012F20 gene, gamma-aminobutyric acid (GABA(A)) receptor-associated protein like 1, ganglioside expression factor 2
1029	9757	AI170693	b		
1030	18905	AI170770	e,s		
1031	16170	AI170894	i		RIKEN cDNA 1300012C15 gene, RIKEN cDNA 2310076L09 gene, adipose differentiation related protein, adipose differentiation-related protein
1032	708g	AI171185	c	hyaluronan mediated motility receptor (RHAMM)	Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:5720466F14, full insert sequence, RIKEN cDNA 0610027D24 gene, TRAF4 associated factor 1, hyaluronan mediated motility receptor (RHAMM), hyaluronan-mediated motility receptor (RHAMM)
1033	17591	AI171354	b		
1034	13285	AI171361	h		heterogeneous nuclear ribonucleoprotein A0
1035	4428	AI171362	a		EST, Moderately similar to NUAM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR [H.sapiens], NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75KD) (NADH-coenzyme Q reductase)
1036	18126	AI171369	w		
1037	23253	AI171448	o		RIKEN cDNA 2010107E04 gene, chromosome 14 open reading frame 2, expressed sequence AU043134, expressed sequence AV124504
1038	4584	AI171492	m,General		
1039	11158	AI171542	f,s		EST, Moderately similar to NI2M_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT [H.sapiens], NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22KD, B22)
1040	15345	AI171587	i		
1041	21183	AI171678	k		
1042	8215	AI171692	i	ferritin light chain 1, ferritin, light polypeptide	ESTs, Highly similar to FRHUL ferritin light chain [H.sapiens], ESTs, Moderately similar to FRHUL ferritin light chain [H.sapiens], PRO0470 protein, RIKEN cDNA 2010009D05 gene, RIKEN cDNA 4933416E14 gene, cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kynurenine aminotransferase), ferritin light chain 2, ferritin, light polypeptide, hypothetical protein 669
1043	11437	AI171794	i		
1044	2625	AI171800	cc		
1045	23579	AI171802	v		
1046	11708	AI171807	l,t		
1047	17204	AI171844	s,y,z		ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit, RIKEN cDNA 2410043G19 gene, expressed sequence AV000645
1048	4420	AI171918	m		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc# No. 44924-888W
					Doc. No. W497.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1049	3266	AI171948	l,m		DKFZP564F0522 protein, ESTs, Weakly similar to T08675 hypothetical protein DKFZp564F0522.1 (H.sapiens)
1050	19012	AI172056	l		
1051	11205	AI172057	a,q,bb		
1052	6057	AI172102	b		
1053	19128	AI172103	m		
1054	15673	AI172107	z		KIAA1863 protein, sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 2, sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)
1055	5630	AI172184	n		
1056	11968	AI172208	bb		Alpha-fetoprotein, ESTs, Weakly similar to ALPHA-FETOPROTEIN PRECURSOR (M.musculus), ESTs, Weakly similar to FPHU alpha-fetoprotein precursor (H.sapiens), alpha fetoprotein, alpha-fetoprotein
1057	6874	AI172263	l,m		
1058	23313	AI172271	d		
1059	2140	AI172272	General		ESTs, Highly similar to Jc4577 transcription elongation factor T1 (H.sapiens), expressed sequence A1326274, transcription elongation factor A (SII), 2
1060	15382	AI172302	l,p,General		
1061	18689	AI172329	l		
1062	17887	AI172414	o		
1063	3042	AI172447	General		ESTs, Highly similar to BCL3 (M.musculus), ESTs, Weakly similar to I-kappa B alpha chain (M.musculus), hypothetical protein MGC15396, nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha, nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon, testis-specific ankyrin motif containing protein
1064	17291	AI172491	bb		
1065	26222	AI172506	p		
1066	13095	AI172595	r		
1067	8795	AI172618	General		
1068	6454	AI175342	l,l,m,y		BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 6 (UBIQUITIN-CONJUGATING BIR-DOMAIN ENZYME APOLLON) (H.sapiens), ESTs, Moderately similar to T31067 BIR repeat containing ubiquitin-conjugating enzyme BRUCE-mouse (M.musculus), baculoviral IAP repeat-containing 6, hypothetical protein FLJ13855, likely ortholog of mouse ubiquitin-conjugating enzyme Ez-230K

TABLE OF HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 44,924-0003/WO Doc. No. 1738837.1
Seq. ID No.	Contig	Seq. ID No.	Model Code	Homologous Gene Name	Cluster Name
1070	4445	AI175466	x		EST, Highly similar to RASIN RAT TRANSFORMING PROTEIN P21/N-RAS [R.norvegicus], EST, Weakly similar to TVHURR transforming protein R-ras [H.sapiens], Harvey rat sarcoma oncogene, subgroup R, RIKEN cDNA 2610016H24 gene, RIKEN cDNA 4930526B11 gene, Ris, expressed sequence A1573425, neuroblastoma RAS viral (v-ras) oncogene homolog, neuroblastoma ras oncogene, related RAS viral (r-ras) oncogene homolog, similar to mouse Ras, dexamethasone-induced 1
1071	3418	AI175475	m		ESTs, Weakly similar to NHPX RAT NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG [R.norvegicus], RIKEN cDNA 2410130M07 gene, non-histone chromosome protein 2 (S. cerevisiae)-like 1, nucleolar protein family A, member 2 (H1ACA small nucleolar RNPs), sperm specific antigen 1
1072	18507	AI175551	bb		ESTs, Highly similar to S25432 translation elongation factor eEF-1 beta chain [H.sapiens], eukaryotic translation elongation factor 1 beta 2
1073	10217	AI175626	w		
1074	7262	AI175633	j,m,x		
1075	19004	AI175875	r		
1076	22352	AI175959	l,General		
1077	7022	AI176041	h,n		
1078	21467	AI176061	t		EST, Moderately similar to TIG2 HUMAN RETINOIC ACID RECEPTOR RESPONDER PROTEIN 2 PRECURSOR [H.sapiens], retinoic acid receptor responder (tazarotene induced) 2
1079	18581	AI176160	General		
1080	14159	AI176169	g		
1081	21742	AI176172	w		
1082	10182	AI176185	v	FBJ osteosarcoma oncogene, v-fos FBJ murine osteosarcoma viral oncogene homolog	
1083	22765	AI176265	General		
1084	6905	AI176275	a		EST, Moderately similar to T02747 phospholipid-hydroperoxide glutathione peroxidase [H.sapiens], EST, Weakly similar to T02747 phospholipid-hydroperoxide glutathione peroxidase [H.sapiens], ESTs, Weakly similar to GSHH RAT PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE PEROXIDASE [R.norvegicus], Homo sapiens PR022593 mRNA, complete cds, RIKEN cDNA 2310016C16 gene, RIKEN cDNA 3110050F08 gene, glutathione peroxidase 4, glutathione peroxidase 4 (phospholipid hydroperoxidase)
1085	12999	AI176276	cc		Homo sapiens cDNA FLJ12570 fis, clone NT2RM4000695, UDP-N-acetylglucosamine pyrophosphorylase 1

TABLE 9: HUMAN HOMOLOGUE ANNOTATIONS					Ally DocId:36030200 Doc No. 1783897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1086	16438	AI176294	e		ESTs, Weakly similar to B Chain B, Crystal Structure Of The D1d2 Sub-Complex From The Human Snrnp Core Domain [H.sapiens], small nuclear ribonucleoprotein D2 polypeptide (16.5kD)
1087	21130	AI176298	y		
1088	3014	AI176362	e		
1089	15015	AI176363	r		
1090	19006	AI176393	x		
1091	20001	AI176396	o		ESTs, Highly similar to C560_HUMAN SUCCINATE DEHYDROGENASE CYTOCHROME B560 SUBUNIT, MITOCHONDRIAL PRECURSOR [H.sapiens], succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
1092	12174	AI176435	j,m		
1093	15191	AI176456	b,o,t,v,cc		ESTs, Moderately similar to AF078844.1 hgp0376 protein [H.sapiens], expressed sequence AA409533
1094	24236	AI176473	d,General		
1095	16518	AI176546	v		ESTs, Highly similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus], Mus musculus, clone IMAGE:3584569, mRNA, partial cds, expressed sequence C81438, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1, heat shock protein, 86 kDa 1
1096	2161	AI176592	General		
1097	12436	AI176610	General		ESTs, Weakly similar to SYC_HUMAN CYSTEINYL-TRNA SYNTHETASE [H.sapiens], cystenyl-tRNA synthetase, hypothetical protein FLJ12118
1098	2536	AI176616	i,v,General		
1099	18525	AI176792	u		with Glu/Asp-rich carboxy-terminal domain, 2, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4, ESTs, Weakly similar to MRG1_HUMAN MSG-RELATED PROTEIN 1 [H.sapiens], expressed sequence AW742964
1100	23449	AI176828	g		
1101	23299	AI176839	General		
1102	3380	AI176848	e		
1103	22103	AI176849	d,General		
1104	16036	AI176855	f		
1105	15588	AI176916	General		
1106	16917	AI176951	t		
1107	16124	AI176963	cc		
1108	15146	AI176969	b,General		
1109	5786	AI177058	f		EST, Moderately similar to APT RAT ADENINE PHOSPHORIBOSYLTRANSFERASE [R.norvegicus], Mouse adenine phosphoribosyltransferase (APRT), complete cds, adenine phosphoribosyl transferase, adenine phosphoribosyltransferase, expressed sequence C85684
1110	2852	AI177059	c		
1112	3156	AI177082	g		
1113	14384	AI177096	a		

TABLE OF HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 41921-3000 WO Doc. No. 1728897-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1114	13310	AI177119	General		ESTs, Weakly similar to COMPLEMENT C10 SUBCOMPONENT, C-CHAIN PRECURSOR [M.musculus]. Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279 IMAGE:4212772. mRNA, complete cds, complement component 1, q subcomponent, beta polypeptide, complement component 1, q subcomponent, c polypeptide, expressed sequence AI385742
1115	24049	AI177341	g.p.s.u		CGI-10 protein
1116	15964	AI177360	c.General		
1117	14989	AI177366	u		ESTs, Highly similar to B27079 fibronectin receptor beta chain precursor [H.sapiens], integrin beta 1 (fibronectin receptor beta), integrin beta 2, integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12), integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1, macrophage antigen 1 (mac-1) beta subunit)
1118	7975	AI177374	aa		
1119	3006	AI177395	k		dicckopf (Xenopus laevis) homolog 3, dicckopf (Xenopus laevis) homolog 4, soggy-1 gene
1120	17570	AI177683	r		ESTs, Highly similar to ROA3_HUMAN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A3 [H.sapiens]. ESTs, Highly similar to S12520 core protein A1 [H.sapiens]. ESTs, Weakly similar to ROA2 MOUSE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 [M.musculus]. Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STs and GSSs, RIKEN cDNA 3010025E17 gene, Ras-GTPase-activating protein SH3-domain binding protein, heterogeneous nuclear ribonucleoprotein A1, heterogeneous nuclear ribonucleoprotein A2/B1, hypothetical protein 23851
1121	9521	AI177706	b		
1122	14425	AI177755	g.General		ESTs, Moderately similar to PBEF_HUMAN PRE-B CELL ENHANCING FACTOR PRECURSOR [H.sapiens], pre-B-cell colony-enhancing factor
1123	10611	AI177790	j,m		
1124	5356	AI177813	cc		modulator recognition factor I
1125	11791	AI177843	General		sarcoma amplified sequence

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44924-5089WO Rec. No. 4796397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1126	14484	AI177867	General		EH-domain containing 3, EH-domain containing 4, ESTs. Highly similar to EP15 MOUSE EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 [M.musculus], Homo sapiens cDNA FL113682 fig. clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15, Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone 9130014G17, full insert sequence, epidermal growth factor receptor pathway substrate 15, epidermal growth factor receptor substrate EPS15R
1127	5780	AI177869	General		EST, Weakly similar to TESTIN 2 [M.musculus], LIM and cysteine-rich domains 1, four and a half LIM domains 2, testis derived transcript, testis derived transcript (3 LIM domains), vascular Rab-GAP/TBC-containing
1128	19184	AI178025	General		ESTs, Weakly similar to TGIF MOUSE 5'-TG-3' INTERACTING FACTOR [M.musculus], Homo sapiens TGF beta induced transcription factor 2-like mRNA, partial sequence, RIKEN cDNA 5430405H02 gene, RIKEN cDNA 5730599O09 gene, TG interacting factor, TGF-beta-induced factor (TALE family homeobox), TGF-beta-induced factor 2 (TALE family homeobox)
1129	6059	AI178245	c.General		ESTs, Highly similar to T13963 formin related protein, lymphocyte specific - mouse [M.musculus], ESTs, Moderately similar to T13963 formin related protein, lymphocyte specific - mouse [M.musculus], Homo sapiens mRNA; cDNA DKFPz762B245 (from clone DKFPz762B245); partial cds, KIAA1902 protein, formin-like
1130	23248	AI178267	y		chromosome 1 open reading frame 9
1131	4073	AI178272	o		
1132	7636	AI178291	e		
1133	18996	AI178326	y		
1134	22488	AI178392	b		EST, Highly similar to I49523 Mouse primary response gene B94 mRNA, 3' end - mouse [M.musculus], Homo sapiens, clone MGC:16332 IMAGE:3942543, mRNA, complete cds, RIKEN cDNA 120000906 gene, RIKEN cDNA 1600013K19 gene, similar to S. cerevisiae Sec5p and R. norvegicus rsec6, tumor necrosis factor, alpha-induced protein 2
1135	18800	AI178504	n.p.aa		
1136	22197	AI178527	g.General		
1137	3401	AI178684	bb		ESTs, Weakly similar to MCM3_HUMAN DNA REPLICATION LICENSING FACTOR MCM3 [H.sapiens], minichromosome maintenance deficient (S. cerevisiae) 3
1138	17713	AI178700	m		
1139	14874	AI178735	e		

TABLE 9. HUMAN HOMOLOGUE ANNOTATIONS					Ally Doclet No. 4184-5059W Doc. No. 179397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster/Name
1140	23567	AI178746	v,General		EST, Moderately similar to HART1 hemoglobin alpha-1 chain - rat [R.norvegicus], EST, Weakly similar to A45964 hemoglobin alpha chain - mouse [M.musculus], ESTs, Moderately similar to HART1 hemoglobin alpha-1 chain - rat [R.norvegicus], Hemoglobin, alpha 1, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2
1141	18907	AI178871	c		
1142	20991	AI178879	i		
1143	5887	AI179099	q,t		biotinidase, vanin 1, vanin 2, vanin 3
1144	8477	AI179167	b,e,General		
1145	3348	AI179288	u,v		
1146	13608	AI179314	e		
1147	8849	AI179315	g,p		
1148	13611	AI179378	v,General		EST, Weakly similar to MAST CELL PROTEASE 7 PRECURSOR [M.musculus], ESTs, Weakly similar to MCT7 RAT MAST CELL PROTEASE 7 PRECURSOR [R.norvegicus], RIKEN cDNA 2410039E16 gene, RIKEN cDNA 4933401F05 gene, marapsin, mast cell protease 7, proleasse, serine, 21 (testisin), protease, serine, 22, proleasse, serine, 8 (prolastin), tryptase delta 1, tryptase, alpha
1149	15438	AI179399	m,x	collagen, type V, alpha 2, procollagen, type V, alpha 2	EST, Highly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to CA25_HUMAN COLLAGEN ALPHA 2(V) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to I49607 procollagen type V alpha 2 - mouse [M.musculus], RIKEN cDNA 281002D19 gene, collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), collagen, type V, alpha 2, hypothetical protein DKFZp434F0316, hypothetical protein MGC12921, procollagen, type III, alpha 1, procollagen, type V, alpha 2, procollagen, type XIII, alpha 1
1150	13614	AI179407	e,t,General		
1151	15042	AI179422	b,General		
1152	2768	AI179481	i,General		
1153	24041	AI179580	b,j		
1154	19822	AI179599	o,General		
1155	23270	AI179601	q,General		
1156	5901	AI179605	e		
1157	18081	AI179610	g,l,p	heme oxygenase (decycling) 1	heme oxygenase (decycling) 1
1158	14564	AI179717	k		
1159	7918	AI179750	General		
1160	6647	AI179795	g		
1161	9097	AI179875	o,General	hypothetical protein similar to mouse aldehyde reductase 6 (renal), renal-specific oxido-reductase	

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc# No. 44927-5039W Doc. No. 192297.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1162	23989	AI179953	a		gap junction membrane channel protein beta 2, gap junction membrane channel protein beta 5, gap junction protein, beta 2, 26kD (connexin 26), gap junction protein, beta 6 (connexin 30)
1163	12899	AI179967	b		
1164	1687	AI179971	c	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HART1 hemoglobin alpha-1 chain - rat [R.norvegicus], ESTs, Moderately similar to HART1 hemoglobin alpha-1 chain - rat [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2
1165	22569	AI179979	General		
1166	23514	AI179986	o,General		phosphoserine phosphatase, phosphoserine phosphatase-like
1167	15892	AI179988	c,General		
1168	12402	AI180004	g		
1169	5443	AI180165	General		DnaJ (Hsp40) homolog, subfamily B, member 3, DnaJ (Hsp40) homolog, subfamily B, member 6, ESTs, Moderately similar to HSJ2_HUMAN DNAJ PROTEIN HOMOLOG 2 [H.sapiens], ESTs, Weakly similar to HSJ2_HUMAN DNAJ PROTEIN HOMOLOG 2 [H.sapiens], Homo sapiens, clone IMAGE:3930327, mRNA, partial cds, RIKEN cDNA 2810451A06 gene, expressed sequence AU020082
1170	5481	AI180170	General		eukaryotic translation termination factor 1
1171	24028	AI180239	i		
1172	17089	AI180281	g		
1173	3701	AI180306	aa		KIAA0273 gene product, KIAA1796 protein
1174	3352	AI180334	m		
1175	24368	AI180392	i,m		ESTs, Highly similar to NBP_HUMAN NUCLEOTIDE-BINDING PROTEIN [H.sapiens], hypothetical protein FLJ12650, nucleotide binding protein 1 (E.coli MinD like), nucleotide binding protein 2 (E.coli MinD like)
1176	14337	AI180414	c		EST, Highly similar to T14106 probable GTPase-activating protein SPA-1 - rat [R.norvegicus], ESTs, Highly similar to T14106 probable GTPase-activating protein SPA-1 - rat [R.norvegicus], KIAA0440 protein, RIKEN cDNA 2610511M17 gene, expressed sequence AW213287, signal-induced proliferation associated gene 1
1177	19080	AI227647	y,z		hypothetical protein, clone 1-53, small inducible cytokine subfamily D (Cys-X3 Cys), member 1 (fractalkine, neuroectin), small inducible cytokine subfamily D, 1
1178	22838	AI227667	aa		
1179	6765	AI227781	i,General		KIAA0665 gene product, KIAA1821 protein

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS				Any Doc. ID No. 4183-318360 Doc. No. 1783877.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1180	24054	AI227867	General		X-linked protein, brain expressed, X-linked 1, hypothetical protein FLJ10097, nerve growth factor receptor (TNFRSF16) associated protein 1
1181	17324	AI227865	i		
1182	23896	AI227967	d		
1183	1651	AI228068	n,w	peptidylglycine alpha-amidating monooxygenase	peptidylglycine alpha-amidating monooxygenase
1184	14237	AI228128	e		
1185	14242	AI228197	General		ESTs, Moderately similar to C21H_HUMAN PUTATIVE PROTEIN C21ORF18 [H.sapiens], chromosome 21 open reading frame 18
1186	16913	AI228236	o		
1187	22915	AI228299	r		
1188	4917	AI228301	General		
1189	15879	AI228313	r,General		
1190	13727	AI228326	o,General		
1191	6102	AI228335	General		
1192	13730	AI228356	a		ESTs, Highly similar to S70642 ubiquitin ligase Nedd4 - rat [R.norvegicus], ESTs, Moderately similar to S70642 ubiquitin ligase Nedd4 - rat [R.norvegicus], ESTs, Weakly similar to NED4 MOUSE NEDD-4 PROTEIN [M.musculus], RIKEN cDNA 2600016C11 gene, neural precursor cell expressed, developmentally down-regulated 4, neural precursor cell expressed, developmentally down-regulated gene 4a
1193	13745	AI228494	b,cc		
1194	4217	AI228567	s		hypothetical protein MGC4614, membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125), next to the Brca1, oxidative stress induced like, sequestosome 1
1195	16053	AI228596	cz		
1196	3557	AI228672	e		
1197	11605	AI228682	e		
1198	13203	AI228728	r		
1199	13771	AI228848	g		DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1, Protein inhibitor of activated STAT X, protein inhibitor of activated STAT protein PIASy, protein inhibitor of activated STAT3
1200	5918	AI229036	r		
1201	8235	AI229154	k		
1202	16203	AI229196	r	vesicle-associated membrane protein 1, vesicle-associated membrane protein 1 (synaptobrevin 1), vesicle-associated membrane protein 2, vesicle-associated membrane protein 2 (synaptobrevin 2)	Rattus norvegicus mRNA for vesicle associated membrane protein 2B, vesicle-associated membrane protein 1, vesicle-associated membrane protein 1 (synaptobrevin 1), vesicle-associated membrane protein 2, vesicle-associated membrane protein 2 (synaptobrevin 2), vesicle-associated membrane protein 5, vesicle-associated membrane protein 5 (myobrevin), vesicle-associated membrane protein 8, vesicle-associated membrane protein 8 (endobrevin)
1203	13826	AI229304	a		
1204	13144	AI229320	g		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any. Doclet No. 4:992-308906
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1205	4640	AI229404	x,aa		
1206	23563	AI229421	l		MAP kinase-activated protein kinase 2, mitogen-activated protein kinase-activated protein kinase 3
1207	15426	AI229497	s		NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)
1208	15193	AI229508	bb		
1209	19243	AI229638	x		thymidine kinase 1, thymidine kinase 1, soluble
1210	23078	AI229647	p		
1211	3099	AI229680	o		NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)
1212	19508	AI229698	bb		
1213	13977	AI229707	x		EST, Moderately similar to I38369 beta tubulin [H.sapiens], EST, Weakly similar to I38369 beta-tubulin [H.sapiens], EST, Weakly similar to TUBULIN BETA-5 CHAIN [M.musculus], ESTs, Highly similar to A25113 tubulin beta chain 15 - rat [R.norvegicus], FK506-binding protein 1A (12kD), RIKEN cDNA 2310061K05 gene, RIKEN cDNA 2410129E14 gene, tubulin, beta 2, tubulin, beta 5, tubulin, beta polypeptide
1214	23963	AI229708	v		quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))
1215	2688	AI229793	e		
1216	13874	AI229832	g		
1217	12587	AI229979	General		ESTs, Weakly similar to MOT2 MOUSE MONOCARBOXYLATE TRANSPORTER 2 [M.musculus], monocarboxylate transporter, monocarboxylate transporter 4, solute carrier 16 (monocarboxylic acid transporters), member 8, solute carrier family 16 (monocarboxylic acid transporters), member 3, solute carrier family 16 (monocarboxylic acid transporters), member 7, solute carrier family 16 (monocarboxylic acid transporters), member 8
1218	20591	AI229993	l,m		
1219	24042	AI230002	a,b,d,General		
1220	13880	AI230042	u		EST, Highly similar to CCAA MOUSE VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT [M.musculus], ESTs, Weakly similar to CCAA MOUSE VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT [M.musculus], Homo sapiens mRNA; cDNA DKFZp434M0223 (from clone DKFZp434M0223); partial cds, Mus musculus calcium channel mRNA, complete cds, calcium channel, P/Q type, alpha 1A, calcium channel, voltage-dependent, alpha 1G subunit, two-pore channel 1, homolog
1221	17672	AI230074	d		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE)

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atiy, Patent No. 44924-3039C Doc No. 1728397
Seq. ID No.	Identifier	SeqBank Acc/ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1222	3652	AI230113	General		ESTs, Highly similar to E2BE RAT TRANSLATION INITIATION FACTOR eIF-2B EPSILON SUBUNIT [R.norvegicus], HSPC028 protein, RIKEN cDNA 1200015E15 gene, Rattus norvegicus initiation factor eIF-2B mRNA, complete cds, basic leucine-zipper protein BZAP45, eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD), expressed sequence C81315
1223	18650	AI230121	aa		EST, Weakly similar to ENPL_HUMAN ENDOPLASMIN PRECURSOR [H.sapiens], ESTs, Highly similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus], ESTs, Weakly similar to ENPL_HUMAN ENDOPLASMIN PRECURSOR [H.sapiens], Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053), RIKEN cDNA 1810014B01 gene, RIKEN cDNA 2410002K23 gene, expressed sequence C81436, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1, tumor rejection antigen (gp96) 1, tumor rejection antigen gp96
1224	13025	AI230173	c		ESTs, Moderately similar to CHD3_HUMAN CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 3 [H.sapiens], chromodomain helicase DNA binding protein 3
1225	4280	AI230247	z	selenoprotein P, plasma, 1	ESTs, Highly similar to A47327 selenoprotein P precursor [H.sapiens], selenoprotein P, plasma, 1
1226	18526	AI230284	General		Homo sapiens, clone IMAGE3845253, mRNA, partial cds
1227	7084	AI230362	p		
1228	20895	AI230549	b,n		
1229	12961	AI230554	General		EST, Moderately similar to GALECTIN-1 [R.norvegicus], Human HL14 gene encoding beta-galactoside-binding lectin, 3' end, clone 2, RIKEN cDNA 2200008F12 gene, beta-galactoside-binding lectin, lectin, galactose binding, soluble 1, lectin, galactoside-binding, soluble, 1 (galectin 1), lectin, galactoside-binding, soluble, 2 (galectin 2)
1230	15636	AI230616	r		
1231	4121	AI230647	l,m		DNA segment, Chr 17, ERATO Doi 441, expressed, hematological end neurological expressed 1
1232	14386	AI230702	General		
1233	18529	AI230716	x,General		EST, Weakly similar to JW0105 synaptotagmin 2 alpha protein - mouse [M.musculus], ESTs, Weakly similar to 2204390A synaptotagmin [R.norvegicus], ESTs, Weakly similar to JW0105 synaptotagmin 2 alpha protein - mouse [M.musculus], expressed sequence AA675315, inositol polyphosphate-5-phosphatase, 75kD, putative phosphatase, suppressor of actin 1, synaptotagmin 2
1234	13618	AI230724	General		
1235	6304	AI230746	cc		

TABLE 9: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Pocket No. 4493-3089/0 Doc. No. 0298897.1
Seq. ID No.	Identifier	SeqBank/Accession/Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1236	4731	A1230773	e		
1237	14430	A1230798	c,k,x		
1238	16627	A1230822	bb		Alg5, S. cerevisiae, homolog of, dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
1239	3125	A1231028	General		DNA segment, Chr 10, ERATO D01398, expressed, EST's, Weakly similar to PTNL RAT PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 21 [R.norvegicus], Homo sapiens, Similar to erythrocyte membrane protein band 4.1-like 3, clone MGC:12343 IMAGE:4044866, mRNA, complete cds, Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:533043010, full insert sequence, Rattus norvegicus protein tyrosine phosphatase 2E (PTP2E) mRNA, complete cds, erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked), erythrocyte membrane protein band 4.1-like 1, erythrocyte membrane protein band 4.1-like 3, erythrocyte protein band 4.1-like 1, erythrocyte protein band 4.1-like 3, protein tyrosine phosphatase, non-receptor type 21
1240	633	A1231127	k		
1241	20846	A1231140	p		EST, Highly similar to 60S RIBOSOMAL PROTEIN L23A [R.norvegicus], EST's, Highly similar to RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [H.sapiens], ribosomal protein L23a
1242	6743	A1231219	d		
1244	26292	A1231391	k		
1245	12343	A1231433	w		
1246	7337	A1231465	aa		
1247	16321	A1231506	General		
1248	8004	A1231532	ll		EST's, Moderately similar to Z183_HUMAN ZINC FINGER PROTEIN 163 [H.sapiens], zinc finger protein 163 (RING finger, C3HC4 type)
1249	15171	A1231792	g		BCL2-associated athanogene 3, Bcl2-associated athanogene 3, RIKEN cDNA 1600025G07 gene, RIKEN cDNA 241011215 gene
1250	6193	A1231797	l		
1252	14227	A1231999	u		RIKEN cDNA 2610411G23 gene, tumor protein D52-like 1
1253	24501	A1232006	w,y,bb		EST, Moderately similar to EF1D_HUMAN ELONGATION FACTOR 1-DELTA [H.sapiens], EST's, Weakly similar to EF1D_HUMAN ELONGATION FACTOR 1-DELTA [H.sapiens], eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein), hypothetical protein FLJ20897
1254	3434	A1232014	g,q,z,cc,General		

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Ally-DogMnNs-43201-43387	Doc. No. 1792387-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Modif. Code	Homologous Gene Name	Homologous Cluster Name	
1255	19094	AI232021	n.General		ESTs, Highly similar to Human Translation Initiation Factor EIf1, Nmr, 29 Structures [H.sapiens], RIKEN cDNA 1500010M16 gene, RIKEN cDNA 3110001N14 gene, putative translation initiation factor, suppressor of initiator codon mutations, related sequence 1 (S. cerevisiae)	
1256	14020	AI232076	u			
1257	6726	AI232157	d			
1258	11549	AI232174	l,m			
1259	23125	AI232266	j,s			
1260	2065	AI232270	bb			
1261	2913	AI232272	o			
1262	14304	AI232281	g			
1263	15955	AI232294	u,bb.General			
1264	15122	AI232303	y		DKFZP566H073 protein, Homo sapiens chromosome 19, cosmid R31343, RIKEN cDNA 1700065B19 gene, RIKEN cDNA 5730408C10 gene, likely ortholog of mouse g1-related zinc finger protein, ring finger protein 13, zinc finger protein 103	
1265	4716	AI232313	y	purinergic receptor P2X, ligand-gated ion channel 4, purinergic receptor P2X, ligand-gated ion channel, 4	purinergic receptor P2X, ligand-gated ion channel 4, purinergic receptor P2X, ligand-gated ion channel, 1, purinergic receptor P2X, ligand-gated ion channel, 4	
1266	15246	AI232332	l,u			
1267	24321	AI232340	o	stromal cell derived factor 1, stromal cell-derived factor 1	stromal cell derived factor 1, stromal cell-derived factor 1	
1268	16172	AI232341	d			
1269	11411	AI232346	h			
1270	19287	AI232379	f	platelet derived growth factor receptor, alpha polypeptide, platelet-derived growth factor receptor, alpha polypeptide		
1271	5601	AI232461	n.General		Flavin-containing monooxygenase 1, flavin containing monooxygenase 1, flavin containing monooxygenase 2, flavin containing monooxygenase 3, flavin containing monooxygenase 4, hypothetical protein PRO1257	
1272	14051	AI232469	l,m			
1273	5572	AI232490	l,i		ESTs, Moderately similar to A27340 complement C7 precursor [H.sapiens], complement component 7	
1274	11157	AI232494	cc			
1275	8709	AI232534	o		DnaJ (Hsp40) homolog, subfamily B, member 3, DnaJ (Hsp40) homolog, subfamily B, member 6, ESTs, Moderately similar to HSJ2_HUMAN DNAJ PROTEIN HOMOLOG 2 [H.sapiens], ESTs, Weakly similar to HSJ2_HUMAN DNAJ PROTEIN HOMOLOG 2 [H.sapiens], Homo sapiens, clone IMAGE:3930327, mRNA, partial cds, RIKEN cDNA 2810451A06 gene, expressed sequence AU020082	
1276	20350	AI232552	j,v,y			
1277	14069	AI232631	e			
1278	4440	AI232643	w			

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 43241-3319 WO Doc. No. 1738397.1
Seq. ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
					2,4-dienoyl CoA reductase 1, mitochondrial, 2,4-dienoyl CoA reductase 2, peroxisomal, ESTs, Weakly similar to S11021 2,4-dienoyl- CoA reductase [R.norvegicus], FabG (beta-ketoacyl-(acyl-carrier-protein) reductase, E coli) like, H2-K region expressed gene 6, Homo sapiens AS10 protein mRNA, partial cds, Mus musculus, clone MGC-6971 IMAGE:3154595, mRNA, complete cds, RIKEN cDNA 0610039E24 gene, RIKEN cDNA 1810026B04 gene, carbonyl reductase, oxidoreductase UCP4, peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase
1279	17695	AI232784	e		
1280	15796	AI232874	v		
1281	12467	AI232924	General		
					ESTs, Highly similar to I49636 DNA- binding protein - mouse [M.musculus], ESTs, Moderately similar to I49636 DNA-binding protein - mouse [M.musculus], ESTs, Weakly similar to OZF_HUMAN ZINC FINGER PROTEIN OZF [H.sapiens], RIKEN cDNA 2310011F05 gene, pancreas zinc finger protein, zinc finger protein 260, zinc finger protein 36 (KOX 18), zinc finger protein 63, zinc finger protein 97
1282	12873	AI232884	i		
1283	5355	AI233031	r		
1284	18794	AI233121	c		
					DNA segment, Chr 17, human D6S81E 1, ESTs, Highly similar to S33681 translation initiation factor eIF- 4A.I [H.sapiens], HLA-B associated transcript 1, Human clone 23933 mRNA sequence, eukaryotic translation initiation factor 4A, isoform 1, mitochondrial DEAD-box polypeptide 28, nuclear RNA helicase, DECD variant of DEAD box family
1285	3823	AI233147	b,g,General		
1286	11967	AI233155	l,c,k,General		
1287	11561	AI233182	d		
1288	3471	AI233183	g		putative receptor protein
1289	21948	AI233181	i		
1290	13558	AI233194	g,p,y		
1291	15552	AI233195	y		
					EST, Moderately similar to EGFR_HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR [H.sapiens], Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (ErbB1), avian erythroblastosis oncogene B 3, epidermal growth factor receptor, epidermal growth factor receptor (avian erythroblastic leukemia viral (v- erb-b) oncogene homolog)
1292	17907	AI233224	bb		
1293	14111	AI233269	cc		
1294	12894	AI233365	d		
1295	7161	AI233407	General		
1296	15906	AI233425	g		
1297	14120	AI233433	d		
1298	14095	AI233468	a,d		

TABLE 9. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 4392-3089WG Doc. No. 3783397.1
Seq. ID No.	Identifier	Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1299	3075	AI233494	u,aa		oxidase (cytochrome c) assembly 1-like
1300	6046	AI233530	General		
1301	18900	AI233570	General		EST, Moderately similar to S56108 26S proteasome regulatory complex chain p31 [H.sapiens], proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
1302	7888	AI233583	General		Homo sapiens, clone MGC:14993 IMAGE:3613406, mRNA, complete cds, arginyl-tRNA synthetase
1303	16709	AI233602	General	adenosine kinase	adenosine kinase, expressed sequence AI255373
1304	5163	AI233712	y		protein phosphatase 1D magnesium-dependent, delta isoform
1305	7243	AI233717	General		coatomer protein complex, subunit alpha, embryonic ectoderm development
1306	3816	AI233729	g		Homo sapiens cDNA FL102633 fls, clone HEMBA1004900, moderately similar to 26S PROTEASOME SUBUNIT S5B, proteasome (prosome, macropain) 26S subunit, non-ATPase, 5
					Aldehyde reductase 1 (low Km aldose reductase) [5.8 kb PstI fragment, probably the functional gene], EST, Highly similar to Aldose Reductase [E.C.1.1.1.21] [H.sapiens], ESTs, Moderately similar to ALDOSE REDUCTASE [R.norvegicus], ESTs, Moderately similar to ALDOSE REDUCTASE-RELATED PROTEIN 2 [M.musculus], Homo sapiens, Similar to RIKEN cDNA 1110018J12 gene, clone IMAGE:3865164, mRNA, partial cds, RIKEN cDNA 2310005E10 gene, aldo-keto reductase family 1, member A4 (aldehyde reductase), aldo-keto reductase family 1, member B1 (aldose reductase), aldo-keto reductase family 1, member B10 (aldose reductase), aldo-keto reductase family 1, member B3 (aldose reductase), fibroblast growth factor regulated protein
1307	13023	AI233740	d,h,General		
1308	14871	AI233743	g		
1309	7469	AI233767	cc		Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2
1310	7804	AI233771	b		
1311	13563	AI233773	e		
1312	2154	AI233818	k,cc	A kinase (PRKA) anchor protein (gravin) 12	
1313	16616	AI234079	h		
					EST, Moderately similar to CYSR RAT CYSTEINE-RICH PROTEIN 1 [R.norvegicus], ESTs, Weakly similar to CYSR RAT CYSTEINE-RICH PROTEIN 1 [R.norvegicus], ESTs, Weakly similar to S12658 cysteine-rich protein [H.sapiens], cysteine and glycine-rich protein 1, cysteine rich protein, cysteine-rich protein 2, cysteine-rich protein 3, epithelial protein lost in neoplasm beta, thymus LIM protein
1314	13393	AI234100	a,d,General		
1315	7071	AI234162	r		

TABLE 8: HUMAN HOMOLOGUE ANNOTATION					Atty. Doc. No. 4421-5063W0 Doc. No. 179837	
Seq. ID No.	Identifier	GenBank Acc. Ref. Seq. ID No.	Model Code	Homologous Gene Name	Accession	Cluster Name
1316	14677	A1234620	General			
1317	4443	A1234629	m			
1318	22453	A1234678	b			
1319	23964	A1234748	General			
1320	19581	A1234753	f			
1321	22152	A1234822	General	RAS, dexamethasone-induced 1		Harvey rat sarcoma oncogene, subgroup R, RAP1B, member of RAS oncogene family, RAP2B, member of RAS oncogene family, RIKEN cDNA 2610016H24 gene, RIKEN cDNA 4021402C18 gene, RIKEN cDNA 4930526B11 gene, RIKEN cDNA 5830461H18 gene, expressed sequence A1573426, rap2A-like protein, ras-related protein
1322	18942	A1234865	d			
1323	22662	A1234939	aa			ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump), subunit 1, EST, Weakly similar to I54197 hypothetical protein [H.sapiens], ESTs, Weakly similar to VAS1, RAT VACUOLAR ATP SYNTHASE SUBUNIT S1 PRECURSOR (V-ATPASE S1 SUBUNIT) (V-ATPASE S1 ACCESSORY PROTEIN) (V-ATPASE AC45 SUBUNIT) (C7-1 PROTEIN) [R.norvegicus], Homo sapiens cDNA FLJ12563 fls, clone NTZRM4000820, weakly similar to VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34)
1324	3875	A1235047	General			ESTs, Moderately similar to CB80 HUMAN 80 KDA NUCLEAR CAP BINDING PROTEIN [H.sapiens], Homo sapiens cDNA FLJ11599 fls, clone HEMBA1003879, nuclear cap binding protein subunit 1, 80kD
1325	19479	A1235135	o			
1326	14906	A1235192	g			ATP-binding cassette, sub-family F (GCN20), member 1, ATP-binding cassette, sub-family F (GCN20), member 2, hypothetical protein FLJ11198
1327	14718	A1235210	e			
1328	15004	A1235224	General			EST, Moderately similar to TIM1 RAT METALLOPROTEINASE INHIBITOR 1 PRECURSOR [R.norvegicus], EST, Weakly similar to TIM1 RAT METALLOPROTEINASE INHIBITOR 1 PRECURSOR [R.norvegicus], tissue inhibitor of metalloproteinase, tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
1329	6632	A1235277	v			
1330	14722	A1235284	x,z			ESTs, Highly similar to A60592 T-cell surface glycoprotein E2 precursor [H.sapiens], Homo sapiens cDNA FLJ13471 fls, clone PLACE1003566, antigen identified by monoclonal antibodies 12E7, F21 and O13, hypothetical protein DKFZp761H2024
1331	1462	A1235585	General			
1332	21061	A1235631	l,m			

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					ALY Accession No. 49321-3089WG Doc. No. 192897.1
Seq. ID No.	Identifier	GenBank/ Acc/ Ref. Seq. ID No.	Model Gene	Homologous Gene Name	Homologous Cluster Name
1333	14665	AI235646	m	MAD (mothers against decapentaplegic, Drosophila) homolog 4, MAD homolog 4 (Drosophila)	MAD (mothers against decapentaplegic, Drosophila) homolog 4
1334	19940	AI235689	General		
1335	5698	AI235692	u		
1336	23745	AI235732	k		ESTs, Weakly similar to LDVR RAT VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR [R.norvegicus], RIKEN cDNA 4933405111 gene, Very low density lipoprotein receptor, nidogen 2, secreted modular calcium-binding protein 1, secreted modular calcium-binding protein 2, very low density lipoprotein receptor
1337	11164	AI235739	General		ESTs, Highly similar to A56716 aromatic ester hydrolase [H.sapiens], biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen)
1338	5212	AI235745	d		
1339	14768	AI235912	h		
1340	14776	AI235950	m		
1341	3051	AI236027	n, General		
1342	14861	AI236045	r		
1343	14862	AI236048	e		integral membrane protein 2 B, integral membrane protein 2B, integral membrane protein 3
1344	16943	AI236097	p		
1345	8336	AI236101	i		
1346	23230	AI236146	v		
1347	22855	AI236150	e		Down syndrome critical region gene 5
1348	14594	AI236152	i		
1349	18406	AI236168	r		
1350	15051	AI236332	General		ESTs, Weakly similar to ATDA_HUMAN DIAMINE ACETYLTRANSFERASE [H.sapiens], RIKEN cDNA 2610016A03 gene, RIKEN cDNA 4930404K22 gene, spermidine/spermine N1-acetyltransferase, spermidine/spermine N1-acetyltransferase
1351	19298	AI236338	bb		ESTs, Highly similar to NHPX RAT NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG [R.norvegicus], RIKEN cDNA 2410130M07 gene, non-histone chromosome protein 2 (S. cerevisiae)-like 1, nucleolar protein family A, member 2 (HACA small nucleolar RNPs), sperm specific antigen 1

TABLE 9. HUMAN HOMOLOGUE ANNOTATIONS				Atty. Docket No. 4:983-5066W Doc. No. 17688v. 1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
					ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D), EST, Highly similar to 2201474A inducible poly(A)-binding protein [H.sapiens], EST, Weakly similar to 2201474A inducible poly(A)-binding protein [H.sapiens], ESTs, Highly similar to HUD RAT PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG [R.norvegicus], ESTs, Moderately similar to HUD RAT PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG [R.norvegicus], ESTs, Moderately similar to POLYADENYLATE-BINDING PROTEIN 1 [M.musculus], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933407N23, full insert sequence, RIKEN cDNA 4932702K14 gene, poly A binding protein, cytoplasmic 1, poly(A)-binding protein, cytoplasmic 4 (inducible form), slash binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1
1352	10667	A1236366	b		
1353	10774	A1236397	f		
1354	9407	A1236402	aa		
1355	26335	A1236460	General		
1356	17950	A1236590	t,General		
1357	18259	A1236601	h,v		
1358	11445	A1236613	j,y		
					S-phase kinase-associated protein 1A (p19A), transcription elongation factor B (SIII), polypeptide 1 (15 kDa), -like, transcription elongation factor B (SIII), polypeptide 1-like
1359	17248	A1236635	o,aa		
1360	16859	A1236753	t,General		
1361	5208	A1236754	g		
1362	24388	A1236772	e,General		chromosome 8 open reading frame 1
					EST, Highly similar to HS96 RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus], EST, Weakly similar to HHMS84 heat shock protein 84 - mouse [M.musculus], ESTs, Highly similar to T46243 hypothetical protein DKFp761K0511.1 [H.sapiens], expressed sequence AL022974, expressed sequence CB1438, heat shock 90KD protein 1, beta, heat shock protein, 84 kDa 1
1363	15850	A1236795	n,v,w		
1364	14800	A1236856	w		
					Human DNA sequence from clone RPS-1057D4 on chromosome 20 Contains a spermidine synthase (SPDSY) pseudogene, a CpG island, ESTs, STSs and GSSs, spermidine synthase
1366	11404	A1237002	m		
1367	18151	A1237212	o,General		hepatitis B virus x-interacting protein (9.6KD)
1368	21653	A1237535	t,General		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4494-3000WO Sec. No. 0798897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1369	11208	AI237586	z		EST, Weakly similar to JC1241 beta-interferon-induced protein - rat [R.norvegicus], ESTs, Moderately similar to JC1241 beta-interferon-induced protein - rat [R.norvegicus], RIKEN cDNA 1110036C17 gene, RIKEN cDNA 4933438K12 gene, interferon induced transmembrane protein 2 (1-8D)
1370	21893	AI237713	l,k,aa		KIAA0101 gene product
1371	14842	AI237724	r		
1372	3467	AI237835	General		ESTs, Highly similar to MX11 RAT MAX INTERACTING PROTEIN 1 [R.norvegicus], MAX dimerization protein, MAX-interacting protein 1, Max dimerization protein, Max interacting protein 1
1373	25840	AI638972	u		
1374	17108	AI639017	n		EST, Highly similar to S30385 Gsa protein [H.sapiens], ESTs, Weakly similar to T17453 ERG-associated protein ESET - mouse [M.musculus], HLA-B associated transcript 8, SET domain, bifurcated 1, expressed sequence C77070, hypothetical protein FLJ12878, suppressor of variegation 3-9 (Drosophila) homolog 2, hypothetical protein FLJ23414
1375	16676	AI639082	c,k,x	mini chromosome maintenance deficient 6 (S. cerevisiae), minichromosome maintenance deficient (mis5, S. pombe) 6	mini chromosome maintenance deficient 6 (S. cerevisiae), minichromosome maintenance deficient (mis5, S. pombe) 6
1376	12400	AI639107	k		
1377	19952	AI639108	q,v		
1379	25907	AI639167	o,w		
1381	18533	AI639231	n		hypothetical protein, hypothetical protein FLJ20333
1382	18353	AI639233	t,aa	decorin	ESTs, Moderately similar to dJ63G5.3 [H.sapiens], RIKEN cDNA 1700034K18 gene, RIKEN cDNA 5530600M07 gene, decorin
1384	15330	AI639285	General		
1385	20026	AI639354	g		
1386	25671	AI639365	r		
1388	19152	AI639387	u,General		
1390	18338	AI639422	y		EST, Weakly similar to CAQC RAT CALSEQUESTRIN, CARDIAC MUSCLE ISOFORM PRECURSOR [R.norvegicus], calsequestrin 1, calsequestrin 1 (fast-twitch, skeletal muscle), calsequestrin 2, calsequestrin 2 (cardiac muscle)
1392	20082	AI639488	t,m		EST, Moderately similar to A Chain A, Mdm2 Bound To The Transactivation Domain Of P53 (SUB 17-125 [H.sapiens], mouse double minute 2, human homolog of: p53-binding protein, transformed mouse 3T3 cell double minute 2
1394	20056	AI639504	a,bb,General		
1395	4713	AI639518	q		

TABLE 9: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44921-580000	Case No. 1795967
Seq. ID No.	Identifier	GenBank Acc. Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
1396	14332	AJ001044	bb		EST, Moderately similar to T42215 zonadhesin - mouse [M.musculus], EST, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens], Homo sapiens SIB 297 intestinal mucin (MUC3) mRNA, partial cds, RIKEN cDNA 3110056H04 gene, RIKEN cDNA 4931407G18 gene, Rattus norvegicus podocalyxin mRNA, complete cds, hepatitis A virus cellular receptor 1, hypothetical protein DKFZp434N185, lymphocyte antigen 64, mucin 1, transmembrane, mucin 2, intestinal/tracheal, zonadhesin	
1397	7602	AJ001929	k			
1398	9867	AJ005424	u		EST, Weakly similar to CGHU3B collagen alpha 3(V) chain precursor, long splice form [H.sapiens], EST, Weakly similar to D40750 proline-rich protein PRB1/2S [H.sapiens], RIKEN cDNA 119004M21 gene, RIKEN cDNA 2410150I18 gene, RIKEN cDNA 6330577E15 gene, expressed sequence AI551093, mitogen-activated protein kinase 7, murine leukemia viral (bcr-1) oncogene homolog, nemo-like kinase, phospholipid scramblase 1	
1400	16351	AJ011811	General	claudin 7	ESTs, Weakly similar to CLD7 MOUSE CLAUDIN-7 [M.musculus], ESTs, Weakly similar to CLD7 RAT CLAUDIN 7 [R.norvegicus], claudin 10, claudin 15, claudin 16, claudin 7	
1401	20116	AJ011969	General	growth differentiation factor 15, prostate differentiation factor		
1402	17635	AJ223355	v,w		ESTs, Moderately similar to BMCP_HUMAN BRAIN MITOCHONDRIAL CARRIER PROTEIN-1 [H.sapiens], ESTs, Weakly similar to M2OM_HUMAN MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN [H.sapiens], ESTs, Weakly similar to brain mitochondrial carrier protein BMCP1 [M.musculus], RIKEN cDNA 1810012H11 gene, expressed sequence AW108044, solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 10, solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10, solute carrier family 25 (mitochondrial carrier, ornithine transporter), member 15, solute carrier family 25 (mitochondrial carrier, oxoglutarate carrier), member 11, uncoupling protein 2, mitochondrial	

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Pat. No. 4,423,518 WO Reg. No. 179,837.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1403	18666	D00729	g	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase)	ESTs, Highly similar to D302 RAT 3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR [R.norvegicus], Homo sapiens, Similar to dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase), clone MGC:3903 IMAGE:3630566, mRNA, complete cds, dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase)
1404	5049	D10655	n,w		ESTs, Weakly similar to ODP2 RAT DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX [R.norvegicus], Mus musculus, clone IMAGE:3586777, mRNA, partial cds, Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein, RIKEN cDNA 1600017E01 gene, RIKEN cDNA 490052C008 gene, dihydrolipoamide S acetyltransferase (E2 component of pyruvate dehydrogenase complex), dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease), dihydrolipoamide branched chain transacylase E2
1405	25257	D13623	j		
1405	15281	D13623	h		
1406	11434	D14014	cc		
1407	1613	D14076	x		EST, Moderately similar to DYN2 MOUSE DYNAMIN 2 [M.musculus], ESTs, Moderately similar to DYN2 MOUSE DYNAMIN 2 [M.musculus], KIAA0820 protein, dynamin 2
1408	1728	D16479	g		
1409	3015	D16554	c,s,v,z		
1410	472	D26111	d,s,bb		
1412	16233	D29960	jj		
1413	9029	D30804	n	proteasome (prosome, macropain) subunit, alpha type 7, proteasome (prosome, macropain) subunit, alpha type, 7	EST, Highly similar to PROTEASOME SUBUNIT RC6-1 [R.norvegicus], EST, Highly similar to PSA7_HUMAN PROTEASOME SUBUNIT ALPHA TYPE 7 (PROTEASOME SUBUNIT RC6-1) (PROTEASOME SUBUNIT XAPC7) [H.sapiens], ESTs, Highly similar to PROTEASOME SUBUNIT RC6-1 [R.norvegicus], ESTs, Weakly similar to PSA7_HUMAN PROTEASOME SUBUNIT ALPHA TYPE 7 (PROTEASOME SUBUNIT RC6-1) (PROTEASOME SUBUNIT XAPC7) [H.sapiens], Human DNA sequence from clone RP11-180/4 on chromosome 9 Contains a proteasome subunit pseudogene, ESTs, STSs, GSSs and a CpG island, RIKEN cDNA 2410072D24 gene, proteasome (prosome, macropain) subunit, alpha type 7, proteasome (prosome, macropain) subunit, alpha type, 7

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4892-Subswg Doc. No. 179887-1
Seq. ID No.	Identifier	GenBank Acc./Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1414	1485	D38222	y,z		PROTEIN-TYROSINE PHOSPHATASE-LIKE N PRECURSOR [H.sapiens], protein tyrosine phosphatase, receptor type, N, protein tyrosine phosphatase, receptor-type, N
1415	9135	D45247	s	proteasome (prosome, macropain) subunit, beta type 5, proteasome (prosome, macropain) subunit, beta type, 5	EST, Moderately similar to PRCE RAT PROTEASOME EPSILON CHAIN PRECURSOR [R.norvegicus], RIKEN cDNA 5830406J20 gene, proteasome (prosome, macropain) subunit, beta type 5, proteasome (prosome, macropain) subunit, beta type, 5
1416	16354	D50564	u		
1417	1884	D50695	i,m,bb		proteasome (prosome, macropain) 26S subunit, ATPase, 4
1418	21147	D63772	General	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1, solute carrier family 1, member 1	
1419	826	D82628	f		CDP-diacylglycerol-inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)
1420	25306	D84485	u		
1421	18867	D88250	t		EST, Moderately similar to MAS2_HUMAN MANNAN-BINDING LECTIN SERINE PROTEASE 2 PRECURSOR [H.sapiens], EST, Weakly similar to JC6554 probable serine proteinase [R.norvegicus], ESTs, Weakly similar to JC6554 probable serine proteinase [R.norvegicus], MASP-2 protein, complement component 1, r subcomponent, complement component 1, s subcomponent, mannan-binding lectin serine protease 1, mannan-binding lectin serine protease 2
1423	22543	H31117	r,v,General		
1424	12360	H31456	w		
1425	20514	H31489	h,i		
1426	11358	H31610	h		DNA segment, Chr 16, Indiana University Medical 21, expressed, ESTs, Highly similar to JC5020 tetraatricopeptide repeat protein [H.sapiens], ESTs, Moderately similar to JW0059 mprd protein - mouse [M.musculus], PRO1880 protein, g1-related zinc finger protein, tetraatricopeptide repeat domain, tetraatricopeptide repeat domain 3
1427	4360	H31813	bb,General		DKFZP586B1621 protein
1428	9343	H32169	i		EST, Moderately similar to COF1_HUMAN COFILIN, NON-MUSCLE ISOFOR [H.sapiens], cofilin 1 (non-muscle), cofilin 1, non-muscle, cofilin 2 (muscle), cofilin 2, muscle
1429	4386	H33093	h,w		
1430	4415	H33636	h		
1431	15374	H34186	i		ESTs, Weakly similar to IF39_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 [H.sapiens]

TABLE 43. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4392-300000
					Doc. No. 172297.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1432	17159	J00797	u, General		ESTs, Highly similar to A23035 tubulin alpha chain [H.sapiens], tubulin alpha 1, tubulin alpha 2, tubulin alpha 3, tubulin alpha 6, tubulin, alpha 2, tubulin, alpha 3, tubulin, alpha, ubiquitous
1433	16260	J01878	f		
1434	17284	J02827	bb	branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease), branched chain ketoacid dehydrogenase E1, alpha polypeptide	
1435	15017	J03752	n		
1436	44	J03819	p, s	thyroid hormone receptor beta, thyroid hormone receptor, beta (avian erythroblastic leukemia viral (v-erb-a) oncogene homolog 2)	
1437	21014	J03914	e, r, General	glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2	ESTs, Moderately similar to GLUTATHIONE S-TRANSFERASE YB1 [R.norvegicus], glutathione S-transferase M1, glutathione S-transferase, mu 1
1438	20429	J05035	f	steroid 5 alpha-reductase 1, steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)
1439	1247	J05181	j, l, m, s, y, z	glutamate-cysteine ligase, catalytic subunit	glutamate-cysteine ligase, catalytic subunit
1440	10464	J05510	n, u, General	inositol 1,4,5-triphosphate receptor 1, inositol 1,4,5-triphosphate receptor, type 1	ESTs, Highly similar to A55713 inositol 1,4,5-triphosphate receptor type 1 [H.sapiens], ESTs, Weakly similar to IP3R MOUSE INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1 RECEPTOR [M.musculus], expressed sequence A1528790, inositol 1,4,5-triphosphate receptor 1, inositol 1,4,5-triphosphate receptor, type 1
1441	20149	K03243	q		
1442	17758	K03249	q		ESTs, Highly similar to ECHP_HUMAN PEROXISOMAL BIFUNCTIONAL ENZYME [H.sapiens], enoyl Coenzyme A hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
1443	381	L00124	w		
1444	2048	L00382	k, x		
1445	10500	L04619	s		
1447	108	L14002	p		
1448	25386	L14003	t		
1449	109	L14004	c, p		
1450	20414	L14323	General	phosphoinositide-specific phospholipase C-beta 1, phospholipase C, beta 1	ESTs, Highly similar to KIAA0581 protein [H.sapiens]
1451	25369	L14937	y		
1452	16119	L16532	k	2',3'-cyclic nucleotide 3' phosphodiesterase, cyclic nucleotide phosphodiesterase 1	2',3'-cyclic nucleotide 3' phosphodiesterase, cyclic nucleotide phosphodiesterase 1, hypothetical gene CG018
1453	25377	L25387	h	phosphoinositide-specific phospholipase C-beta 1, phospholipase C, beta 1	

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Pocket No. 4392A-60890C Doc. No. 798897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1453	12058	L25387	h	phosphofructokinase, platelet	ESTs, Highly similar to JC2055 6-phosphofructokinase [H.sapiens], ESTs, Weakly similar to JC2055 6-phosphofructokinase [H.sapiens], Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone 2210403E17, full insert sequence, expressed sequence AA407869, phosphofructokinase, liver, B-type, phosphofructokinase, muscle, phosphofructokinase, platelet
1455	21146	L35558	General	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1, solute carrier family 1, member 1	
1456	106	L37203	w		
1458	13682	L38482	f,j,k,m,z		
1459	6405	L38515	p	glutathione synthetase	
1461	15189	M11794	n,v		
1462	17086	M13011	j		
1464	21053	M18481	o		
1465	25405	M18330	l,i		
1466	25415	M19648	a		
1468	14967	M22366	w		
1469	20481	M22631	bb		
1471	15048	M24542	q		EST, Moderately similar to UCRI RAT UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR [R.norvegicus], EST, Weakly similar to UCRI_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR [H.sapiens], ESTs, Moderately similar to UCRI_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR [H.sapiens], Human DNA sequence from clone RP1-228J4 on chromosome 6 Contains a pseudogene similar to UOCRF51 (ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1), ESTs, an STS and GSSs, RIKEN cDNA 4430402G14 gene, expressed sequence A1875505, ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
1472	20921	M29853	m	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE 4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, 4a14, cytochrome P450, subfamily IVA, polypeptide 1 cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13
1473	1224	M31931	u		
1474	15579	M33648	q		
1474	15580	M33648	q		

TABLE OF HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 494-933WO Pat. No. 179897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1475	17211	M34331	g,n,q,v		EST, Moderately similar to 60S RIBOSOMAL PROTEIN L35 [R.norvegicus], EST, Moderately similar to G01477 ribosomal protein L35 [H.sapiens], EST, Weakly similar to 60S RIBOSOMAL PROTEIN L35 [R.norvegicus], ESTs, Highly similar to G01477 ribosomal protein L35 [H.sapiens], Human DNA sequence from clone RP1-34P24 on chromosome 22 Contains a pseudogene similar to ribosomal protein L35, ESTs, STSs and GSSs, RIKEN cDNA 2410039E09 gene, ribosomal protein L35
1476	20699	M35601	b,x,bb	fibrinogen, A alpha polypeptide	Homo sapiens clone HQ0582, expressed sequence A1303526, fibrinogen, A alpha polypeptide, fibrinogen, gamma polypeptide
1476	20700	M35601	b,l,bb	fibrinogen, A alpha polypeptide	Homo sapiens clone HQ0582, expressed sequence A1303528, fibrinogen, A alpha polypeptide, fibrinogen, gamma polypeptide
1477	9223	M36151	o		H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes, expressed sequence A1845868
1479	1585	M57728	j,m,y		Homo sapiens mRNA; cDNA DKFZp434M2227 (from clone DKFZp434M2227), Homo sapiens prostate-specific membrane antigen PSM mRNA, exon 6 alternative splice variant, partial cds, RIKEN cDNA 2610028K12 gene, isolate hydrolase, transferrin receptor, transferrin receptor (p90, CD71), transferrin receptor 2
1480	24844	M58040	c		
1481	25057	M58495	h		
1482	457	M60666	d,General	tropomyosin 1 (alpha),	ESTs, Moderately similar to alpha-tropomyosin slow (M.musculus), tropomyosin 4
1483	1223	M75281	f	tropomyosin 1, alpha	
1484	5733	M81855	i,k,aa	ATP-binding cassette, sub-family B (MDR/TAP), member 1, ATP-binding cassette, sub-family B (MDR/TAP), member 1B	ATP-binding cassette, sub-family B (MDR/TAP), member 1, ATP-binding cassette, sub-family B (MDR/TAP), member 10, ATP-binding cassette, sub-family B (MDR/TAP), member 8, EST, Highly similar to MDR3 MOUSE MULTIDRUG RESISTANCE PROTEIN 3 [M.musculus], EST, Weakly similar to MDR1 RAT MULTIDRUG RESISTANCE PROTEIN 1 [R.norvegicus], ESTs, Weakly similar to MDR1 MOUSE MULTIDRUG RESISTANCE PROTEIN 1 [M.musculus]
1485	4198	M83143	m		ESTs, Highly similar to A41734 beta-galactoside alpha-2,6-sialyltransferase [H.sapiens]
1485	4199	M83143	m		ESTs, Highly similar to A41734 beta-galactoside alpha-2,6-sialyltransferase [H.sapiens]
1486	24651	M83678	k,w,z		RAB13, member RAS oncogene family, RIKEN cDNA 0610007N03 gene, expressed sequence AW107754

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS				Atty. Docket No. 4384-5389WC Doc. No. 1793877.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model/Code	Homologous Gene Name	Homologous Cluster Name
1487	1430	M84648	General	dopa decarboxylase, dopa decarboxylase (aromatic L-amino acid decarboxylase)	EST, Highly similar to AROMATIC-L-AMINO-ACID DECARBOXYLASE [R.norvegicus], EST, Moderately similar to AROMATIC-L-AMINO-ACID DECARBOXYLASE [R.norvegicus], Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610109O21, full insert sequence, dopa decarboxylase, dopa decarboxylase (aromatic L-amino acid decarboxylase)
1488	25467	M93267	c		
1489	729	M95762	a.y		ESTs, Highly similar to NTG3 MOUSE SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 3 [M.musculus], ESTs, Weakly similar to NTG3 HUMAN SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 3 [H.sapiens], expressed sequence AA589632, solute carrier family 6 (neurotransmitter transporter, GABA), member 13
1490	23698	NM_012489	q		DNA segment, Chr 9, ERATO Dcl 25, expressed, Homo sapiens clone 23623 mRNA, partial cds, Homo sapiens, Similar to Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal, clone MGC:18173 IMAGE:4155269, mRNA, complete cds, Homo sapiens, Similar to acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase), clone MGC:23127 IMAGE:4908159, mRNA, complete cds, RIKEN cDNA 0610011L04 gene, acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase), expressed sequence AI255831, expressed sequence AI265397, l-complex protein 1, related sequence 1
1490	23699	NM_012489	q		DNA segment, Chr 9, ERATO Dcl 25, expressed, Homo sapiens clone 23623 mRNA, partial cds, Homo sapiens, Similar to Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal, clone MGC:18173 IMAGE:4155269, mRNA, complete cds, Homo sapiens, Similar to acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase), clone MGC:23127 IMAGE:4908159, mRNA, complete cds, RIKEN cDNA 0610011L04 gene, acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase), expressed sequence AI255831, expressed sequence AI265397, l-complex protein 1, related sequence 1

TABLE 30: HUMAN HOMOLOGUE ANNOTATIONS				Any DocId: No. 44984583W2 Doc. No. 1793867.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Gender	Homologous Gene Name	Homologous Cluster Name
1491	7062	NM_012495	d	aldolase 1, A isoform, aldolase A, fructose-bisphosphate	EST, Moderately similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], EST, Weakly similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], EST, Weakly similar to I39435 fructose-bisphosphate aldolase [H.sapiens], ESTs, Moderately similar to aldolase A [M.musculus], Homo sapiens, aldolase 1, A isoform, clone MGC:16171 (IMAGE:4155253, mRNA, complete cds, RIKEN cDNA 4833425L11 gene, aldolase 1, A isoform, aldolase 3, C isoform, aldolase A, fructose-bisphosphate
1492	15511	NM_012498	u	aldo-keto reductase family 1, member B1 (aldose reductase), aldo-keto reductase family 1, member B3 (aldose reductase)	
1494	7427	NM_012515	General	benzodiazepine receptor (peripheral), benzodiazepine receptor, peripheral	Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazepine receptor (MBR,PBR, PBKS, IBP, Isoquinoline-binding protein)) LIKE protein, the gene for a novel protein similar to part of APOBEC1 (Phorbol 1, Apolipoprotein B mRNA editing protein), and the NFYA gene for nuclear transcription factor Y, alpha (CCAAT-binding transcription factor subunit B, CBF-B, CAAT-Box DNA binding protein subunit A). Contains ESTs, STSs, GSSs, two putative CpG islands and a ca repeat polymorphism, RIKEN cDNA 2510027D20 gene, benzodiazepine receptor (peripheral), benzodiazepine receptor, peripheral
1495	24433	NM_012527	i	cholinergic receptor, muscarinic 3, cholinergic receptor, muscarinic 3, cardiac	cholinergic receptor, muscarinic 1, CNS, cholinergic receptor, muscarinic 3, cholinergic receptor, muscarinic 3, cardiac
1496	4467	NM_012529	d	creatine kinase, brain	EST, Moderately similar to CREATINE KINASE, B CHAIN [R.norvegicus], EST, Weakly similar to KIHUCB creatine kinase [H.sapiens], creatine kinase, brain
1497	16520	NM_012532	General	ceruloplasmin, ceruloplasmin (ferroxidase)	DNA segment, Chr 3, ERATO Doc 555, expressed, EST, Highly similar to 1012298A factor VIIIc [H.sapiens], ESTs, Weakly similar to CERU MOUSE CERULOPLASMIN PRECURSOR [M.musculus], ESTs, Weakly similar to CERU RAT CERULOPLASMIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to KUHU ferroxidase [H.sapiens], Hermansky-Pudlak syndrome 3, ceruloplasmin, ceruloplasmin (ferroxidase), hephaestin

TABLE 10. HUMAN HOMOLOGUE ANNOTATIONS				Any Pocket No. 4497-5689WG Data No. 119837-1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Class	Homologous Gene Name	Homologous Cluster Name
1498	225	NM_012544	x,z	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1, angiotensin converting enzyme	ESTs, Highly similar to A31759 peptidyl-dipeptidase A [H.sapiens], ESTs, Highly similar to JC2038 peptidyl-dipeptidase A [R.norvegicus], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933424D04, full insert sequence, RIKEN cDNA 2010305L05 gene, angiotensin I converting enzyme (peptidyl-dipeptidase A) 1, angiotensin converting enzyme
1499	1431	NM_012545	General	dopa decarboxylase, dopa decarboxylase (aromatic L-amino acid decarboxylase)	EST, Highly similar to AROMATIC-L-AMINO-ACID DECARBOXYLASE [R.norvegicus], EST, Moderately similar to AROMATIC-L-AMINO-ACID DECARBOXYLASE [R.norvegicus], Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2510109O21, full insert sequence, dopa decarboxylase, dopa decarboxylase (aromatic L-amino acid decarboxylase)
1500	23868	NM_012551	l,m,v,General	early growth response 1	ESTs, Weakly similar to I53869 zinc finger protein - mouse [M.musculus], early growth response 1, repressor of GATA, testis zinc finger protein
1500	23872	NM_012551	l,v,cc,General	early growth response 1	ESTs, Weakly similar to I53869 zinc finger protein - mouse [M.musculus], early growth response 1, repressor of GATA, testis zinc finger protein
1500	23869	NM_012551	v,General	early growth response 1	ESTs, Weakly similar to I53869 zinc finger protein - mouse [M.musculus], early growth response 1, repressor of GATA, testis zinc finger protein
1501	19407	NM_012554	z	enolase 1, (alpha), enolase 1, alpha non-neuron	EST, Moderately similar to ALPHA ENOLASE [R.norvegicus], EST, Weakly similar to A29170 phosphopyruvate hydratase [H.sapiens], Homo sapiens cDNA FLJ12774 fls, clone NT2RP2001663, moderately similar to ENOLASE (EC 4.2.1.11), enolase 1, (alpha), enolase 1, alpha non-neuron, enolase alpha, lung-specific, expressed sequence A1427012
1501	19408	NM_012554	n,s,y,z	enolase 1, (alpha), enolase 1, alpha non-neuron	EST, Moderately similar to ALPHA ENOLASE [R.norvegicus], EST, Weakly similar to A29170 phosphopyruvate hydratase [H.sapiens], Homo sapiens cDNA FLJ12774 fls, clone NT2RP2001663, moderately similar to ENOLASE (EC 4.2.1.11), enolase 1, (alpha), enolase 1, alpha non-neuron, enolase alpha, lung-specific, expressed sequence A1427012
1502	21836	NM_012555	k	E26 avian leukemia oncogene 1, 5' domain, v-ets avian erythroblastosis virus E26 oncogene homolog 1	E26 avian leukemia oncogene 1, 5' domain, ESTs, Moderately similar to FLI1 MOUSE RETROVIRAL INTEGRATION SITE PROTEIN FLI-1 [M.musculus], FEV protein, Rattus norvegicus ETS domain transcription factor Pcl-1 mRNA, complete cds, v-ets avian erythroblastosis virus E26 oncogene homolog 1

TABLE 8: HUMAN HOMOLOGUE ANNOTATIONS					Pub. Patent No. 44921-5638WG	Doc. No. 1799387-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
1503	16895	NM_012558	g,s		EST, Weakly similar to FRUCTOSE-1,6-BISPHOSPHATASE ISOZYME 2 [M.musculus], fructose biphosphatase 1, fructose biphosphatase 2, fructose-1,6-bisphosphatase 1, fructose-1,6-bisphosphatase 2	
1504	25317	NM_012559	bb		EST, Moderately similar to FGHUGB fibrinogen gamma-B chain precursor [H.sapiens], EST, Moderately similar to Recombinant Human Gamma-Fibrinogen Carboxyl Terminal Fragment [H.sapiens], ESTs, Weakly similar to FIBG RAT FIBRINOGEN GAMMA-A/B CHAIN PRECURSOR [R.norvegicus], RIKEN cDNA 1110007F23 gene, expressed sequence A303526, fibrinogen, gamma polypeptide, fibrinogen-like 1, ficolin A, ficolin B	
1504	6477	NM_012559	b,bb	fibrinogen, gamma polypeptide	EST, Moderately similar to FGHUGB fibrinogen gamma-B chain precursor [H.sapiens], EST, Moderately similar to Recombinant Human Gamma-Fibrinogen Carboxyl Terminal Fragment [H.sapiens], ESTs, Weakly similar to FIBG RAT FIBRINOGEN GAMMA-A/B CHAIN PRECURSOR [R.norvegicus], RIKEN cDNA 1110007F23 gene, expressed sequence A303526, fibrinogen, gamma polypeptide, fibrinogen-like 1, ficolin A, ficolin B	
1504	6478	NM_012559	bb	fibrinogen, gamma polypeptide	folistatin, folistatin-like 3, folistatin-like 3 (secreted glycoprotein), transmembrane protein with EGF-like and two folistatin-like domains 1	
1505	11731	NM_012561	k	folistatin	group specific component, group-specific component (vitamin D binding protein)	
1507	4254	NM_012564	a	H1 histone family, member 0	H1 histone family, member 0	
1508	16026	NM_012578	r	H1 histone family, member 0	H1 histone family, member 0	
1508	16024	NM_012578	r	H1 histone family, member 0	H1 histone family, member 0	
1508	16025	NM_012578	r	H1 histone family, member 0	H1 histone family, member 0	
1509	16080	NM_012580	g,m	heme oxygenase (decycling) 1	heme oxygenase (decycling) 1	
1510	15098	NM_012588	bb	insulin-like growth factor binding protein 3	insulin-like growth factor binding protein 3, protease, sarin, 11 (igf binding)	
1511	4450	NM_012592	bb	isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	RIKEN cDNA 1300003O09 gene, RIKEN cDNA 2310016C19 gene, acetyl-Coenzyme A dehydrogenase, short chain, isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	
1511	4451	NM_012592	l,bb	isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	RIKEN cDNA 1300003O09 gene, RIKEN cDNA 2310016C19 gene, acetyl-Coenzyme A dehydrogenase, short chain, isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44921-303BWO Doc. No. 1998397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1511	4452	NM_012592	bb	isovaleryl-Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	RIKEN cDNA 1300003008 gene, RIKEN cDNA 2310016C19 gene, acetyl-Coenzyme A dehydrogenase, short chain, isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase
1512	17198	NM_012593	a,x	kalikrein 1, renal/pancreas/salivary, kalikrein 6	kalikrein 1, renal/pancreas/salivary, kalikrein 21, kalikrein 24, kalikrein 27, kalikrein 5
1512	17197	NM_012593	x	kalikrein 1, renal/pancreas/salivary, kalikrein 6	kalikrein 1, renal/pancreas/salivary, kalikrein 21, kalikrein 24, kalikrein 27, kalikrein 5
1513	18749	NM_012600	a,h	malic enzyme 1, NADP(+)-dependent, cytosolic, malic enzyme, supernatant	
1514	2628	NM_012603	General	myelocytomatosis oncogene, v-myc avian myelocytomatosis viral oncogene homolog	
1514	2629	NM_012603	x,General	myelocytomatosis oncogene, v-myc avian myelocytomatosis viral oncogene homolog	RIKEN cDNA 2900002K07 gene, myelocytomatosis oncogene, v-myc avian myelocytomatosis viral oncogene homolog
1515	16849	NM_012608	n,o,q	membrane metallo-endopeptidase, membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	endothelin converting enzyme-like 1, expressed sequence AW322500, mei transforming oncogene-like 1, membrane metallo-endopeptidase, membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10), membrane metallo-endopeptidase-like 2
1517	15540	NM_012620	General	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
1518	24568	NM_012630	General	prolactin receptor	cytokine receptor-like factor 1, interleukin 13 receptor, alpha 2, interleukin 5 receptor, alpha, prolactin receptor, prolactin receptor related sequence 1
1518	24566	NM_012630	General	prolactin receptor	cytokine receptor-like factor 1, interleukin 13 receptor, alpha 2, interleukin 5 receptor, alpha, prolactin receptor, prolactin receptor related sequence 1
1519	18553	NM_012631	k	prion protein, prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Sträussler-Scheinker syndrome, fatal familial insomnia)	prion protein, prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Sträussler-Scheinker syndrome, fatal familial insomnia)
1520	1844	NM_012637	General		ESTs, Highly similar to TPYHUN1 protein-tyrosine-phosphatase (H.sapiens), protein tyrosine phosphatase, non-receptor type 1
1521	24668	NM_012642	f	renin, renin 1 structural	expressed sequence C18352, renin, renin 1 structural, renin 2 tandem duplication of Ren1
1522	18632	NM_012645	a		
1523	25435	NM_012647	g		
1524	9423	NM_012649	b,cc	syndecan 4, syndecan 4 (amphiglycan, ryudocan)	syndecan 4, syndecan 4 (amphiglycan, ryudocan)

TABLE 31 HUMAN HOMOLOGUE ANNOTATIONS					Atiy, DocId:314191-5086W6 Doc. No. 5198397-1	
Seq. ID No.	Identifier	GenBank Acc./ R-L Seq. ID No.	Model Code	Homologous Gene Name	Homologous Gene Name	
1525	24496	NM_012654	n	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3, solute carrier family 9 (sodium/hydrogen exchanger), member 3	ESTs, Weakly similar to NAH1 MOUSE SODIUM/HYDROGEN EXCHANGER 1 [M.musculus], Homo sapiens mRNA: cDNA DKFPz434D0818 (from clone DKFPz434D0818), RIKEN cDNA 0610040A22 gene, RIKEN cDNA 6430709P13 gene, expressed sequence A182282, solute carrier family 9 (sodium/hydrogen exchanger), isoform 3, solute carrier family 9 (sodium/hydrogen exchanger), isoform 6, solute carrier family 9 (sodium/hydrogen exchanger), member 1	
1526	7101	NM_012679	x.bb.General		DNA segment, Chr. 14, University of California at Los Angeles 3, EST, Moderately similar to A41386 clusterin precursor [H.sapiens], ESTs, Moderately similar to A41386 clusterin precursor [H.sapiens], clusterin, clusterin (complement lysis inhibitor, SP-40.40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J), expressed sequence A1893575	
1527	24707	NM_012683	i		cytochrome P450, 2a12, cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13, cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7, pseudogene 1, cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7, pseudogene 2	
1528	1850	NM_012696	t	kininogen	EST, Weakly similar to KNG_MOUSE KININOGEN PRECURSOR [CONTAINS: BRADYKININ] [M.musculus], kininogen	
1528	1854	NM_012696	t	kininogen	EST, Weakly similar to KNG_MOUSE KININOGEN PRECURSOR [CONTAINS: BRADYKININ] [M.musculus], kininogen	
1529	1603	NM_012697	General		EST, Weakly similar to OCN2_MOUSE ORGANIC CATION/CARNITINE TRANSPORTER 2 [M.musculus], ESTs, Highly similar to OCN2_HUMAN ORGANIC CATION/CARNITINE TRANSPORTER 2 [H.sapiens], solute carrier family 22 (organic cation transporter), member 1, solute carrier family 22 (organic cation transporter), member 4, solute carrier family 22 (organic cation transporter), member 5, solute carrier family 22 (organic cation transporter), member 9	
1530	1372	NM_012734	u	hexokinase 1	ESTs, Highly similar to HXK1 RAT HEXOKINASE, TYPE I [R.norvegicus], hexokinase 1, hypothetical protein FLJ22761	
1531	1478	NM_012744	bb.General		expressed sequence C79630, methylcrotonoyl-Coenzyme A carboxylase 1 (alpha), pyruvate carboxylase, pyruvate decarboxylase	

TABLE 9. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 439A1-5049V Doc. No. 1793897.1
Seq. ID No.	Identifier	GenBank Acc. Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1532	343	NM_012747	h,t		Signal transducer and activator of transcription 1, signal transducer and activator of transcription 1, signal transducer and activator of transcription 1, 91kD, signal transducer and activator of transcription 3, signal transducer and activator of transcription 3 (acute-phase response factor)
1533	8629	NM_012749	General		
1534	20628	NM_012752	General	CD24 antigen (small cell lung carcinoma cluster 4 antigen), CD24a antigen	CD24 antigen (small cell lung carcinoma cluster 4 antigen), CD24a antigen
1534	20629	NM_012752	General	CD24 antigen (small cell lung carcinoma cluster 4 antigen), CD24a antigen	CD24 antigen (small cell lung carcinoma cluster 4 antigen), CD24a antigen
1534	20630	NM_012752	General	CD24 antigen (small cell lung carcinoma cluster 4 antigen), CD24a antigen	CD24 antigen (small cell lung carcinoma cluster 4 antigen), CD24a antigen
1535	15174	NM_012756	b		ESTs, Highly similar to 1312358A IGF II receptor [H.sapiens], expressed sequence A1661837, insulin-like growth factor 2 receptor
1536	21685	NM_012760	m,n		EST, Weakly similar to ZF37_RAT ZINC FINGER PROTEIN 37 (ZFP-37) [R.nonvegus], ESTs, Weakly similar to S59069 Z13 protein - mouse [M.musculus], Homo sapiens chromosome 19, BAC 273239 (CIT-8-320G13), Homo sapiens, clone MGC:23189 IMAGE:4854518, mRNA, complete cds, RIKEN cDNA 2410081M15 gene, RIKEN cDNA 2810019F01 gene, RIKEN cDNA 2810011C24 gene, hypothetical protein FLJ12488, hypothetical zinc finger protein MGC2396, zinc finger protein 37, zinc finger protein homologous to Zfp37 in mouse
1537	18068	NM_012762	t		CARD only protein, ESTs, Moderately similar to A55084 Interleukin-1beta converting enzyme beta isozyme [H.sapiens], ESTs, Weakly similar to Interleukin-1beta converting enzyme gamma isozyme [H.sapiens], Homo sapiens mRNA; cDNA DKFZp586A181 (from clone DKFZp586A181); partial cds, ICEBERG caspase-1 inhibitor, caspase 1, caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
1538	1246	NM_012770	a,General		ESTs, Weakly similar to ANPA MOUSE ATRIAL NATRIURETIC PEPTIDE RECEPTOR A PRECURSOR [M.musculus], guanylate cyclase 1, soluble, alpha 3, guanylate cyclase 1, soluble, beta 2, guanylate cyclase 1, soluble, beta 3, natriuretic peptide receptor 1
1539	1346	NM_012776	f	adrenergic receptor kinase, beta 1, adrenergic, beta, receptor kinase 1	G protein-coupled receptor kinase 2, groucho gene related (Drosophila), G protein-coupled receptor kinase 5, G protein-coupled receptor kinase 6, adrenergic, beta, receptor kinase 1, modopsin kinase

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Ally, DocRefNo. 4382-588W Doc. No. 179887.1	
Seq. ID No.	Identifier	GenBank Acc. Ref. Seq. ID No.	Modif. Code	Homologous Gene Name	Homologous Cluster Name	
1540	18135	NM_012791	w	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	ESTs, Moderately similar to DYRK RAT DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORYLATION REGULATED KINASE [R.norvegicus], ESTs, Weakly similar to DYRK MOUSE DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORYLATION REGULATED KINASE [M.musculus], Homo sapiens chromosome 19, CIT-HSP BAC 470n8, Mus musculus, clone MGC:6599 IMAGE:3584001, mRNA, complete cds, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b, dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2, homeodomain-interacting protein kinase 2	
1541	16947	NM_012793	p.bb	guanidinoacetate N-methyltransferase, guanidinoacetate methyltransferase	GAMT, HUMAN GUANIDINOACETATE N-METHYLTRANSFERASE [H.sapiens], Homo sapiens, clone MGC:14390 IMAGE:4300887, mRNA, complete cds, guanidinoacetate N-methyltransferase, guanidinoacetate methyltransferase	
1542	960	NM_012796	u	glutathione S-transferase (theta 2, glutathione S-transferase, theta 2	ESTs, Highly similar to GTT2 RAT GLUTATHIONE S-TRANSFERASE YRS-YRS [R.norvegicus], Homo sapiens mRNA: cDNA DKFZp762N226 (from clone DKFZp762N226), expressed sequence A1265894, glutathione S-transferase theta 2, glutathione S-transferase, theta 2, hypothetical protein	
1543	260	NM_012798	f.u	mal, T-cell differentiation protein, myelin and lymphocyte protein; T-cell differentiation protein	BENE protein, Mus musculus, Similar to BENE protein, clone MGC:19097 IMAGE:4205488, mRNA, complete cds, RIKEN cDNA 2700018N07 gene, expressed sequence A1461653, mal, T-cell differentiation protein, mal, T-cell differentiation protein 2, myelin and lymphocyte protein; T-cell differentiation protein	
1544	556	NM_012803	d	protein C, protein C (inactivator of coagulation factors Va and VIIIa)	B-factor, properdin, DKFZP586H2123 protein, ESTs, Weakly similar to PRTC RAT VITAMIN-K DEPENDENT PROTEIN C PRECURSOR [R.norvegicus], protein C, protein C (inactivator of coagulation factors Va and VIIIa)	
1545	21729	NM_012804	q	ATP-binding cassette, sub-family D (ALD), member 3	ATP-binding cassette, sub-family D (ALD), member 1, ATP-binding cassette, sub-family D (ALD), member 2, ATP-binding cassette, sub-family D (ALD), member 3, ESTs, Weakly similar to ABD3 RAT ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3 [R.norvegicus]	
1546	15032	NM_012816	General	insulin-like growth factor binding protein 5	alpha-methylacyl-CoA racemase, hypothetical protein FLJ11808	
1547	24895	NM_012817	General	insulin-like growth factor binding protein 5	insulin-like growth factor binding protein 5	

TABLE B: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 449A-3083WG Case No. 17988P-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Gene Name
1548	18109	NM_012823	u, General		EST, Weakly similar to ANXA_HUMAN ANNEXIN XI [H.sapiens], annexin A10, annexin A3
1549	373	NM_012833	h, l, q, General	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	ATP-binding cassette, sub-family C (CFTR/MRP), member 10, ATP-binding cassette, sub-family C (CFTR/MRP), member 1a, ATP-binding cassette, sub-family C (CFTR/MRP), member 2, ATP-binding cassette, sub-family C (CFTR/MRP), member 4, ATP-binding cassette, sub-family C (CFTR/MRP), member 6, ESTs, Weakly similar to A40303 cystic fibrosis transmembrane conductance regulator - mouse [M.musculus], expressed sequence A1132311
1550	2855	NM_012838	e	cystatin B, cystatin B (steffin B)	cystatin B, cystatin B (steffin B), expressed sequence A4060480
1551	11136	NM_012839	s	cytochrome c, cytochrome c, somatic	ESTs, Highly similar to 630485A cytochrome c [H.sapiens], ESTs, Weakly similar to CYTOCHROME C, SOMATIC [M.musculus], Homo sapiens pseudogene for cytochrome c-like protein, clone pHGC4E1, Human DNA sequence from clone RP11-169017 on chromosome 13 Contains ESTs, GSSs, STSs and four CpG Islands. Contains a novel protein similar to cytochrome c, part of a novel gene similar to TPTE encoding a transmembrane phosphatase with tensin homology and the ADPRT11 gene encoding ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) like protein 1 (vslu) protein, KIAA0177, cytochrome c, cytochrome c, somatic
1552	20885	NM_012842	a	epidermal growth factor, epidermal growth factor (beta-urogastrone)	EST, Moderately similar to EPIDERMAL GROWTH FACTOR PRECURSOR [M.musculus], ESTs, Moderately similar to EPIDERMAL GROWTH FACTOR PRECURSOR [M.musculus], ESTs, Weakly similar to EGRT epidermal growth factor precursor - rat [R.norvegicus], Homo sapiens mRNA; cDNA DKFZp434O0213 (from clone DKFZp434O0213); partial cds, epidermal growth factor, epidermal growth factor (beta-urogastrone), nidogen 2
1552	20884	NM_012842	a, bb	epidermal growth factor, epidermal growth factor (beta-urogastrone)	EST, Moderately similar to EPIDERMAL GROWTH FACTOR PRECURSOR [M.musculus], ESTs, Moderately similar to EPIDERMAL GROWTH FACTOR PRECURSOR [M.musculus], ESTs, Weakly similar to EGRT epidermal growth factor precursor - rat [R.norvegicus], Homo sapiens mRNA; cDNA DKFZp434O0213 (from clone DKFZp434O0213); partial cds, epidermal growth factor, epidermal growth factor (beta-urogastrone), nidogen 2

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Publ. Packet No. 49921-6693/WO Doc. No. 169387.1	
Seq. ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
1553	16770	NM_012857	e	lysosomal membrane glycoprotein 1, lysosomal- associated membrane protein 1	CD68 antigen, ESTs, Weakly similar to LMP1 RAT LYOSOME- ASSOCIATED MEMBRANE GLYCOPROTEIN 1 PRECURSOR [R.norvegicus], lysosomal membrane glycoprotein 1, lysosomal-associated membrane protein 1, similar to S68401 (cattle) glucose induced gene	
1554	20674	NM_012861	i	O-6-methylguanine-DNA methyltransferase, O-6- methylguanine-DNA methyltransferase	ESTs, Highly similar to 1207289A reverse transcriptase related protein [H.sapiens], ESTs, Highly similar to S21348 probable polypeptide- related protein 4 - rat [R.norvegicus], ESTs, Moderately similar to GNMSLL retrovirus-related reverse transcriptase homolog - mouse retrotransposon [M.musculus], ESTs, Weakly similar to 1207289A reverse transcriptase related protein [H.sapiens], ESTs, Weakly similar to B34087 hypothetical protein [H.sapiens], Homo sapiens cDNA FLJ12202 fs, clone MAMMA1000908, Mus musculus, Similar to L1 repeat, Tt subfamily, member 30, clone MGC:7372 IMAGE:3487559, mRNA, complete cds, RIKEN cDNA 1700082M22 gene, T lymphoma oncogene, expressed sequence AJ267024, hypothetical protein FLJ21032, pheromone receptor V3R4	
1555	13151	NM_012862	a,r,General	matrix Gla protein, matrix gamma-carboxyglutamate (gla) protein	MATRIX GLA-PROTEIN PRECURSOR [H.sapiens], matrix Gla protein, matrix gamma- carboxyglutamate (gla) protein	
1556	24617	NM_012870	General	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	Nerve growth factor receptor, fast, RIKEN cDNA 2610311B09 gene, nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16), tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin), tumor necrosis factor receptor superfamily, member 21	
1557	20945	NM_012875	a,v		EST, Moderately similar to 60S RIBOSOMAL PROTEIN L39 [R.norvegicus], ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L39 [R.norvegicus], ESTs, Highly similar to G02654 ribosomal protein L39 [H.sapiens], ESTs, Moderately similar to G02654 ribosomal protein L39 [H.sapiens], RIKEN cDNA 2810465O16 gene, RIKEN cDNA 4930517K11 gene, ribosomal protein L39, ribosomal protein L39-like 1	

TABLE 3: HUMAN HOMOLOGUS ANNOTATIONS					Aty. Accession No. and Source Ref. No. 133837.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1558	15872	NM_012879	c,r	solute carrier family 2 (facilitated glucose transporter), member 2	ESTs, Highly similar to A31318 glucose transporter-like protein [H.sapiens], ESTs, Weakly similar to GLUCOSE TRANSPORTER TYPE 2, LIVER [R.norvegicus], ESTs, Weakly similar to S05319 glucose transport protein, hepatic - mouse [M.musculus], solute carrier family 2 (facilitated glucose transporter), member 10, solute carrier family 2 (facilitated glucose transporter), member 2, solute carrier family 2, (facilitated glucose transporter) member 8
1559	495	NM_012880	z	superoxide dismutase 3, extracellular	RIKEN cDNA 1700105P06 gene, superoxide dismutase 3, extracellular
1559	494	NM_012880	c	superoxide dismutase 3, extracellular	RIKEN cDNA 1700105P06 gene, superoxide dismutase 3, extracellular
1560	23651	NM_012881	d,u,General	secreted phosphoprotein 1, secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1)	
1562	19477	NM_012891	q		
1563	18564	NM_012899	v,General	aminolevulinate, delta-, dehydratase	aminolevulinate, delta-, dehydratase
1564	7197	NM_012904	f,r,cc,General	annexin A1	EST, Weakly similar to A Chain A, Nmr Solution Structure Of Domain 1 Of Human Annexin I (SUB 41-113 [H.sapiens], annexin A1
1564	7196	NM_012904	v,cc,General	annexin A1	
1565	20202	NM_012909	b,r	aquaporin 2, aquaporin 2 (collecting duct), aquaporin 6, aquaporin 6, kidney specific	
1566	16581	NM_012911	c,j		Mus musculus retinal cone arrestin 3 (Arr3) mRNA, complete cds, RIKEN cDNA 1200006117 gene, arrestin, beta 2, expressed sequence A1326910, retinal S-antigen
1566	16582	NM_012911	c		Mus musculus retinal cone arrestin 3 (Arr3) mRNA, complete cds, RIKEN cDNA 1200006117 gene, arrestin, beta 2, expressed sequence A1326910, retinal S-antigen
1567	24431	NM_012912	General	activating transcription factor 3	ESTs, Highly similar to 1604249C transcription factor ATF3 [H.sapiens], ESTs, Weakly similar to ATF3 RAT CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-3 [R.norvegicus], Jun dimerization protein 2, activating transcription factor 3, basic leucine zipper transcription factor, ATF-like
1568	18118	NM_012913	p	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 3 polypeptide	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 3 polypeptide, ESTs, Highly similar to G02485 Na <sup>+</sup> /K <sup>+</sup> -exchanging ATPase [H.sapiens], expressed sequence A1654000
1569	6108	NM_012915	n		ATPase inhibitor, ATPase inhibitor precursor, ESTs, Moderately similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [R.norvegicus], Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610204M17, full insert sequence

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS				Atty. Patent No. 4,197,508BWO Doc. No. 179387.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Metad. Code	Homologous Gene Name	Homologous Cluster Name
1570	20757	NM_012923	c,i,aa	cyclin G, cyclin G1	cyclin G, cyclin G1, cyclin G2, cyclin I
1570	20755	NM_012923	i	cyclin G, cyclin G1	cyclin G, cyclin G1, cyclin G2, cyclin I
1571	2830	NM_012925	f	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344), CD59a antigen	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344), CD59a antigen, ESTs, Weakly similar to CD59 RAT CD59 GLYCOPROTEIN PRECURSOR [R.norvegicus]
1571	2831	NM_012925	f	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344), CD59a antigen	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344), CD59a antigen, ESTs, Weakly similar to CD59 RAT CD59 GLYCOPROTEIN PRECURSOR [R.norvegicus]
1572	1977	NM_012930	q	camitine palmitoyltransferase 2, camitine palmitoyltransferase II	EST, Moderately similar to CPT2 RAT CARNTINE O-PALMITOYLTRANSFERASE II, MITOCHONDRIAL PRECURSOR [R.norvegicus], camitine palmitoyltransferase 2, camitine palmitoyltransferase II, expressed sequence A1323687
1573	18694	NM_012931	j,i,m,z		CD2-associated protein, HEF like Protein, Homo sapiens cDNA FLJ14854 fis, clone PLACE1000972, breast cancer anti-estrogen resistance 1, enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related), neural precursor cell expressed, developmentally down-regulated gene 9, v-crk-associated tyrosine kinase substrate
1574	13723	NM_012935	n	crystallin, alpha B	
1575	9109	NM_012939	j,y,z	cathepsin H	ESTs, Highly similar to KHHUH cathepsin H [H.sapiens], ESTs, Weakly similar to CATHEPSIN H PRECURSOR [R.norvegicus], Homo sapiens cDNA: FLJ22499 fis, clone HRC11250, highly similar to HSCATH4 Human mRNA for cathepsin H (EC 3.4.22.16), cathepsin H, cathepsin W, cathepsin W (lymphopain)
1575	19398	NM_012939	aa		
1576	223	NM_012945	b,cc	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), heparin binding epidermal growth factor-like growth factor	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor), expressed sequence AWW047313, heparin binding epidermal growth factor-like growth factor
1577	15056	NM_012950	cc	coagulation factor II (thrombin) receptor	ESTs, Weakly similar to GPRY_MOUSE PROBABLE G PROTEIN-COUPLED RECEPTOR GPR34 [M.musculus], G protein-coupled receptor 41, G protein-coupled receptor 43, Rattus norvegicus protease activated receptor 3 mRNA, complete cds, coagulation factor II (thrombin) receptor

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any Pocket No. 44931-50370 Doc. No. 199337.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1579	19111	NM_012963	g	high mobility group box 1, high-mobility group (nonhistone chromosomal) protein 1	EST, Moderately similar to A Chain A, Crystal Structure Of Hmg1 Domain A Bound To A Cisplatin- Modified Dna Duplex [R.norvegicus], EST, Weakly similar to A Chain A, Crystal Structure Of Hmg1 Domain A Bound To A Cisplatin- Modified Dna Duplex [R.norvegicus], ESTs, Highly similar to S02826 nonhistone chromosomal protein HMG-1 [H.sapiens], ESTs, Moderately similar to HIGH MOBILITY GROUP PROTEIN HMG1 [M.musculus], RIKEN cDNA 4932431P20 gene, high mobility group box 1, high mobility group box 3, high-mobility group (nonhistone chromosomal) protein 1, high-mobility group (nonhistone chromosomal) protein 1-like 10, high-mobility group (nonhistone chromosomal) protein 1-like 3
1580	19374	NM_012964	x	hyaluronan mediated motility receptor (RHAMM), hyaluronan-mediated motility receptor (RHAMM)	Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:5720466F14, full insert sequence, RIKEN cDNA 0610027D24 gene, TRAF4 associated factor 1, hyaluronan mediated motility receptor (RHAMM), hyaluronan-mediated motility receptor (RHAMM)
1581	2554	NM_012967	t	intercellular adhesion molecule, intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	Homo sapiens mRNA; cDNA DKFZp434E0516 (from clone DKFZp434E0516), intercellular adhesion molecule, intercellular adhesion molecule 1 (CD54), human rhinovirus receptor, intercellular adhesion molecule 3, intercellular adhesion molecule 5, telencephalin
1581	2555	NM_012967	t,cc,General	intercellular adhesion molecule, intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	Homo sapiens mRNA; cDNA DKFZp434E0516 (from clone DKFZp434E0516), intercellular adhesion molecule, intercellular adhesion molecule 1 (CD54), human rhinovirus receptor, intercellular adhesion molecule 3, intercellular adhesion molecule 5, telencephalin
1582	24526	NM_012973	c	potassium voltage-gated channel, Isk-related family, member 1, potassium voltage-gated channel, Isk-related subfamily, member 1	potassium voltage-gated channel, Isk-related family, member 1, potassium voltage-gated channel, Isk-related subfamily, member 1
1583	956	NM_012976	c		ESTs, Highly similar to LEG9 RAT GALECTIN-9 [R.norvegicus], ESTs, Highly similar to LEG9_HUMAN GALECTIN-9 [H.sapiens], ESTs, Weakly similar to LEG9 RAT GALECTIN-9 [R.norvegicus], expressed sequence A1265545, lectin, galactose binding, soluble 12, lectin, galactose binding, soluble 9, lectin, galactoside-binding, soluble, 9 (galectin 9)
1584	16417	NM_012991	g	nucleoporin 50kD, nucleoprotein 50	nucleoporin 50kD, nucleoprotein 50

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					Any DocId: No. 44924-5089W6 Doc. No. 1798867.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1565	17393	NM_012992	d	nucleophosmin (nucleolar phosphoprotein B23, numatrin), nucleophosmin 1	ESTs, Moderately similar to NPM_HUMAN NUCLEOPHOSMIN [H.sapiens], ESTs, Weakly similar to NPM_HUMAN NUCLEOPHOSMIN [H.sapiens], nucleophosmin (nucleolar phosphoprotein B23, numatrin), nucleophosmin 1, nucleophosmin/nucleoplasmin 3, nucleoplasmin 3
1586	23544	NM_013013	s	prosaposin, prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	ESTs, Weakly similar to 1504251A sphingolipid activator [H.sapiens], RIKEN cDNA 2310020A21 gene, prosaposin, prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
1587	1588	NM_013026	k	syndecan 1	syndecan 1
1588	17894	NM_013027	m	selenoprotein W, 1, selenoprotein W, muscle 1	ESTs, Weakly similar to SELW MOUSE SELENOPROTEIN W [M.musculus], selenoprotein W, 1, selenoprotein W, muscle 1
1589	18300	NM_013030	s,v.General		ESTs, Weakly similar to NPT2 RAT RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [R.norvegicus], ESTs, Weakly similar to NPT2_HUMAN RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [H.sapiens], Homo sapiens, Similar to solute carrier family 34 (sodium phosphate), member 1, clone MGC:18179 IMAGE:4155326, mRNA, complete cds, Solute carrier family 17 (sodium/hydrogen exchanger), member 2, expressed sequence A1549385, solute carrier family 34 (sodium phosphate), member 1, solute carrier family 34 (sodium phosphate), member 2
1589	18076	NM_013030	g,s,z	solute carrier family 34 (sodium phosphate), member 1	ESTs, Weakly similar to NPT2 RAT RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [R.norvegicus], ESTs, Weakly similar to NPT2_HUMAN RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [H.sapiens], Homo sapiens, Similar to solute carrier family 34 (sodium phosphate), member 1, clone MGC:18179 IMAGE:4155326, mRNA, complete cds, Rattus norvegicus mRNA for Neph-2 alpha, complete cds, expressed sequence A1549385, solute carrier family 34 (sodium phosphate), member 1, solute carrier family 34 (sodium phosphate), member 2

TABLE 1: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4424-3389/0 Doc. No. 179337-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Accession Code	Homologous Gene Name	Homologous Cluster Name
1589	18078	NM_013030	s	solute carrier family 34 (sodium phosphate), member 1	ESTs, Weakly similar to NPT2 RAT RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [R.norvegicus], ESTs, Weakly similar to NPT2_HUMAN RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [H.sapiens], Homo sapiens, Similar to solute carrier family 34 (sodium phosphate), member 1, clone MGC:18179 IMAGE:4155326, mRNA, complete cds, Rattus norvegicus mRNA for NaPi-2 alpha, complete cds, Solute carrier family 17 (sodium/hydrogen exchanger), member 2, expressed sequence A1649385, solute carrier family 34 (sodium phosphate), member 1, solute carrier family 34 (sodium phosphate), member 2
1589	18077	NM_013030	s, s.2	solute carrier family 34 (sodium phosphate), member 1	ESTs, Weakly similar to NPT2 RAT RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [R.norvegicus], ESTs, Weakly similar to NPT2_HUMAN RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [H.sapiens], Homo sapiens, Similar to solute carrier family 34 (sodium phosphate), member 1, clone MGC:18179 IMAGE:4155326, mRNA, complete cds, Rattus norvegicus mRNA for NaPi-2 alpha, complete cds, expressed sequence A1649385, solute carrier family 34 (sodium phosphate), member 1, solute carrier family 34 (sodium phosphate), member 2
1591	730	NM_013040	w	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	ATP-binding cassette, sub-family C (CFTR/MRP), member 8, ATP-binding cassette, sub-family C (CFTR/MRP), member 9, ESTs, Highly similar to ACC8_HUMAN SULFONYLUREA RECEPTOR 1 [H.sapiens], ESTs, Weakly similar to T42728 sulfonylurea receptor 2, isoform B - mouse [M.musculus], Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330439B14, full insert sequence
1592	17401	NM_013043	l.o.General	transforming growth factor beta 1 induced transcript 4, transforming growth factor beta-stimulated protein TSC-22	ESTs, Moderately similar to DIP_HUMAN DIP PROTEIN [H.sapiens], delta sleep inducing peptide, immunoreactor, glucocorticoid induced leucine zipper, transforming growth factor beta 1 induced transcript 4, transforming growth factor beta-stimulated protein TSC-22
1593	16684	NM_013052	General	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide, tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					ALY DocId:34461508
					Reg. No. 5726287-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Similar Name
1594	14421	NM_013053	u		RIKEN cDNA 2700028P07 gene, tyrosine 3-monooxygenase/tyrosophan 5-monooxygenase activation protein, theta polypeptide
1595	15254	NM_013058	k		inhibitor of DNA binding 3, inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
1596	14997	NM_013059	s,z		alkaline phosphatase, liver/bone/kidney
1596	14996	NM_013059	General		alkaline phosphatase, liver/bone/kidney
1597	25676	NM_013069	aa		
1597	16924	NM_013069	o		CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated), Ia-associated invariant chain, KIAA0275 gene product, sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican), sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1, sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2
1598	24748	NM_013070	h,q	utrophin, utrophin (homologous to dystrophin)	Dystrophin, dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS235, DXS268, DXS269, DXS270, DXS272, dystrophin, muscular dystrophy, dystrophin-related protein 2 A-form splice variant, utrophin, utrophin (homologous to dystrophin)
1599	1529	NM_013082	d,General		syndecan 2, syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
1600	1521	NM_013091	j,l,z,General		tumor necrosis factor receptor superfamily, member 12, tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein), tumor necrosis factor receptor superfamily, member 1A, tumor necrosis factor receptor superfamily, member 1a, tumor necrosis factor receptor superfamily, member 1a-like 1, tumor necrosis factor receptor superfamily, member 1a-like 2
1601	1685	NM_013096	c,aa	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	
1601	26150	NM_013096	c,j		
1601	1688	NM_013096	p	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	
1601	1689	NM_013096	c,p	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HART1 hemoglobin alpha-1 chain - rat [R.norvegicus], ESTs, Moderately similar to HART1 hemoglobin alpha-1 chain - rat [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc# No. 4991-5087W Doc. No. 198397.1
Seq. ID No.	Identif.	GenBank Acc / Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1601	1684	NM_013096	c,s,aa	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HART1 hemoglobin alpha-1 chain - rat [R.norvegicus], ESTs, Moderately similar to HART1 hemoglobin alpha-1 chain - rat [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2
1602	20886	NM_013097	u,x,bb		
1602	20887	NM_013097	u,x,bb		ESTs, Weakly similar to DRN1 RAT DEOXYRIBONUCLEASE I PRECURSOR [R.norvegicus], Mus musculus DNaseI precursor mRNA, complete cds, RIKEN cDNA 4733401H14 gene, deoxyribonuclease II, expressed sequence A1758550
1603	1321	NM_013098	c		ESTs, Weakly similar to G6PT RAT GLUCOSE-6-PHOSPHATASE [R.norvegicus], Homo sapiens, clone IMAGE:3050476, mRNA, partial cds, RIKEN cDNA 0710001K01 gene, expressed sequence AW545836, glucose-6-phosphatase, catalytic, glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease), glucose-6-phosphatase, catalytic, related sequence, islet-specific glucose-6-phosphatase catalytic subunit-related protein
1604	15296	NM_013102	l,m	FK506 binding protein 1a (12 kDa), FK506-binding protein 1A (12kD)	ESTs, Moderately similar to 1613455A FK506 binding protein FKBP [H.sapiens], FK506 binding protein 1a (12 kDa), FK506 binding protein 1b (12.6 kDa), FK506 binding protein 2 (13 kDa), FK506 binding protein 4 (59 kDa), FK506 binding protein 5 (51 kDa), FK506-binding protein 1A (12kD)
1606	23709	NM_013113	c,s,z,aa		
1606	23711	NM_013113	p		ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1 polypeptide
1606	23710	NM_013113	s		ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1 polypeptide
1607	1976	NM_013118	u		guanylate cyclase activator 1B (retina), guanylate cyclase activator 2 (guanylin 2, intestinal, heatstable), guanylate cyclase activator 2A (guanylin)
1609	870	NM_013130	h		MAD (mothers against decapentaplegic, Drosophila) homolog 1, MAD (mothers against decapentaplegic, Drosophila) homolog 5, MAD (mothers against decapentaplegic, Drosophila) homolog 8
1610	16650	NM_013132	u,General	annexin A5	annexin A5
1611	650	NM_013134	h		3-hydroxy-3-methylglutaryl-Coenzyme A reductase, ESTs, Moderately similar to hydroxymethylglutaryl-CoA reductase [M.musculus], SREBP CLEAVAGE-ACTIVATING PROTEIN

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4-99-388WO Doc. No. 1782497.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Clusite Name
1611	651	NM_013134	h,j,l		3-hydroxy-3-methylglutaryl-Coenzyme A reductase, ESTs, Moderately similar to hydroxymethylglutaryl-CoA reductase [M.musculus], SREBP CLEAVAGE-ACTIVATING PROTEIN
1612	1712	NM_013138	General	inositol 1,4,5-triphosphate receptor 3, inositol 1,4,5-triphosphate receptor, type 3	ESTs, Moderately similar to INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1 RECEPTOR [M.musculus], Mus musculus, Similar to Purkinje cell protein 1, clone MGC:11943 IMAGE:3600031, mRNA, complete cds, RIKEN cDNA 9330127120 gene, inositol 1,4,5-triphosphate receptor 1, inositol 1,4,5-triphosphate receptor 2, inositol 1,4,5-triphosphate receptor 5, inositol 1,4,5-triphosphate receptor, type 3
1613	16982	NM_013144	o,v,General		insulin-like growth factor binding protein 1, protease, serine, 11 (IGF binding)
1614	21683	NM_013154	t,cc,General	CCAAT/enhancer binding protein (C/EBP), delta	CCAAT/enhancer binding protein (C/EBP), delta
1614	21682	NM_013154	cc	CCAAT/enhancer binding protein (C/EBP), delta	CCAAT/enhancer binding protein (C/EBP), delta
1615	3431	NM_013156	b,g,n	cathepsin L	ESTs, Weakly similar to CATHEPSIN L PRECURSOR [M.musculus], RIKEN cDNA 2310051M13 gene, RIKEN cDNA 4930486L24 gene, cathepsin 7, cathepsin F, cathepsin L, cathepsin L2, cathepsin O
1615	25567	NM_013156	v,General		
1615	3430	NM_013156	General	cathepsin L	ESTs, Weakly similar to CATHEPSIN L PRECURSOR [M.musculus], RIKEN cDNA 2310051M13 gene, RIKEN cDNA 4930486L24 gene, cathepsin 7, cathepsin F, cathepsin L, cathepsin L2, cathepsin O
1616	1309	NM_013159	w		RIKEN cDNA 4833415K22 gene, expressed sequence AA675335, insulin degrading enzyme, insulin-degrading enzyme
1616	1310	NM_013159	w		RIKEN cDNA 4833415K22 gene, expressed sequence AA675336, insulin degrading enzyme, insulin-degrading enzyme
1617	21723	NM_013174	w		TGF beta 2 protein, transforming growth factor, beta 2, transforming growth factor, beta 3
1618	1314	NM_013181	m		EST, Moderately similar to CAMP-DEPENDENT PROTEIN KINASE TYPE I-ALPHA REGULATORY CHAIN [R.norvegicus], protein kinase, cAMP dependent regulatory, type 1, alpha, protein kinase, cAMP dependent regulatory, type 1 beta, protein kinase, cAMP-dependent, regulatory, type 1, alpha (tissue specific extinguisher 1)
1619	17357	NM_013183	p,bb,General	meprin 1 beta, meprin A, beta	expressed sequence C67576, meprin 1 beta, meprin A, beta
1620	1300	NM_013190	y		Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210403E17, full insert sequence, expressed sequence AA407869, phosphofructokinase, liver, phosphofructokinase, liver, B-type, phosphofructokinase, muscle

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any Doc No. 44921-58806 Doc No. 1793897.1	
Seq. ID No.	Identifier	GenBank Acc# R.L. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
1621	16448	NM_013197	c		EST, Highly similar to HEMO RAT 5-AMINOLEVULINIC ACID SYNTHASE, ERYTHROID-SPECIFIC, MITOCHONDRIAL PRECURSOR [R.norvegicus], ESTs, Highly similar to SYHUA 5-aminolevulinate synthase [H.sapiens], aminolevulinic acid synthase 2 (sideroblastic/hypochromic anemia), aminolevulinic acid synthase 1, aminolevulinic acid synthase 2, erythroid, glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase), glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	
1622	20856	NM_013200	b	camitine palmitoyltransferase 1, muscle, camitine palmitoyltransferase 1, muscle	ESTs, Moderately similar to CPTM RAT CARNITINE O-PALMITOYLTRANSFERASE 1, MITOCHONDRIAL MUSCLE ISOFORM [R.norvegicus], ESTs, Weakly similar to CPT1 MOUSE CARNITINE O-PALMITOYLTRANSFERASE 1, MITOCHONDRIAL LIVER ISOFORM [M.musculus], camitine palmitoyltransferase 1, liver, camitine palmitoyltransferase 1, muscle, camitine palmitoyltransferase 1, muscle	
1623	397	NM_013214	f		ESTs, Highly similar to AR72_HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE 1 (AFB1-AR 1) (ALDOKETOREDUCTASE 7) [H.sapiens], ESTs, Moderately similar to AFAR RAT AFLATOXIN B1 ALDEHYDE REDUCTASE [R.norvegicus], RIKEN cDNA 0610025K21 gene, Rattus norvegicus alar mRNA for androgen-inducible aldehyde reductase, complete cds, aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase), aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	
1624	20864	NM_013215	g.n.y		ESTs, Moderately similar to T30969 serine/threonine protein kinase NIK - mouse [M.musculus], Mus musculus, Similar to zinc finger protein 347, clone MGC:18913 IMAGE:4242025, mRNA, complete cds, RIKEN cDNA 1500031A17 gene, mitogen-activated protein kinase kinase kinase 4, mitogen-activated protein kinase kinase kinase 6, myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4, syntaxin binding protein 4	
1625	20728	NM_013217	v		ESTs, Highly similar to ALR RAT AUGMENTER OF LIVER REGENERATION [R.norvegicus], growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	
1626	11396	NM_013222	j		ESTs, Highly similar to ALR RAT AUGMENTER OF LIVER REGENERATION [R.norvegicus], growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Any DocId: 44924338 Doc No: 1798897	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
1627	815	NM_013224	w		ESTs, Highly similar to R526_HUMAN 40S RIBOSOMAL PROTEIN S26 [H.sapiens], Homo sapiens, clone IMAGE:4100953, mRNA, Human DNA sequence from PAC 384D21 on chromosome X contains ribosomal protein S26 pseudogene, STS, polymerase (RNA) II (DNA directed) polypeptide D, ribosomal protein S26	
1628	18306	NM_013226	v			
1629	21078	NM_016986	d	acetyl-Coenzyme A dehydrogenase, medium chain, acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	ESTs, Highly similar to ACDM MOUSE ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR [M.musculus], acetyl-Coenzyme A dehydrogenase, medium chain, acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	
1630	24649	NM_016988	v	acid phosphatase 2, lysosomal	ESTs, Weakly similar to PPAL RAT LYSSOMAL ACID PHOSPHATASE PRECURSOR [R.norvegicus], acid phosphatase 2, lysosomal, acid phosphatase 6, lysophosphatidic, acid phosphatase, prostate, acid phosphatase, testicular	
1631	15239	NM_016989	q,w		EST, Weakly similar to RL15 RAT 60S RIBOSOMAL PROTEIN L15 [R.norvegicus], ESTs, Highly similar to RL15_HUMAN 60S RIBOSOMAL PROTEIN L15 [H.sapiens], ESTs, Moderately similar to RL15 RAT 60S RIBOSOMAL PROTEIN L15 [R.norvegicus], RIKEN cDNA 2510008H07 gene, ribosomal protein L15	
1632	45	NM_016996	General	calcium-sensing receptor, calcium-sensing receptor (hypocalcemic hypercalcemia 1, severe neonatal hyperparathyroidism)	EST, Weakly similar to EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR [R.norvegicus], ESTs, Weakly similar to CASR_HUMAN EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR [H.sapiens], ESTs, Weakly similar to JC7160 metabotropic glutamate receptor subtype 3 precursor - mouse [M.musculus], G protein coupled receptor, family C, group 1, member A, G protein coupled receptor, family C, group 1, member C, calcium-sensing receptor (hypocalcemic hypercalcemia 1, severe neonatal hyperparathyroidism), vomeronasal 2, receptor, 11, vomeronasal 2, receptor, 12	
1633	20714	NM_016999	t	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105.22 gene, cytochrome P450, 4a10, cytochrome P450, 4a14, cytochrome P450, subfamily IVA, polypeptide 11	

TABLE 1. HUMAN HOMOLOGUE ANNOTATIONS					Ally. DocId: No. 41941-608 (W)
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1633	20713	NM_016999	t	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, 4a14, cytochrome P450, subfamily IVA, polypeptide 11
1633	20711	NM_016999	q,t	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, 4a14, cytochrome P450, subfamily IVA, polypeptide 11
1633	20715	NM_016999	q,t	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, 4a14, cytochrome P450, subfamily IVA, polypeptide 11
1634	1698	NM_017000	e,n,p,General	diaphorase (NADH/NADPH) (cytochrome b-5 reductase), diaphorase 4 (NADH/NADPH)	ESTs, Weakly similar to DHOU RAT NAD(P)H DEHYDROGENASE [R.norvegicus], NAD(P)H menedione oxidoreductase 2, dioxin inducible, NAD(P)H menedione oxidoreductase 2, dioxin-inducible, diaphorase (NADH/NADPH) (cytochrome b-5 reductase), diaphorase 4 (NADH/NADPH)
1635	1399	NM_017006	h,n,General	glucose-6-phosphate dehydrogenase, glucose-6-phosphate dehydrogenase X-linked	glucose-6-phosphate dehydrogenase, glucose-6-phosphate dehydrogenase 2, glucose-6-phosphate dehydrogenase X-linked, hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
1637	18989	NM_017013	n	glutathione S-transferase A2, glutathione S-transferase, alpha 2 (Yc2)	glutathione S-transferase A2, glutathione S-transferase, alpha 2 (Yc2)
1638	21013	NM_017014	e,f	glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2	ESTs, Moderately similar to GLUTATHIONE S-TRANSFERASE YB1 [R.norvegicus], glutathione S-transferase M1, glutathione S-transferase, mu 1
1638	21015	NM_017014	e,General	glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2	ESTs, Moderately similar to GLUTATHIONE S-TRANSFERASE YB1 [R.norvegicus], glutathione S-transferase M1, glutathione S-transferase, mu 1
1639	11836	NM_017023	b	potassium inwardly-rectifying channel, subfamily J, member 1	EST, Weakly similar to IRKF MOUSE ATP-SENSITIVE INWARD RECTIFIER POTASSIUM CHANNEL 15 [M.musculus], potassium inwardly-rectifying channel, subfamily J, member 1, potassium inwardly-rectifying channel, subfamily J, member 10, potassium inwardly-rectifying channel, subfamily J, member 15

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 4392-3081WS Doc. No. 170287-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Cert.	Homologous Gene Name	Homologous Cluster Name
1639	5475	NM_017023	b	potassium inwardly-rectifying channel, subfamily J, member 1	ESTs, Weakly similar to IRKF MOUSE ATP-SENSITIVE INWARD RECTIFIER POTASSIUM CHANNEL 15 [M.musculus], potassium inwardly-rectifying channel, subfamily J, member 1, potassium inwardly-rectifying channel, subfamily J, member 10, potassium inwardly-rectifying channel, subfamily J, member 15
1639	25546	NM_017023	b.bb	potassium inwardly-rectifying channel, subfamily J, member 1	
1640	17807	NM_017025	i.General	lactate dehydrogenase 1, A chain, lactate dehydrogenase A	ESTs, Highly similar to DEHULM L-lactate dehydrogenase [H.sapiens], ESTs, Moderately similar to DEHULM L-lactate dehydrogenase [H.sapiens], ESTs, Moderately similar to L-LACTATE DEHYDROGENASE M CHAIN [R.norvegicus], ESTs, Weakly similar to DEMSLM L-lactate dehydrogenase [M.musculus], Homo sapiens, Similar to lactate dehydrogenase 1, A chain, clone MGC:23940 IMAGE:3935569, mRNA, complete cds, expressed sequence A1325310, lactate dehydrogenase 1, A chain, lactate dehydrogenase A, lactate dehydrogenase C
1641	24597	NM_017040	u	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform, protein phosphatase 2a, catalytic subunit, beta isoform	Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600017J22, full insert sequence, RIKEN cDNA 2310003C10 gene, expressed sequence A115466, protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform, protein phosphatase 2a, catalytic subunit, beta isoform, protein phosphatase 4, catalytic subunit
1642	24696	NM_017048	f,j,z	solute carrier family 4 (anion exchanger), member 2, solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	ESTs, Moderately similar to A25104 band 3 protein, nonerythroid [H.sapiens], Human DNA sequence from clone RP4-79418 on chromosome 20 Contains a gene for a putative oncogene protein, parts of 2 novel genes, ESTs, STSs, GSSs and CpG islands, solute carrier family 4 (anion exchanger), member 2, solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1), solute carrier family 4, sodium bicarbonate cotransporter, member 4, solute carrier family 4, sodium bicarbonate cotransporter, member 9, solute carrier family 4, sodium bicarbonate transporter-like, member 11

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc#pt No. 44921-3183WG Reg. No. 1793877
Seq. ID No.	GenBank Accession No.	Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Gene Description
1643	24695	NM_017049	u		EST, Highly similar to B3A3 RAT ANION EXCHANGE PROTEIN 3 [R.norvegicus], ESTs, Weakly similar to 138495 anion exchanger 3 brain isoform [H.sapiens], Human DNA sequence from clone RP4-79416 on chromosome 20 Contains a gene for a putative oncogene protein, parts of 2 novel genes, ESTs, STSs, GSSs and CpG islands, solute carrier family 4 (anion exchanger), member 3, solute carrier family 4, anion exchanger, member 3, solute carrier family 4, sodium bicarbonate transporter-like, member 11
1644	20876	NM_017050	j,n,z	superoxide dismutase 1, soluble, superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	ESTs, Moderately similar to SUPEROXIDE DISMUTASE [M.musculus], copper chaperone for superoxide dismutase, superoxide dismutase 1, soluble, superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
1645	910	NM_017059	f,j,m	BCL2-associated X protein, Bcl2-associated X protein	BCL2-associated X protein, Bcl2-associated X protein
1645	912	NM_017059	i	BCL2-associated X protein, Bcl2-associated X protein	BCL2-associated X protein, Bcl2-associated X protein
1646	1946	NM_017061	h	lysyl oxidase	ESTs, Moderately similar to LYOX_HUMAN PROTEIN-LYSINE 6-OXIDASE PRECURSOR [H.sapiens], ESTs, Moderately similar to PROTEIN-LYSINE 6-OXIDASE PRECURSOR [R.norvegicus], hypothetical protein FLJ21889, lysyl oxidase, lysyl oxidase-like 1, lysyl oxidase-like 2
1646	1942	NM_017061	t,General	lysyl oxidase	ESTs, Moderately similar to LYOX_HUMAN PROTEIN-LYSINE 6-OXIDASE PRECURSOR [H.sapiens], ESTs, Moderately similar to PROTEIN-LYSINE 6-OXIDASE PRECURSOR [R.norvegicus], hypothetical protein FLJ21889, lysyl oxidase, lysyl oxidase-like 1, lysyl oxidase-like 2
1646	1943	NM_017061	t	lysyl oxidase	ESTs, Moderately similar to LYOX_HUMAN PROTEIN-LYSINE 6-OXIDASE PRECURSOR [H.sapiens], ESTs, Moderately similar to PROTEIN-LYSINE 6-OXIDASE PRECURSOR [R.norvegicus], hypothetical protein FLJ21889, lysyl oxidase, lysyl oxidase-like 1, lysyl oxidase-like 2
1647	8062	NM_017066	d	pleiotrophin, pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	EST, Moderately similar to JH0385 midline precursor [H.sapiens], EST, Weakly similar to PTN MOUSE PLEIOTROPHIN PRECURSOR [R.norvegicus], midline, midline (neurite growth-promoting factor 2), pleiotrophin, pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Check No. 4-976-6388W0 Doc. No. 1193837.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Gene Name
1648	6654	NM_017068	w	lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2	CD68 antigen, ESTs, Highly similar to LAMP2 RAT LYSOSOME ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR [R.norvegicus], ESTs, Weakly similar to A48042 lysosomal membrane glycoprotein lamp-2 homolog [H.sapiens], lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2
1649	11153	NM_017073	s	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase
1650	923	NM_017076	General		DNA segment, Chr 7, ERATO D01 458, expressed, RIKEN cDNA 2610301B19 gene, RIKEN cDNA 3830421F03 gene, poliovirus receptor, poliovirus receptor-related 2 (herpesvirus entry mediator B), poliovirus receptor-related 3, poliovirus sensitivity, tumor-associated antigen 1
1651	1523	NM_017079	s		CD1b antigen, b polypeptide, CD1d antigen, d polypeptide, CD1e antigen, e polypeptide, CD1d1 antigen, CD1d2 antigen
1652	23660	NM_017080	s	hydroxysteroid (11-beta) dehydrogenase 1, hydroxysteroid 11-beta dehydrogenase 1	DNA segment, Chr 14, University of California at Los Angeles 2, ESTs, Weakly similar to CORTICOSTEROID 11-BETA-DEHYDROGENASE, ISOZYME 1 [R.norvegicus], expressed sequence C79874, hydroxysteroid (11-beta) dehydrogenase 1, hydroxysteroid 11-beta dehydrogenase 1, hydroxysteroid 17-beta dehydrogenase 11, retinal short-chain dehydrogenase/reductase retSDR2
1653	275	NM_017081	b,d,General	hydroxysteroid (11-beta) dehydrogenase 2, hydroxysteroid 11-beta dehydrogenase 2	Mus musculus, Similar to hydroxysteroid 11-beta dehydrogenase 2, clone MGC:25647 (IMAGE:4235545, mRNA, complete cde, hydroxysteroid (11-beta) dehydrogenase 2
1654	16211	NM_017082	j,s,z	uromodulin, uromodulin (uromucoid, Tamm-Horsfall glycoprotein)	RIKEN cDNA 2310037118 gene, tectorin beta, uromodulin, uromodulin (uromucoid, Tamm-Horsfall glycoprotein), zona pellucida glycoprotein 1
1655	1552	NM_017084	j	glycine N-methyltransferase	glycine N-methyltransferase
1655	1550	NM_017084	y	glycine N-methyltransferase	glycine N-methyltransferase
1656	22552	NM_017087	a,k,x	biglycan	ESTs, Weakly similar to BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR [R.norvegicus], ESTs, Weakly similar to PGS1_HUMAN BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR [H.sapiens], asporin, asporin (LRR class 1), biglycan, optican

TABLE 1. HUMAN HOMOLOGUE ANNOTATIONS				Any. Doc# No. 43921-5038W6 Doc. No. 179387.1	
Seq. ID No.	Manifiler	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1657	8888	NM_017090	m	guanylate cyclase 1, soluble, alpha 3	ESTs, Weakly similar to ANPA MOUSE ATRIAL NATRIURETIC PEPTIDE RECEPTOR A PRECURSOR [M.musculus], ESTs, Weakly similar to GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN [R.norvegicus], guanylate cyclase 1, soluble, alpha 2, guanylate cyclase 1, soluble, alpha 3, guanylate cyclase 1, soluble, beta 3, natriuretic peptide receptor 1, soluble guanylyl cyclase alpha2 subunit
1658	10887	NM_017094	a.General	growth hormone receptor	growth hormone receptor
1659	4393	NM_017101	a.y	peptidylprolyl isomerase A, peptidylprolyl isomerase A (cyclophilin A)	ESTs, Highly similar to A Chain A, Cyclophilin A [H.sapiens], ESTs, Weakly similar to PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [R.norvegicus], KIAA1228 protein, RIKEN cDNA 2310076A22 gene, RIKEN cDNA 4930520F12 gene, expressed sequence A1256741, expressed sequence AW457192, peptidylprolyl isomerase A, peptidylprolyl isomerase A (cyclophilin A), peptidylprolyl isomerase E (cyclophilin E)
1660	24770	NM_017111	d	solute carrier family 21 (organic anion transporter), member 1	blood-brain barrier specific anion transporter, solute carrier family 21 (organic anion transporter) member 10, solute carrier family 21 (organic anion transporter), member 1, solute carrier family 21 (organic anion transporter), member 10, solute carrier family 21 (organic anion transporter), member 14, solute carrier family 21 (organic anion transporter), member 3, solute carrier family 21 (organic anion transporter), member 6, solute carrier family 21 (organic anion transporter), member 8
1661	20745	NM_017113	e	granulin	granulin
1661	20746	NM_017113	a	granulin	granulin
1662	1375	NM_017122	w	hippocalcin	DNA segment, Chr 15, ERATO Dcl 412, expressed, ESTs, Highly similar to HIPP RAT NEURON SPECIFIC CALCIUM-BINDING PROTEIN HIPPOCALCIN [R.norvegicus], ESTs, Highly similar to VIS3 MOUSE VISININ LIKE PROTEIN 3 [M.musculus], hippocalcin, hippocalcin-like 1, hypothetical protein FL20481
1663	12903	NM_017124	k	CD37 antigen	CD37 antigen, EST, Highly similar to A47629 cell surface glycoprotein CD37 [H.sapiens], Mus musculus, Similar to CD37 antigen, clone MGC:7983 IMAGE:3585492, mRNA, complete cds, occluspanin

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					App. Deposit No. 449A-Subtype Doc. No. 179387.1
Seq. ID No.	Identifier	GenBank Acc# Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1664	24885	NM_017138	r	laminin receptor 1 (67kD, ribosomal protein SA)	EST, Moderately similar to 40S RIBOSOMAL PROTEIN SA [R.norvegicus], ESTs, Highly similar to A31233 ribosomal protein RS.40K, cytosolic [H.sapiens], ESTs, Highly similar to A56880 laminin receptor, 67K [H.sapiens], ESTs, Moderately similar to A29395 ribosomal protein RS.40K - mouse [M.musculus], ESTs, Weakly similar to 1405340A protein 40kD [M.musculus], Homo sapiens laminin receptor-like protein LAMRL5 mRNA, complete cds, laminin receptor 1 (67kD, ribosomal protein SA)
1664	24886	NM_017138	d,g	laminin receptor 1 (67kD, ribosomal protein SA)	EST, Moderately similar to 40S RIBOSOMAL PROTEIN SA [R.norvegicus], ESTs, Highly similar to A31233 ribosomal protein RS.40K, cytosolic [H.sapiens], ESTs, Highly similar to A56880 laminin receptor, 67K [H.sapiens], ESTs, Moderately similar to A29395 ribosomal protein RS.40K - mouse [M.musculus], ESTs, Weakly similar to 1405340A protein 40kD [M.musculus], Homo sapiens laminin receptor-like protein LAMRL5 mRNA, complete cds, laminin receptor 1 (67kD, ribosomal protein SA)
1665	15363	NM_017147	n,u	cofilin 1 (non-muscle), cofilin 1, non-muscle	EST, Moderately similar to COF1_HUMAN COFILIN, NON-MUSCLE ISOFORM [H.sapiens], ESTs, Highly similar to DEST_HUMAN DESTRIN [H.sapiens], ESTs, Moderately similar to COF1 RAT COFILIN, NON-MUSCLE ISOFORM [R.norvegicus], ESTs, Moderately similar to COF1_HUMAN COFILIN, NON-MUSCLE ISOFORM [H.sapiens], cofilin 1 (non-muscle), cofilin 1, non-muscle, cofilin 2 (muscle), cofilin 2, muscle, destrin
1666	13392	NM_017148	u,General		EST, Moderately similar to CYSR RAT CYSTEINE-RICH PROTEIN 1 [R.norvegicus], ESTs, Weakly similar to CYSR RAT CYSTEINE-RICH PROTEIN 1 [R.norvegicus], ESTs, Weakly similar to S12658 cysteine-rich protein [H.sapiens], cysteine and glycine-rich protein 1, cysteine rich protein, cysteine-rich protein 2, cysteine-rich protein 3, epithelial protein lost in neoplasm beta, thymus LIM protein

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Any. Locat. No. 44941-50396	Doc. No. 199397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
1667	5351	NM_017150	g	ribosomal protein L29	EST, Moderately similar to 60S RIBOSOMAL PROTEIN L29 [R.norvegicus], EST, Weakly similar to S65784 ribosomal protein L29, cytosolic [H.sapiens], ESTs, Highly similar to S65784 ribosomal protein L29, cytosolic [H.sapiens], ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L29 [M.musculus], Human DNA sequence from clone RP4-505K12 on chromosome 1p31.2-31.3 Contains a pseudogene similar to 60S RPL29 (ribosomal protein L29 (cell surface heparin binding protein HIP)), a chromosome 1 specific mRNA (K1AA0499), a novel mRNA (K1AA0433), ESTs, STSs, GSSs and a CpG island, ribosomal protein L29	
1668	16954	NM_017151	a,n	ribosomal protein S15	EST, Moderately similar to R3HU15 ribosomal protein S15, cytosolic [H.sapiens], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S15 [R.norvegicus], ESTs, Highly similar to R3HU15 ribosomal protein S15, cytosolic [H.sapiens], Homo sapiens, clone IMAGE-447080, mRNA, partial cds, ribosomal protein S15	
1669	21643	NM_017152	g	ribosomal protein S17	EST, Weakly similar to 40S RIBOSOMAL PROTEIN S17 [M.musculus], ESTs, Highly similar to R4HU17 ribosomal protein S17, cytosolic [H.sapiens], ESTs, Moderately similar to R4HU17 ribosomal protein S17, cytosolic [H.sapiens], ribosomal protein S17	
1670	1694	NM_017153	a,q	ribosomal protein S3A, ribosomal protein S3a	EST, Weakly similar to RS3A MOUSE 40S RIBOSOMAL PROTEIN S3A [M.musculus], ESTs, Highly similar to JC4662 ribosomal protein S3a, cytosolic [H.sapiens], ribosomal protein S3A, ribosomal protein S3a	
1671	17104	NM_017160	bb,General	ribosomal protein S6	EST, Moderately similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S6 [R.norvegicus], ESTs, Moderately similar to 40S RIBOSOMAL PROTEIN S6 [M.musculus], Homo sapiens cDNA: FLJ23534 fls, clone LNC06974, highly similar to HUMRPS6A Human ribosomal protein S6 mRNA, RIKEN cDNA 5830405M20 gene, ribosomal protein S6	
1671	17106	NM_017160	u	ribosomal protein S6	EST, Moderately similar to R3HU6 ribosomal protein S6, cytosolic [H.sapiens], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S6 [R.norvegicus], ESTs, Moderately similar to 40S RIBOSOMAL PROTEIN S6 [M.musculus], Homo sapiens cDNA: FLJ23534 fls, clone LNC06974, highly similar to HUMRPS6A Human ribosomal protein S6 mRNA, RIKEN cDNA 5830405M20 gene, ribosomal protein S6	

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Ally, pocket No. 4, 921-58976 acc. No. 179387
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model/Grade	Homologous Gene Name	Homologous Gene Description
1671	17107	NM_017160	d,e	ribosomal protein S6	EST, Moderately similar to R3H06 ribosomal protein S6, cytosolic [H.sapiens], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S6 [R.norvegicus], ESTs, Moderately similar to 40S RIBOSOMAL PROTEIN S6 [M.musculus], Homo sapiens cDNA: FLJ23534 fs, clone LNG06974, highly similar to HUMRPS6A Human ribosomal protein S6 mRNA, RIKEN cDNA 5830405M20 gene, ribosomal protein S6
1672	17686	NM_017165	n,q	glutathione peroxidase 4, glutathione peroxidase 4 (phospholipid hydroperoxidase)	EST, Moderately similar to T02747 phospholipid-hydroperoxide glutathione peroxidase [H.sapiens], EST, Weakly similar to T02747 phospholipid-hydroperoxide glutathione peroxidase [H.sapiens], ESTs, Weakly similar to GS-HI RAT PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE PEROXIDASE [R.norvegicus], Homo sapiens PRO2893 mRNA, complete cds, RIKEN cDNA 2310016C16 gene, RIKEN cDNA 3110050F08 gene, glutathione peroxidase 4, glutathione peroxidase 4 (phospholipid hydroperoxidase)
1673	20702	NM_017166	c	leukemia-associated gene, stathmin 1/oncoprotein 18	ESTs, Weakly similar to STHM MOUSE STATHMIN [M.musculus], Homo sapiens (clone B3B3E13) Huntington's disease candidate region mRNA fragment, leukemia-associated gene, stathmin 1/oncoprotein 18
1674	3513	NM_017177	r	choline kinase-like, choline/ethanolamine kinase	EST, Weakly similar to KICE MOUSE CHOLINE/ETHANOLAMINE KINASE [M.musculus], ESTs, Weakly similar to KICE RAT CHOLINE/ETHANOLAMINE KINASE [R.norvegicus], Homo sapiens, Similar to hypothetical protein FLJ10761, clone MGC:19512 IMAGE:4329734, mRNA, complete cds, Mus musculus mRNA for choline/ethanolamine kinase, complete cds, RIKEN cDNA 4930555L11 gene, choline kinase-like, choline/ethanolamine kinase, ethanolamine kinase, hypothetical protein FLJ10761
1675	19031	NM_017180	v,General	T-cell death associated gene, pleckstrin homology-like domain, family A, member 1	ESTs, Weakly similar to S58222 PQ-rich protein [H.sapiens], MARCKS-like protein, Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730519L10, full insert sequence, Myristoylated alanine-rich protein kinase C substrate, myristoylated alanine rich protein kinase C substrate, myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L), pleckstrin homology-like domain, family A, member 1, pleckstrin homology-like domain, family A, member 3, tumor suppressing subtransferable candidate 3

TABLE 2. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4494-5089WC Reg. No. 1793877-1
Seq. ID No.	Identifier	GenBank Acc. Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologue (Gene) Name
1676	15437	NM_017187	x.z		EST, Moderately similar to HMG2 RAT HIGH MOBILITY GROUP PROTEIN HMG2 [R.norvegicus], EST, Weakly similar to HMG2 RAT HIGH MOBILITY GROUP PROTEIN HMG2 [R.norvegicus], ESTs, Weakly similar to 2001363A high mobility group protein 2 [H.sapiens], ESTs, Weakly similar to HMG2 RAT HIGH MOBILITY GROUP PROTEIN HMG2 [R.norvegicus], Human DNA sequence from clone RP3-527B10 on chromosome 6q25.1-25.3 Contains a pseudogene similar to HMG (high mobility group) protein, STSs and GSSs, Human DNA sequence from clone RP5-1007G16 on chromosome 1p34.2-35.3. Contains part of the gene for a novel CUB and Sushi (SCR repeat) domain protein, a novel high-mobility group (nonhistone chromosomal) protein 2 (HMG2) like protein (pseudo) gene, a heat shock 60kD protein 1 (chaperonin) (HSPD1) pseudogene, ESTs, STSs and GSSs, RIKEN cDNA 2610021J01 gene, expressed sequence A326135, expressed sequence C80539, high mobility group box 2, high-mobility group (nonhistone chromosomal) protein 2
1676	15433	NM_017187	y		EST, Moderately similar to HMG2 RAT HIGH MOBILITY GROUP PROTEIN HMG2 [R.norvegicus], EST, Weakly similar to HMG2 RAT HIGH MOBILITY GROUP PROTEIN HMG2 [R.norvegicus], ESTs, Weakly similar to 2001363A high mobility group protein 2 [H.sapiens], ESTs, Weakly similar to HMG2 RAT HIGH MOBILITY GROUP PROTEIN HMG2 [R.norvegicus], Human DNA sequence from clone RP3-527B10 on chromosome 6q25.1-25.3 Contains a pseudogene similar to HMG (high mobility group) protein, STSs and GSSs, Human DNA sequence from clone RP5-1007G16 on chromosome 1p34.2-35.3. Contains part of the gene for a novel CUB and Sushi (SCR repeat) domain protein, a novel high-mobility group (nonhistone chromosomal) protein 2 (HMG2) like protein (pseudo) gene, a heat shock 60kD protein 1 (chaperonin) (HSPD1) pseudogene, ESTs, STSs and GSSs, RIKEN cDNA 2610021J01 gene, expressed sequence A326135, expressed sequence C80539, high mobility group box 2, high-mobility group (nonhistone chromosomal) protein 2

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Allyl Docetaxel No. 43924-503876 Doc. No. 179337-1
Seq. ID No.	Identifier	GenBank/ACGI Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
					EST, Moderately similar to HMG2 RAT HIGH MOBILITY GROUP PROTEIN HMG2 [R.norvegicus], EST, Weakly similar to HMG2 RAT HIGH MOBILITY GROUP PROTEIN HMG2 [R.norvegicus], ESTs, Weakly similar to 2001363A high mobility group protein 2 [H.sapiens], ESTs, Weakly similar to HMG2 RAT HIGH MOBILITY GROUP PROTEIN HMG2 [R.norvegicus], Human DNA sequence from clone RP3-527B10 on chromosome 6q25.1-25.3 Contains a pseudogene similar to HMG (high mobility group) protein, STSs and GSSs, Human DNA sequence from clone RP5-1007G16 on chromosome 1p34.2-35.3. Contains part of the gene for a novel CUB and Sushi (SCR repeat) domain protein, a novel high-mobility group (nonhistone chromosomal) protein 2 (HMG2) like protein (pseudo) gene, a heat shock 60kD protein 1 (chaperonin) (HSPD1) pseudogene, ESTs, STSs and GSSs, RIKEN cDNA 2610021A1 gene, expressed sequence A1326135, expressed sequence C80539, high mobility group box 2, high-mobility group (nonhistone chromosomal) protein 2
1676	15434	NM_017187	x,z		
1677	24437	NM_017190	p	malignancy-associated protein, myelin-associated glycoprotein	CD33 antigen, CD33 antigen (gp67), ESTs, Weakly similar to MYELIN-ASSOCIATED GLYCOPROTEIN PRECURSOR [R.norvegicus], Homo sapiens HSPC078 mRNA, partial cds, myelin associated glycoprotein, myelin-associated glycoprotein
1678	1542	NM_017193	l,j,m,z	L-tryptophan/alpha-aminoadipate aminotransferase, kynurenine aminotransferase II	ESTs, Weakly similar to S48737 kynurenine aminotransferase - rat [R.norvegicus], cysteine conjugate-beta lyase, cytoplasmic [glutamine transaminase K, kynurenine aminotransferase], hypothetical protein 669
1679	14695	NM_017202	q,s		EST, Weakly similar to COX4_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR [H.sapiens], cytochrome c oxidase subunit IV, cytochrome c oxidase subunit IV isoform 2, cytochrome c oxidase subunit IV isoform 2 precursor, cytochrome c oxidase, subunit IVa, cytochrome c oxidase, subunit IVb, expressed sequence AL024441
1679	14694	NM_017202	s,z		EST, Weakly similar to COX4_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR [H.sapiens], cytochrome c oxidase subunit IV, cytochrome c oxidase subunit IV isoform 2, cytochrome c oxidase subunit IV isoform 2 precursor, cytochrome c oxidase, subunit IVa, cytochrome c oxidase, subunit IVb, expressed sequence AL024441

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Alta DocuID: 44993-3089W
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1680	1428	NM_017213	m	outer dense fiber of sperm tails 2, outer dense fibre of sperm tails 2	ESTs, Highly similar to T09400 outer dense fiber protein 2 - mouse [M.musculus], KIAA1229 protein, Myosin heavy chain 11, Myosin, heavy polypeptide 9, non-muscle, expressed sequence C80049, myosin, heavy polypeptide 9, non-muscle, outer dense fiber of sperm tails 2, outer dense fibre of sperm tails 2
1681	1622	NM_017216	g,j,s,z	solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1, solute carrier family 3, member 1	ESTs, Moderately similar to 1914205A AA transporter [H.sapiens], putative L-type neutral amino acid transporter, solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2, solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1, solute carrier family 3, member 1
1682	13642	NM_017220	v		
1682	19976	NM_017220	w		
1683	1510	NM_017224	General		EST, Moderately similar to JC4884 organic cation transporter protein 2 - rat [R.norvegicus], EST, Weakly similar to OCN2 MOUSE ORGANIC CATION/CARNITINE TRANSPORTER 2 [M.musculus], ESTs, Highly similar to OCN2_HUMAN ORGANIC CATION/CARNITINE TRANSPORTER 2 [H.sapiens], ESTs, Highly similar to organic cation transporter [H.sapiens], solute carrier family 22 (organic cation transporter), member 1, solute carrier family 22 (organic cation transporter), member 4, solute carrier family 22 (organic cation transporter), member 5, solute carrier family 22 (organic cation transporter), member 9, solute carrier family 22, member 2, solute carrier family 22, member 3
1684	1811	NM_017228	j,l,m,z	dentatorubral pallidolysian atrophy, dentatorubral-pallidolysian atrophy (atrophin-1)	ESTs, Moderately similar to DRPL RAT ATROPHIN-1 [R.norvegicus], ESTs, Weakly similar to G01763 atrophin-1 [H.sapiens], Homo sapiens, clone IMAGE:4153246, mRNA, partial cds, RIKEN cDNA 231009E07 gene, RIKEN cDNA 2810012K09 gene, arginine-glutamic acid dipeptide (RE) repeats, dentatorubral pallidolysian atrophy, dentatorubral-pallidolysian atrophy (atrophin-1), expressed sequence C78339, formin
1686	17553	NM_017245	s,c,e,g	eukaryotic translation elongation factor 2	EST, Weakly similar to EFHJ2 translation elongation factor eEF-2 [H.sapiens], ESTs, Highly similar to ELONGATION FACTOR 2 [R.norvegicus], ESTs, Weakly similar to ELONGATION FACTOR 2 [R.norvegicus], G1 to phase transition 1, G1 to phase transition 2, RIKEN cDNA 4930594C11 gene, U5 snRNP-specific protein, 116 kD, eukaryotic translation elongation factor 1 alpha 1, eukaryotic translation elongation factor 2, expressed sequence AA451340, hypothetical protein FLJ21661

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 4-923 4363W0 Doc. No. 1793347, 1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1687	17502	NM_017248	r	heterogeneous nuclear ribonucleoprotein A1	ESTs, Highly similar to ROA1 RAT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 [R.norvegicus], ESTs, Moderately similar to Up1, The Two Rna-Recognition Motif Domain Of Hnmp A1 (SUB 3-184 [H.sapiens], ESTs, Weakly similar to ROA1 RAT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 [R.norvegicus], ESTs, Weakly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], Human DNA sequence from clone RP11-51N22 on chromosome 13 Contains ESTs, STSs and GSSs. Contains an HNRPA1 (heterogeneous nuclear ribonucleoprotein A1) pseudogene, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear ribonucleoprotein A1
1687	17501	NM_017248	x	heterogeneous nuclear ribonucleoprotein A1	ESTs, Highly similar to ROA1 RAT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 [R.norvegicus], ESTs, Moderately similar to Up1, The Two Rna-Recognition Motif Domain Of Hnmp A1 (SUB 3-184 [H.sapiens], ESTs, Weakly similar to ROA1 RAT HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 [R.norvegicus], ESTs, Weakly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], Human DNA sequence from clone RP11-51N22 on chromosome 13 Contains ESTs, STSs and GSSs. Contains an HNRPA1 (heterogeneous nuclear ribonucleoprotein A1) pseudogene, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear ribonucleoprotein A1
1688	19	NM_017258	v,General	B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative, ESTs, Weakly similar to BTG1 RAT BTG1 PROTEIN [R.norvegicus], transducer of ERBB2, 1, transducer of ERBB2, 2, transducer of ErbB-2, 1
1689	15300	NM_017259	l,v,cc,General	B-cell translocation gene 2, anti-proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 3, B-cell translocation gene 4, BTG family, member 2, BTG family, member 3, BTG family, member 4, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]
1689	15301	NM_017259	l,m,v,aa,cc,General	B-cell translocation gene 2, anti-proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 3, B-cell translocation gene 4, BTG family, member 2, BTG family, member 3, BTG family, member 4, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4394-568WG Doc. No. 179497.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1689	15299	NM_017259	l.y.cc.General	B-cell translocation gene 2, anti-proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 3, B-cell translocation gene 4, BTG family, member 2, BTG family, member 3, BTG family, member 4, ESTs, Highly similar to BTG2 HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]
1690	15224	NM_017264	d	protease (prosome, macropain) 28 subunit, alpha, proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	EST, Moderately similar to A Chain A, Proteasome Activator Reg(Alpha) (SUB 4-63 [H.sapiens]), proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
1691	3987	NM_017280	bb	proteasome (prosome, macropain) subunit, alpha type 3, proteasome (prosome, macropain) subunit, alpha type, 3	multicatalytic endopeptidase complex [H.sapiens], ESTs, Highly similar to PRC8 MOUSE PROTEASOME COMPONENT C8 [M.musculus], ESTs, Highly similar to PROTEASOME COMPONENT C8 [R.norvegicus], ESTs, Weakly similar to SNHUC8 multicatalytic endopeptidase complex [H.sapiens], proteasome (prosome, macropain) subunit, alpha type 3, proteasome (prosome, macropain) subunit, alpha type, 3
1692	1447	NM_017281	i	proteasome (prosome, macropain) subunit, alpha type 4, proteasome (prosome, macropain) subunit, alpha type, 4	EST, Weakly similar to SNHUC9 multicatalytic endopeptidase complex [H.sapiens], proteasome (prosome, macropain) subunit, alpha type 4, proteasome (prosome, macropain) subunit, alpha type, 4
1693	15535	NM_017283	s.bb	proteasome (prosome, macropain) subunit, alpha type 6, proteasome (prosome, macropain) subunit, alpha type, 6	ESTs, Weakly similar to PRC1_HUMAN PROTEASOME IOTA CHAIN [R.norvegicus], proteasome (prosome, macropain) subunit, alpha type 6, proteasome (prosome, macropain) subunit, alpha type, 6
1694	12349	NM_017290	General	ATPase, Ce++ transporting, cardiac muscle, slow twitch 2	
1695	15819	NM_017298	p	calcium channel, voltage-dependent, L type, alpha 1D subunit	EST, Highly similar to CCAD MOUSE VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL ALPHA-1D SUBUNIT [M.musculus], EST, Moderately similar to CCAD MOUSE VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL ALPHA-1D SUBUNIT [M.musculus], EST, Moderately similar to CCAD RAT VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL ALPHA-1D SUBUNIT [R.norvegicus], RIKEN cDNA 8430418G19 gene, calcium channel, voltage-dependent, alpha 1F subunit, calcium channel, voltage-dependent, L type, alpha 1D subunit, calcium channel, voltage-dependent, alpha 1F subunit, polycystic kidney disease 2-like 2

TABLE 3: HUMAN HOMOLOGUE/ANNOTATIONS					Atty-Bracket No. 4924-4987w Doc. No. 178387.1
Seq. ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1696	23825	NM_017299	v	solute carrier family 19 (folate transporter), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 1	expressed sequence AW322295, solute carrier family 19 (folate transporter), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 1, solute carrier family 19 (thiamine transporter), member 2, solute carrier family 19, member 3
1696	23826	NM_017299	v	solute carrier family 19 (folate transporter), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 1	expressed sequence AW322295, solute carrier family 19 (folate transporter), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 1, solute carrier family 19 (sodium/hydrogen exchanger), member 3, solute carrier family 19 (thiamine transporter), member 2, solute carrier family 19, member 3
1697	14003	NM_017305	l,m,y,z	glutamate-cysteine ligase, modifier subunit, glutamate-cysteine ligase, modifier subunit	ESTs, Highly similar to GSH0, HUMAN, GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT [H.sapiens], glutamate-cysteine ligase, modifier subunit, glutamate-cysteine ligase, modifier subunit
1698	26109	NM_017306	q,s		ESTs, Highly similar to D3D2 RAT 3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR [R.norvegicus], Homo sapiens, Similar to dodecanoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase), clone MGC:3903 IMAGE:3630566, mRNA, complete cds, dodecanoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase), dodecanoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase) A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase)
1698	18687	NM_017306	q,t	dodecanoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase), dodecanoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase)	EST, Moderately similar to S12583 polyubiquitin 4 - mouse [M.musculus], EST, Weakly similar to JE0190 polyubiquitin unit [H.sapiens], Homo sapiens UBBP2 pseudogene for ubiquitin UBB, RIKEN cDNA 2700054O04 gene, expressed sequence AI194771, expressed sequence AL033289, ubiquitin B, ubiquitin C
1699	18142	NM_017314	q,s,aa		Calmodulin S
1700	1894	NM_017320	t		Calmodulin I (phosphorylase kinase, delta), Calmodulin III, ESTs, Highly similar to A Chain A, Calmodulin Complexed With Calmodulin-Binding Peptide From Smooth Muscle Myosin Light Chain Kinase (SUB 2-148 [H.sapiens], R.norvegicus CalMII retrotransposon (clone lambda SC27), RIKEN cDNA 231006B022 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3
1701	20809	NM_017326	u	calmodulin 2, calmodulin 2 (phosphorylase kinase, delta)	
1702	355	NM_017334	icc		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Design No. 4492-5003WG Doc. No. 1732827.1	
Seq. ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Homologue Gene Name	Homologue Cluster Name	
					ESTs, Highly similar to ACYL-COENZYME A OXIDASE, PEROXISOMAL (R.norvegicus), ESTs, Highly similar to CAOP_HUMAN ACYL-COENZYME A OXIDASE, PEROXISOMAL (H.sapiens), RIKEN cDNA 1300003O09 gene, RIKEN cDNA 2310016C19 gene, acetyl-Coenzyme A dehydrogenase, short chain, acyl-Coenzyme A oxidase 2, branched chain, isovaleryl coenzyme A dehydrogenase	
1703	16148	NM_017340	q,s			
					ESTs, Highly similar to ACYL-COENZYME A OXIDASE, PEROXISOMAL (R.norvegicus), ESTs, Highly similar to CAOP_HUMAN ACYL-COENZYME A OXIDASE, PEROXISOMAL (H.sapiens), RIKEN cDNA 1300003O09 gene, RIKEN cDNA 2310016C19 gene, acetyl-Coenzyme A dehydrogenase, short chain, acyl-Coenzyme A oxidase 2, branched chain, isovaleryl coenzyme A dehydrogenase	
1703	16150	NM_017340	a			
					ESTs, Weakly similar to MOHULP myosin regulatory light chain, placental (H.sapiens), RIKEN cDNA 2900073G15 gene, expressed sequence C77744, myosin, light polypeptide, regulatory, non-sarcomeric (20kD)	
1704	20849	NM_017343	r,u,General			
					ESTs, Weakly similar to MOHULP myosin regulatory light chain, placental (H.sapiens), RIKEN cDNA 2900073G15 gene, expressed sequence C77744, myosin, light polypeptide, regulatory, non-sarcomeric (20kD)	
1704	20848	NM_017343	b,General			
					GPI-anchored metastasis-associated protein homolog, metastasis-associated GPI-anchored protein, plasminogen activator, urokinase receptor, urokinase plasminogen activator receptor	
1705	606	NM_017350	b			
					ESTs, Weakly similar to LIM PROTEIN CLP36 (R.norvegicus), PDZ and LIM domain 1 (elfin), PDZ and LIM domain 3, PDZ-LIM protein mystique, RIKEN cDNA 1110003B01 gene, Rattus norvegicus LIM-domain protein LMP-1 mRNA, complete cds, Z-band alternatively spliced PDZ-motif, actinin alpha 2 associated LIM protein, alpha-actinin-2-associated LIM protein, reversion induced LIM gene	
1706	1581	NM_017365	General	PDZ and LIM domain 1 (elfin)		
				tropomyosin 1 (alpha), tropomyosin 1, alpha	ESTs, Moderately similar to alpha-tropomyosin slow (M.musculus), tropomyosin 4	
1707	455	NM_019131	x			
				tropomyosin 1 (alpha), tropomyosin 1, alpha	ESTs, Moderately similar to alpha-tropomyosin slow (M.musculus), tropomyosin 4	
1707	456	NM_019131	y,z			
				tropomyosin 1 (alpha), tropomyosin 1, alpha	ESTs, Moderately similar to alpha-tropomyosin slow (M.musculus), tropomyosin 4	

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4394-0000 Reg. No. 170247-1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Annotation F. Summary	Homologous Cluster Name	
				solute carrier family 12 (sodium/potassium/chloride transporters), member 1, solute carrier family 12, member 1	EST, Weakly similar to NKCC2_HUMAN BUMETANIDE-SENSITIVE SODIUM-(POTASSIUM)-CHLORIDE COTRANSPORTER 2 (KIDNEY-SPECIFIC NA-K-CL SYMPORTER) [H.sapiens], expressed sequence A1788571, hypothetical protein FLJ23188, solute carrier family 12 (sodium/potassium/chloride transporters), member 1, solute carrier family 12, member 1, solute carrier family 12, member 2	
1708	4532	NM_019134	b		ESTs, Moderately similar to SNG1 RAT SYNAPTOGYRIN 1 [R.norvegicus], synaptogyrin 1, synaptogyrin 3, synaptogyrin 4	
1709	1608	NM_019166	i,y,z	synaptogyrin 1, synuclein, alpha, synuclein, alpha (non A4 component of amyloid precursor)	synuclein, alpha, synuclein, alpha (non A4 component of amyloid precursor), synuclein, beta, synuclein, gamma	
1710	7489	NM_019169	c,General		ESTs, Weakly similar to JC5284 carbonyl reductase (NADPH) (EC 1.1.1.184), inducible - rat [R.norvegicus], Homo sapiens, clone MGC:23280 IMAGE:4637504, mRNA, complete cds, RIKEN cDNA 1110001J05 gene, RIKEN cDNA 9430059D04 gene, carbonyl reductase 1, carbonyl reductase 3, expressed sequence C81353	
1711	17066	NM_019170	p		ESTs, Weakly similar to CARBONIC ANHYDRASE IV PRECURSOR [R.norvegicus], carbonic anhydrase 15, carbonic anhydrase 4, carbonic anhydrase IV, carbonic anhydrase XIV, expressed sequence AW456718	
1712	23924	NM_019174	bb	carbonic anhydrase 4, carbonic anhydrase IV	ADP-ribosylation factor-like 4, ADP-ribosylation factor-like 7, ADP-ribosylation-like 4, ESTs, Weakly similar to ARL4 MOUSE ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 4 [M.musculus], Mus musculus, Similar to ADP-ribosylation-like 4, clone MGC:5774 IMAGE:3595701, mRNA, complete cds	
1713	24019	NM_019186	t	ADP-ribosylation factor-like 4, ADP-ribosylation-like 4	CD47 antigen (Rb-related antigen, integrin-associated signal transducer), integrin-associated protein	
1714	22063	NM_019195	d		ESTs, Weakly similar to GRG MOUSE GRG PROTEIN [R.norvegicus], amino-terminal enhancer of split	
1715	2079	NM_019220	j,k,z			

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4492-388WC Doc. No. 179937-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model/Contig	Homologous Gene Name	Homologous Cluster Name
1716	16284	NM_019229	l,m	solute carrier family 12 (potassium/chloride transporters), member 4, solute carrier family 12, member 4	EST, Moderately similar to T31429 K-Cl cotransport protein KCC1, furosemide-sensitive - rat [R.norvegicus], EST, Weakly similar to T31429 K-Cl cotransport protein KCC1, furosemide-sensitive - rat [R.norvegicus], ESTs, Highly similar to T17275 hypothetical protein DKFZp434D2135.1 [H.sapiens], Mus musculus strain ILS K-Cl cotransporter (Slc12a5) mRNA, complete cds, Rattus norvegicus ccd5 mRNA for cation-chloride cotransporter 6, complete cds, expressed sequence AW546649, solute carrier family 12 (potassium/chloride transporters), member 4, solute carrier family 12 (potassium/chloride transporters), member 6, solute carrier family 12 (potassium/chloride transporters), member 7, solute carrier family 12, member 2, solute carrier family 12, member 4, solute carrier family 12, member 7
1717	985	NM_019233	b,cc	small inducible cytokine subfamily A (Cys-Cys), member 20, small inducible cytokine subfamily A20	small inducible cytokine subfamily A (Cys-Cys), member 20, small inducible cytokine subfamily A20
1718	15503	NM_019237	k,x	procollagen C-endopeptidase enhancer, procollagen C-proteinase enhancer protein	EST, Weakly similar to PCO1_HUMAN PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR [H.sapiens], Homo sapiens cDNA FLJ12558 fs, clone NT2RM4000787, Mus musculus CSMD1 (Csm1) mRNA, complete cds, RIKEN cDNA 2400001O18 gene, expressed sequence A1043106, membrane-type frizzled-related protein, procollagen C-endopeptidase enhancer, procollagen C-endopeptidase enhancer 2, procollagen C-proteinase enhancer protein
1718	15504	NM_019237	k,x	procollagen C-endopeptidase enhancer, procollagen C-proteinase enhancer protein	EST, Weakly similar to PCO1_HUMAN PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR [H.sapiens], Homo sapiens cDNA FLJ12558 fs, clone NT2RM4000787, Mus musculus CSMD1 (Csm1) mRNA, complete cds, RIKEN cDNA 2400001O18 gene, expressed sequence A1043106, membrane-type frizzled-related protein, procollagen C-endopeptidase enhancer, procollagen C-endopeptidase enhancer 2, procollagen C-proteinase enhancer protein
1719	17908	NM_019242	l,v,cc,General	interferon-related developmental regulator 1	ESTs, Weakly similar to INTERFERON RELATED PROTEIN PC4 [R.norvegicus], interferon-related developmental regulator 1, interferon-related developmental regulator 2
1720	11218	NM_019247	c	paired-like homeodomain transcription factor 3	paired-like homeodomain transcription factor 1, paired-like homeodomain transcription factor 2, paired-like homeodomain transcription factor 3

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Aty. Order No. 43924-50890C Doc. No. 1728997.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Group Name	Homologous Cluster Name
				complement component 1, q subcomponent binding protein	DNA segment, Chr 11, Wayne State University 182, expressed, complement component 1, q subcomponent binding protein, expressed sequence AA986492
1721	15259	NM_019259	d.f		C1q-related factor, Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279 IMAGE:4212772, mRNA, complete cds, complement component 1, q subcomponent, beta polypeptide, complement component 1, q subcomponent, c polypeptide, expressed sequence AJ385742
1722	21443	NM_019262	aa.General	complement component 1, q subcomponent, beta polypeptide	C1q-related factor, Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279 IMAGE:4212772, mRNA, complete cds, complement component 1, q subcomponent, beta polypeptide, complement component 1, q subcomponent, c polypeptide, expressed sequence AJ385742
1722	21444	NM_019262	t.General	complement component 1, q subcomponent, beta polypeptide	C1q-related factor, Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279 IMAGE:4212772, mRNA, complete cds, complement component 1, q subcomponent, beta polypeptide, complement component 1, q subcomponent, c polypeptide, expressed sequence AJ385742
				sodium channel, voltage gated, type VIII, alpha polypeptide, sodium channel, voltage-gated, type VIII, alpha polypeptide	ESTs, Highly similar to voltage gated Na channel Scn8a [M.musculus], Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230108N10, full insert sequence, hypothetical protein MGC15619, sodium channel, voltage gated, type VIII, alpha polypeptide, sodium channel, voltage-gated, type II, alpha 2 polypeptide, sodium channel, voltage-gated, type III, alpha polypeptide, sodium channel, voltage-gated, type VIII, alpha polypeptide
1723	117	NM_019266	o.bb		
				gap junction membrane channel protein alpha 5, gap junction protein, alpha 5, 40kD (connexin 40)	
1724	1145	NM_019280	w		
				alcohol dehydrogenase 1, complex, alcohol dehydrogenase 1A (class I), alpha polypeptide	ESTs, Weakly similar to ADHA MOUSE ALCOHOL DEHYDROGENASE A CHAIN [M.musculus], alcohol dehydrogenase 1A (class I), alpha polypeptide, alcohol dehydrogenase 1B (class I), beta polypeptide, expressed sequence A1194826, nuclear receptor binding factor 1
1725	22220	NM_019286	c		EST, Highly similar to AR41_HUMAN ARP2/3 COMPLEX 41 KDA SUBUNIT [H.sapiens], ESTs, Moderately similar to AR41_HUMAN ARP2/3 COMPLEX 41 KDA SUBUNIT [H.sapiens], actin related protein 2/3 complex, subunit 1A (41 kD), actin related protein 2/3 complex, subunit 1A (41 kDa), actin related protein 2/3 complex, subunit 1B (41 kDa), expressed sequence AA408064, suppressor of profilin/p41 of actin-related complex 2/3
1726	10015	NM_019289	lm,Lx.General		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any DocId No. 4934-SubWC Doc. No. 1793377.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model/Code	Homologous Gene Name	Homologous Cluster Name
1726	10016	NM_019289	bb,General		EST, Highly similar to AR41_HUMAN ARP2/3 COMPLEX 41 KDA SUBUNIT [H.sapiens], ESTs, Moderately similar to AR41_HUMAN ARP2/3 COMPLEX 41 KDA SUBUNIT [H.sapiens], actin related protein 2/3 complex, subunit 1A (41 kD), actin related protein 2/3 complex, subunit 1A (41 kDa), actin related protein 2/3 complex, subunit 1B (41 kDa), expressed sequence AA408064, suppressor of profilin/p41 of actin-related complex 2/3
1727	21651	NM_019296	c,f,x		RIKEN cDNA 2310015O17 gene, RIKEN cDNA 4933411O17 gene, cell division cycle 2 homolog A (S. pombe), cell division cycle 2, G1 to S and G2 to M, cyclin-dependent kinase-like 1 (CDC2-related kinase), cyclin-dependent kinase-like 2 (CDC2-related kinase), cyclin-dependent kinase-like 3, expressed sequence A1852479, serine/threonine kinase NIGATRE beta
1728	20751	NM_019301	s		CUB and Sushi multiple domains 1, ESTs, Highly similar to I73012 complement C3b/C4b receptor, membrane-bound form precursor [H.sapiens], ESTs, Weakly similar to JC2054 complement regulatory protein, 512 antigen precursor - rat [R.norvegicus], Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730478H20, full insert sequence, complement component (3b/4b) receptor 1, including Knops blood group system, complement receptor related protein, decay accelerating factor 1, decay accelerating factor 2, membrane cofactor protein
1729	645	NM_019345	bb	solute carrier family 12 (sodium/chloride transporters), member 3, solute carrier family 12, member 3	ESTs, Moderately similar to PC4180 thiazide-sensitive sodium-chloride cotransporter [H.sapiens], ESTs, Moderately similar to thiazide-sensitive Na-Cl cotransporter [M.musculus], ESTs, Weakly similar to BUMETANIDE-SENSITIVE SODIUM-(POTASSIUM)-CHLORIDE COTRANSPORTER 2 [M.musculus], expressed sequence A1788571, solute carrier family 12 (sodium/chloride transporters), member 3, solute carrier family 12, member 1, solute carrier family 12, member 3
1730	1301	NM_019349	c		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any. Doc# No. 44924-5089W
					Doc. No. 179389W
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1731	3776	NM_019354	a.u		ESTs, Moderately similar to BACP, HUMAN BRAIN MITOCHONDRIAL CARRIER PROTEIN-1 (H.sapiens), RIKEN cDNA 3632410G24 gene, RIKEN cDNA 4933433D23 gene, expressed sequence AW108044, solute carrier family 25 (mitochondrial carrier, brain), member 14, solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 10, solute carrier family 25 (mitochondrial carrier, ornithine transporter), member 15, uncoupling protein 2 (mitochondrial, proton carrier), uncoupling protein 2, mitochondrial
1732	4592	NM_019356	General		RIKEN cDNA 0910001O23 gene, eukaryotic translation initiation factor 2, subunit 1 (alpha, 35K), eukaryotic translation initiation factor 2A
1733	1324	NM_019371	w		EGL nine (C.elegans) homolog 1, EGL nine (C.elegans) homolog 2, EGL nine (C.elegans) homolog 3, EGL nine homolog 3 (C. elegans), ESTs, Moderately similar to A53770 growth factor-responsive protein, vascular smooth muscle - rat [R.norvegicus], ESTs, Weakly similar to A53770 growth factor-responsive protein, vascular smooth muscle - rat [R.norvegicus], SCAN domain-containing 2
1734	19577	NM_019377	e	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide, tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	
1735	24626	NM_019381	s	testis enhanced gene transcript, testis enhanced gene transcript (BAX inhibitor 1)	CGI-119 protein, RIKEN cDNA 5031405P05 gene, testis enhanced gene transcript (BAX inhibitor 1)
1736	744	NM_019622	p		ESTs, Highly similar to T42716 ankryrin 3, splice form 4 - mouse [M.musculus], ESTs, Moderately similar to A55575 ankryrin 3, long splice form [H.sapiens], ESTs, Weakly similar to T42716 ankryrin 3, splice form 4 - mouse [M.musculus], RIKEN cDNA 2310026G15 gene, RIKEN cDNA 4833425P12 gene, RIKEN cDNA 4930400E23 gene, RIKEN cDNA C430011H05 gene, ankryrin 3, node of Ranvier (ankryrin 3), hypothetical protein FLJ20189, phospholipase A2, group VI, phospholipase A2, group VI (cytosolic, calcium-independent), proteasome (prosome, macropain) 26S subunit, non-ATPase, 10

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any. Accession No. 4:001-500W0 Doc. No. 172697.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1737	20716	NM_019623	c		EST, Weakly similar to CPPI RAT CYTOCHROME P450 4F1 [R.norvegicus], ESTs, Weakly similar to S45702 leukotriene-B4 20-monooxygenase [H.sapiens], Mus musculus, Similar to RIKEN cDNA 1810054N16 gene, clone MGC:7384 [IMAGE:3487830, mRNA, complete cds, RIKEN cDNA 231002.1J05 gene, cytochrome P450 isoform 4F12, cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVF, polypeptide 11, cytochrome P450, subfamily IVF, polypeptide 2, cytochrome P450, subfamily IVF, polypeptide 8, expressed sequence AJ787289
1738	20709	NM_019904	x	lectin, galactose binding, soluble 1, lectin, galactoside-binding, soluble, 1 (galectin 1)	EST, Moderately similar to 1713410A beta galactoside soluble lectin [H.sapiens], EST, Moderately similar to GALECTIN-1 [R.norvegicus], Human HL14 gene encoding beta-galactoside-binding lectin, 3' end, clone 2, RIKEN cDNA 2200008F12 gene, Rattus norvegicus mRNA for galectin-2 related protein, complete cds, lectin, galactose binding, soluble 1, lectin, galactoside-binding, soluble, 1 (galectin 1), lectin, galactoside-binding, soluble, 2 (galectin 2)
1739	574	NM_019905	u,General	hydroxyacid oxidase (glycolate oxidase) 3, hydroxyacid oxidase 3 (medium-chain)	ESTs, Highly similar to (S)-2-HYDROXY-ACID OXIDASE, PEROXISOMAL [R.norvegicus], ESTs, Highly similar to LUH036 annexin II [H.sapiens], RIKEN cDNA 1110003P15 gene, RIKEN cDNA B43031.1C09 gene, annexin A2, annexin A2 pseudogene 2, caspase recruitment domain family, member 6, expressed sequence AW215814, hydroxyacid oxidase (glycolate oxidase) 3, hydroxyacid oxidase 1, liver, hydroxyacid oxidase 2 (long chain), nuclear protein 3 (apoptosis repressor with CARD domain)
1740	9096	NM_019908	j	hypothetical protein similar to mouse aldehyde reductase 6 (renal), renal-specific oxido-reductase	
1741	20457	NM_020073	i,General		parathyroid hormone receptor, parathyroid hormone receptor 1
1741	20458	NM_020073	General		parathyroid hormone receptor, parathyroid hormone receptor 1
1741	20460	NM_020073	General		parathyroid hormone receptor, parathyroid hormone receptor 1
1742	18713	NM_020075	r	eukaryotic translation initiation factor 5	DNA segment, Chr 12, ERATO D01549, expressed, KIAA1856 protein, eukaryotic translation initiation factor 5
1742	18715	NM_020075	r	eukaryotic translation initiation factor 5	DNA segment, Chr 12, ERATO D01549, expressed, KIAA1856 protein, eukaryotic translation initiation factor 5
1743	20493	NM_020076	p		3-hydroxyanthranilate 3,4-dioxygenase, RIKEN cDNA 0610007K21 gene, RIKEN cDNA 0610012J07 gene

TABLE OF HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4494-500TWG Doc. No. 179337	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Transcript Name	Gene	Homologues Cluster Name
1744	16375	NM_020976	g			angiotensin I converting enzyme (peptidyl-dipeptidase A) 2, kidney-specific membrane protein
1745	20816	NM_021261	k, General			EST, Highly similar to THYMOSIN BETA-10 [R.norvegicus], ESTs, Highly similar to TYB4 MOUSE THYMOSIN BETA-4 [M.musculus], expressed sequence AW544206, thymosin, beta 10, thymosin, beta 4, X chromosome
1746	15335	NM_021264	a		ribosomal protein L35a	EST, Weakly similar to 60S RIBOSOMAL PROTEIN L35A [R.norvegicus], EST, Weakly similar to R35A MOUSE 60S RIBOSOMAL PROTEIN L35A [M.musculus], EST, Weakly similar to RSHU35 ribosomal protein L35a [H.sapiens], Homo sapiens cDNA FLJ11509 fis, clone HEMBA1002166, RIKEN cDNA 2810431L15 gene, ribosomal protein L35a, uncharacterized hypothalamus protein HSMNP1
1747	18729	NM_021578	k, z		transforming growth factor, beta 1	transforming growth factor, beta 1
1748	19060	NM_021587	cc		latent transforming growth factor beta binding protein 1	EST, Weakly similar to TGFB_HUMAN LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR [H.sapiens], ESTs, Weakly similar to TGFB RAT LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR [R.norvegicus], RIKEN cDNA 2310046A13 gene, hypothetical protein MGC13010, latent transforming growth factor beta binding protein 1, latent transforming growth factor beta binding protein 2, latent transforming growth factor beta binding protein 3
1749	17324	NM_021593	o, General			ESTs, Moderately similar to TYPE I IODOTHYRONINE DEIODINASE [R.norvegicus], deiodinase, iodothyronine, type I
1750	19679	NM_021653	General		deiodinase, iodothyronine, type I	ESTs, Moderately similar to TYPE I IODOTHYRONINE DEIODINASE [R.norvegicus], deiodinase, iodothyronine, type I
1751	19678	NM_021653	a, y, General		deiodinase, iodothyronine, type I	ESTs, Moderately similar to TYPE I IODOTHYRONINE DEIODINASE [R.norvegicus], deiodinase, iodothyronine, type I
1751	19665	NM_021688	u, General			potassium channel, subfamily K, member 1 (TWIK-1), potassium channel, subfamily K, member 3 (TASK-1), potassium channel, subfamily K, member 6 (TWIK-2), potassium channel, subfamily K, member 7

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any. Doc# No. 43921-3331WO Doc. No. 1793837.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1752	19667	NM_021690	m		EST, Highly similar to GUANINE NUCLEOTIDE RELEASING PROTEIN [R.norvegicus], EST, Weakly similar to 2009427A guanine nucleotide-releasing protein [H.sapiens], ESTs, Highly similar to 2009427A guanine nucleotide-releasing protein [H.sapiens], ESTs, Weakly similar to S28407 guanine nucleotide-exchange activator CDC25 homolog - mouse [M.musculus], RAS protein-specific guanine nucleotide-releasing factor 1, RAS protein-specific guanine nucleotide-releasing factor 2, RIKEN cDNA 4921528G01 gene, Rap1 guanine-nucleotide-exchange factor directly activated by cAMP, Rettus norvegicus strain Wistar RAS guanine nucleotide-releasing factor 1 (Rasgrf1) mRNA, partial cds, guanine nucleotide-releasing factor 2 (specific for crk proto oncogene)
1754	22816	NM_021740	a	prothymosin alpha, prothymosin, alpha (gene sequence 28)	ESTs, Highly similar to THYA_HUMAN PROTHYMOSIN ALPHA [H.sapiens], RIKEN cDNA 2610009E16 gene, prothymosin a 14, prothymosin alpha, prothymosin, alpha (gene sequence 28)
1755	19710	NM_021744	t		CD14 antigen, ESTs, Weakly similar to CD14 RAT MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR [R.norvegicus]
1755	19711	NM_021744	t		CD14 antigen, ESTs, Weakly similar to CD14 RAT MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR [R.norvegicus]
1756	19712	NM_021745	f		EST, Weakly similar to 138975 nuclear orphan receptor LXR-alpha [H.sapiens], ESTs, Moderately similar to JC4014 steroid hormone-nuclear receptor NER [H.sapiens], expressed sequence A1957360, nuclear receptor subfamily 1, group H, member 3, nuclear receptor subfamily 1, group H, member 4
1757	19824	NM_021750	a,bb		Homo sapiens, clone MGC:18185 IMAGE:4155381, mRNA, complete cds, KIAA0251 hypothetical protein, RIKEN cDNA 1110027M19 gene, cysteine sulfinic acid decarboxylase-related protein 2, glutamic acid decarboxylase 2
1758	25198	NM_021754	h		DKFZP566J153 protein, ESTs, Moderately similar to T17299 hypothetical protein
1758	20035	NM_021754	b,n,s,v,General		DKFZp564H2171.1 [H.sapiens], nuclear protein NOP5/NOP58

TABLE B: HUMAN HOMOLOGUE ANNOTATIONS					Any. DocId: No. 4494-5089W Doc. No. 1795897.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model/Code	Homologous Gene Name	Homologous Cluster Name	
1759	20090	NM_021757	m	pleiotropic regulator 1 (PRL1, Arabidopsis homolog), pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	EST, Weakly similar to LIS1 MOUSE [PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus], ESTs, Weakly similar to LIS1 MOUSE [PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus], Homo sapiens mRNA for FLJ00083 protein, partial cds, WD repeat domain 5, f-box and WD-40 domain protein 2, hypothetical protein, platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta), platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit, platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD), recombination protein REC14	
1760	17885	NM_021765	aa		ESTs, Weakly similar to COPP RAT COATOMER BETA' SUBUNIT [R.norvegicus], Mus musculus, Similar to RIKEN cDNA 1500041N16 gene, clone MGC:12068 IMAGE:3708188, mRNA, complete cds, RIKEN cDNA 2510040007 gene, coatomer protein complex, subunit beta 2 (beta prime), expressed sequence AA08785, expressed sequence A1256832, expressed sequence C77982, glutamate rich WD repeat protein GRWD, platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	
1762	20161	NM_021836	cc,General		Jun-B oncogene, Jun B proto-oncogene	
1764	1203	NM_021997	k,z	cytoplasmic linker 2	DKFZP586N1922 protein, ESTs, Moderately similar to S22695 restin [H.sapiens], ESTs, Weakly similar to T42734 cytoplasmic linker protein CLIP-115 - rat [R.norvegicus], RIKEN cDNA 1500005P14 gene, RIKEN cDNA 4831428H07 gene, RIKEN cDNA 5830409B12 gene, cytoplasmic linker 2, hypothetical protein FLJ20364, restin (Reed-Steinberg cell-expressed intermediate filament-associated protein), restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	
1765	23151	NM_022005	b	FXYP domain-containing ion transport regulator 6	EST, Moderately similar to PLM RAT PHOSPHOLEMMAN PRECURSOR [R.norvegicus], EST, Weakly similar to PLM_HUMAN PHOSPHOLEMMAN PRECURSOR [H.sapiens], FXYP domain-containing ion transport regulator 1, FXYP domain-containing ion transport regulator 1 (phospholemmann), FXYP domain-containing ion transport regulator 3, FXYP domain-containing ion transport regulator 4, FXYP domain-containing ion transport regulator 5, FXYP domain-containing ion transport regulator 6, FXYP domain-containing ion transport regulator 7, hypothetical protein MGC13186	

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any DocId:364492-6081WO Doc. No. 199397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1767	17101	NM_022179	bb		EST, Moderately similar to HXK3_HUMAN HEXOKINASE TYPE III [H.sapiens], EST, Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], ESTs, Moderately similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], ESTs, Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], hexokinase 2, hexokinase 3 (white cell)
1767	17100	NM_022179	bb		EST, Moderately similar to HXK3_HUMAN HEXOKINASE TYPE III [H.sapiens], EST, Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], ESTs, Moderately similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], ESTs, Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], hexokinase 2, hexokinase 3 (white cell)
1768	20257	NM_022180	w.General		expressed sequence AA986699, hepatic nuclear factor 4, hepatocyte nuclear factor 4, alpha
1768	25699	NM_022180	i		expressed sequence AA986699, hepatic nuclear factor 4, hepatocyte nuclear factor 4, alpha
1768	10860	NM_022180	p		
1769	23780	NM_022183	k,x	topoisomerase (DNA) II alpha, topoisomerase (DNA) II alpha (170kD)	ESTs, Moderately similar to A40493 DNA topoisomerase [H.sapiens], ESTs, Moderately similar to TP2A MOUSE DNA TOPOISOMERASE II, ALPHA [M.musculus], topoisomerase (DNA) II alpha, topoisomerase (DNA) II beta, topoisomerase (DNA) II beta (180kD)
1770	20312	NM_022224	o		expressed sequence A1790318, expressed sequence A1836570, phospholipase related
1771	6585	NM_022266	d,p,cc		WNT1 inducible signaling pathway protein 1, WNT1 inducible signaling pathway protein 2, WNT1 inducible signaling pathway protein 3, connective tissue growth factor
1772	17161	NM_022298	l,v,cc,General		ESTs, Highly similar to A23035 tubulin alpha chain [H.sapiens], tubulin alpha 1, tubulin alpha 2, tubulin alpha 3, tubulin alpha 6, tubulin, alpha 2, tubulin, alpha 3, tubulin, alpha, ubiquitous
1772	17162	NM_022298	u		ESTs, Highly similar to A23035 tubulin alpha chain [H.sapiens], tubulin alpha 1, tubulin alpha 2, tubulin alpha 3, tubulin alpha 6, tubulin, alpha 2, tubulin, alpha 3, tubulin, alpha, ubiquitous
1772	17160	NM_022298	u		ESTs, Highly similar to A23035 tubulin alpha chain [H.sapiens], tubulin alpha 1, tubulin alpha 2, tubulin alpha 3, tubulin alpha 6, tubulin, alpha 2, tubulin, alpha 3, tubulin, alpha, ubiquitous

TABLE 8: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44924-8889WO (Doc. No. 6798267.1)
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1772	17158	NM_022298	q		ESTs, Highly similar to A23035 tubulin alpha chain [H.sapiens], tubulin alpha 1, tubulin alpha 2, tubulin alpha 3, tubulin alpha 6, tubulin, alpha 2, tubulin, alpha 3, tubulin, alpha, ubiquitous
1773	11454	NM_022381	I,aa.General		EST, Moderately similar to E Chain E, Human Pcn [H.sapiens], proliferating cell nuclear antigen
1773	11455	NM_022381	I.General		EST, Moderately similar to E Chain E, Human Pcn [H.sapiens], proliferating cell nuclear antigen
1774	13480	NM_022390	s		RIKEN cDNA 261008L04 gene, quinoid dihydropteridine reductase
1775	15184	NM_022391	z	pituitary tumor-transforming 1	
1776	22413	NM_022392	h		EST, Highly similar to ISI1_HUMAN INSULIN-INDUCED PROTEIN 1 [H.sapiens], ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [R.norvegicus], Mus musculus, clone MGC:18904 IMAGE:4240711, mRNA, complete cds, insulin induced gene 1, Insulin induced protein 2
1776	22414	NM_022392	n		EST, Highly similar to ISI1_HUMAN INSULIN-INDUCED PROTEIN 1 [H.sapiens], ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [R.norvegicus], Mus musculus, clone MGC:18904 IMAGE:4240711, mRNA, complete cds, insulin induced gene 1, Insulin induced protein 2
1777	22499	NM_022393	t		C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 10, C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 6, C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6, CD72 antigen, Mus musculus Ly-49Q mRNA for NK receptor Ly-49Q, complete cds, Mus musculus, Similar to macrophage galactose N-acetyl-galactosamine specific lectin, clone MGC:25983 IMAGE:4456238, mRNA, complete cds, RIKEN cDNA 4930572L20 gene, asialoglycoprotein receptor 1, macrophage lectin 2 (calcium dependent)
1779	24537	NM_022399	e		ESTs, Weakly similar to CALRETICULIN PRECURSOR [R.norvegicus], Homo sapiens, Similar to RIKEN cDNA 1700031L01 gene, clone MGC:26577 IMAGE:4822010, mRNA, complete cds, RIKEN cDNA 1700031L01 gene, RIKEN cDNA 633056I20 gene, calreticulin

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					App. Doc. No. 4-199-5081W0 Sec. No. 199897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Gene Name	Homologous EMBL Name
1779	24539	NM_022399	y		ESTs, Weakly similar to CALRETICULIN PRECURSOR [R.norvegicus], Homo sapiens. Similar to RIKEN cDNA 1700031L01 gene, clone MGC:26577 IMAGE:4822010, mRNA, complete cds, RIKEN cDNA 1700031L01 gene, RIKEN cDNA 6330586I20 gene, calreticulin
1780	1141	NM_022401	q.General		ESTs, Highly similar to 139161 dystonin isoform 2 [H.sapiens], ESTs, Weakly similar to T42725 actin binding protein ACF7, neural isoform 1 - mouse (fragment) [M.musculus], Leman coiled-coil protein, actin-crosslinking protein 7, expressed sequence AA591047, expressed sequence AW554249, plectin 1, intermediate filament binding protein, 500kD, serologically defined colon cancer antigen 8
1781	1059	NM_022402	g		EST, Highly similar to R5HUP0 acidic ribosomal protein P0, cytosolic [H.sapiens], EST, Moderately similar to RLA0 RAT 60S ACIDIC RIBOSOMAL PROTEIN P0 [R.norvegicus], ESTs, Highly similar to R5HUP0 acidic ribosomal protein P0, cytosolic [H.sapiens], ESTs, Highly similar to RLA0 MOUSE 60S ACIDIC RIBOSOMAL PROTEIN P0 [M.musculus], RIKEN cDNA 2810012O22 gene, acidic ribosomal phosphoprotein P0, hypothetical protein IMAGE3455200, ribosomal protein, large, P0
1782	8211	NM_022500	j,n,s	ferritin light chain 1, ferritin, light polypeptide	ESTs, Highly similar to FRHUL ferritin light chain [H.sapiens], ESTs, Moderately similar to FRHUL ferritin light chain [H.sapiens], PRO0470 protein, RIKEN cDNA 4933416E14 gene, ferritin light chain 2, ferritin, light polypeptide
1782	8212	NM_022500	n,s	ferritin light chain 1, ferritin, light polypeptide	ESTs, Highly similar to FRHUL ferritin light chain [H.sapiens], ESTs, Moderately similar to FRHUL ferritin light chain [H.sapiens], PRO0470 protein, RIKEN cDNA 4933416E14 gene, ferritin light chain 2, ferritin, light polypeptide
1783	6815	NM_022503	s	cytochrome c oxidase subunit VIIa polypeptide 3 (liver), cytochrome c oxidase, subunit VIIa 3	EST, Moderately similar to OSHU7L cytochrome-c oxidase [H.sapiens], cytochrome c oxidase subunit VIIa polypeptide 2 (liver), cytochrome c oxidase, subunit VIIa 1, cytochrome c oxidase, subunit VIIa 3
1784	4259	NM_022504	q,w	ribosomal protein L36	EST, Moderately similar to T08720 ribosomal protein L36 [H.sapiens], ESTs, Weakly similar to RL36, HUMAN 60S RIBOSOMAL PROTEIN L36 [H.sapiens], RIKEN cDNA 1110038G14 gene, ribosomal protein L36

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4927-3180W0
					Doc. No. 17928P/1
Seq. ID No.	Identifier	SanBank/Accession Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1785	1611	NM_022509	j		ESTs, Weakly similar to SMN1_HUMAN SURVIVAL MOTOR NEURON PROTEIN 1 [H.sapiens], RIKEN cDNA 2410004J23 gene, expressed sequence AB849087, expressed sequence AW122358, splicing factor 30, survival of motor neuron-related, survival motor neuron, survival motor neuron pseudogene, survival of motor neuron 1, telomeric, survival of motor neuron 2, centromeric
1786	2236	NM_022512	y,z		ESTs, Weakly similar to acyl-CoA dehydrogenase [R.norvegicus], RIKEN cDNA 1300003O09 gene, RIKEN cDNA 2310018C19 gene, acetyl-Coenzyme A dehydrogenase, short chain, acyl-Coenzyme A dehydrogenase family, member 8, acyl Coenzyme A dehydrogenase, C-2 to C-3 short chain, hypothetical protein FLJ12592, hypothetical protein MGC5601, isovaleryl coenzyme A dehydrogenase
1787	3026	NM_022514	a		EST, Weakly similar to 60S RIBOSOMAL PROTEIN L27 [R.norvegicus], EST, Weakly similar to S43505 ribosomal protein L27, cytosolic [H.sapiens], ribosomal protein L27
1787	3027	NM_022514	a,q,r,aa		EST, Weakly similar to 60S RIBOSOMAL PROTEIN L27 [R.norvegicus], EST, Weakly similar to S43505 ribosomal protein L27, cytosolic [H.sapiens], ribosomal protein L27
1788	2696	NM_022515	a,d		ESTs, Highly similar to RL24_HUMAN 60S RIBOSOMAL PROTEIN L24 [H.sapiens], RIKEN cDNA 0610008L05 gene, ribosomal protein L24
1788	2697	NM_022515	n,w,aa		ESTs, Highly similar to RL24_HUMAN 60S RIBOSOMAL PROTEIN L24 [H.sapiens], RIKEN cDNA 0610008L05 gene, ribosomal protein L24
1789	3900	NM_022516	h	neural polypyrimidine tract binding protein, polypyrimidine tract binding protein	ESTs, Moderately similar to S15552 polypyrimidine tract-binding protein 1 - rat [R.norvegicus], ESTs, Weakly similar to S15552 polypyrimidine tract-binding protein 1 - rat [R.norvegicus], RIKEN cDNA 2810036L13 gene, expressed sequence AW107884, heterogeneous nuclear ribonucleoprotein L, neural polypyrimidine tract binding protein, polypyrimidine tract binding protein, polypyrimidine tract binding protein 2
1790	4151	NM_022518	o		ADP-ribosylation factor 1, ADP-ribosylation factor domain protein 1, 64kD, ADP-ribosylation factor-like 1, ARF protein, Homo sapiens, Similar to DKFPZ727C091 protein, clone MGC:10677 IMAGE:3948445, mRNA, complete cds

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4892-3089WO Doc. No. 1792817.1
Seq. ID No.	Accession	Gene/Protein/Accession/Ref. Seq. ID No.	Model Code	Homologue Gene Name	Homologue Cluster Name
1791	4242	NM_022521	c		ESTs, Highly similar to ORNITHINE AMINOTRANSFERASE PRECURSOR [R. norvegicus], RIKEN cDNA 1300019H02 gene, RIKEN cDNA 2900006B13 gene, hypothetical protein MGC15875, ornithine aminotransferase, ornithine aminotransferase (gyrate atrophy)
1792	4412	NM_022523	o		CD151 antigen, Homo sapiens cDNA FLJ14609 fs, clone NT2RP1000944, RIKEN cDNA 1110014F12 gene, RIKEN cDNA 1110031P12 gene, RIKEN cDNA 2700063A19 gene, transmembrane 4 superfamily member (tetraspan NET-2), transmembrane 4 superfamily member 6
1793	6641	NM_022533	General		ESTs, Weakly similar to A55046 plasmolipin - rat [R. norvegicus], ESTs, Weakly similar to PLIP - HUMAN PLASMOLIPIN [H. sapiens], Homo sapiens cDNA FLJ14787 fs, clone NT2RP4000878, highly similar to MYELOID UPREGULATED PROTEIN, Mus musculus, Similar to BENE protein, clone MGC:19097 IMAGE:4205488, mRNA, complete cds, RIKEN cDNA 2700018N07 gene, expressed sequence A461653, myelin and lymphocyte protein; T-cell differentiation protein, plasmolipin
1794	8097	NM_022536	a		ESTs, Moderately similar to A Chain A, Cyclophilin B Complexed With [H. sapiens], RIKEN cDNA 1110060C10 gene, RIKEN cDNA 3732410E19 gene, RIKEN cDNA 4833408F11 gene, expressed sequence AA408962, expressed sequence AA553318, peptidylprolyl isomerase B, peptidylprolyl isomerase B (cyclophilin B)
1795	8597	NM_022538	c,r,u		
1795	8598	NM_022538	u		
1796	9296	NM_022541	o		EST, Highly similar to IMB8_MOUSE MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM8 B (DEAFNESS DYSTONIA PROTEIN 2 HOMOLOG) [R. norvegicus], translocase of inner mitochondrial membrane 8 (yeast) homolog B, translocase of inner mitochondrial membrane 8 homolog b (yeast)
1797	21063	NM_022585	h	ornithine decarboxylase antizyme inhibitor	ESTs, Weakly similar to A Chain A, Crystal Structure Ornithine Decarboxylase From Mouse, Truncated 37 Residues From The C-Terminus, To 1.6 Angstrom Resolution [M. musculus], ESTs, Weakly similar to ORNITHINE DECARBOXYLASE [R. norvegicus], Ornithine decarboxylase, ornithine decarboxylase 1, ornithine decarboxylase antizyme inhibitor, ornithine decarboxylase, structural, ornithine decarboxylase-like protein

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Ally, Doclet No. 4-924-438W0 Doc. No. 1193897.1
Seq. ID No.	Accession No.	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Gene Name
1799	20781	NM_022591	z		apoptotic protease activating factor, telomerase associated protein 1, telomerase-associated protein 1 RIKEN cDNA 4933401f19 gene, hypothetical protein DKFZp434L1717, transketolase, transketolase (Wernicke Korsakoff syndrome), transketolase-like 1
1800	20803	NM_022592	n		
1801	20925	NM_022594	g	enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1, peroxisomal	AU RNA-binding protein/enoyl-coenzyme A hydratase, EST, Weakly similar to ECH1, HUMAN DELTA3,5-DELTA2,4-DIENOYL-COA ISOMERASE PRECURSOR [H.sapiens], RIKEN cDNA 2610009M20 gene, enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1, peroxisomal, expressed sequence AA617331
1802	20944	NM_022597	aa		cathepsin B, lipocalin 7, tubulointerstitial nephritis antigen
1803	21024	NM_022599	o, General		EST, Highly similar to OM25_RAT MITOCHONDRIAL OUTER MEMBRANE PROTEIN 25 (NPW16) [R.norvegicus], EST, Weakly similar to OM25_RAT MITOCHONDRIAL OUTER MEMBRANE PROTEIN 25 (NPW16) [R.norvegicus], ErbB2 interacting protein, discs, large homolog 4 (Drosophila), expressed sequence A118201, hypothetical protein FLJ11271, synaptotagmin 2 binding protein
1804	2250	NM_022643	General		H2B histone family, member D, H2B histone family, member K, RIKEN cDNA 2610022J01 gene, expressed sequence A1413321, expressed sequence R74621
1805	17567	NM_022672	a, y	ribosomal protein S14	EST, Moderately similar to 40S RIBOSOMAL PROTEIN S14 [R.norvegicus], EST, Weakly similar to A25220 ribosomal protein S14, cytosolic [H.sapiens], EST, Weakly similar to JE0129 ribosomal protein S14 - mouse [M.musculus], ESTs, Highly similar to A25220 ribosomal protein S14, cytosolic [H.sapiens], ribosomal protein S14
1806	17651	NM_022674	bb	H2A histone family, member Z	EST, Weakly similar to histone H2A-F/Z variant [H.sapiens], ESTs, Highly similar to HISTONE H2A.Z [R.norvegicus], H2A histone family, member Z, RIKEN cDNA C530002L11 gene, histone H2A-F/Z variant
1807	24563	NM_022676	b	protein phosphatase 1, regulatory (inhibitor) subunit 1A	EST, Weakly similar to IPP1_HUMAN PROTEIN PHOSPHATASE INHIBITOR 1 [H.sapiens], ESTs, Weakly similar to IPP1_HUMAN PROTEIN PHOSPHATASE INHIBITOR 1 [H.sapiens], RIKEN cDNA 4930579P15 gene, protein phosphatase 1, regulatory (inhibitor) subunit 1A, protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 4:192-3801WO
					Doc. No. 179:3397.1
Seq. ID No.	Identifier	Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1807	24564	NM_022676	b,x	protein phosphatase 1, regulatory (inhibitor) subunit 1A	EST, Weakly similar to IPP1_HUMAN PROTEIN PHOSPHATASE INHIBITOR 1 [H.sapiens], ESTs, Weakly similar to IPP1_HUMAN PROTEIN PHOSPHATASE INHIBITOR 1 [H.sapiens], RIKEN cDNA 4930579P15 gene, protein phosphatase 1, regulatory (inhibitor) subunit 1A, protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)
1808	20506	NM_022686	i		
1809	20508	NM_022688	g		
1810	17586	NM_022694	k		EBNA-2 co-activator (100kD), ESTs, Moderately similar to 138968 100 kDa coactivator [H.sapiens]
1811	17730	NM_022697	a		DNA segment, Chr 7, Wayne State University 21, expressed, EST, Highly similar to S55915 ribosomal protein L28 [H.sapiens], ESTs, Highly similar to S55915 ribosomal protein L28 [H.sapiens], ribosomal protein L28
1811	17729	NM_022697	q		DNA segment, Chr 7, Wayne State University 21, expressed, EST, Highly similar to S55915 ribosomal protein L28 [H.sapiens], ESTs, Highly similar to S55915 ribosomal protein L28 [H.sapiens], ribosomal protein L28
1812	154	NM_022649	t	crp-ductin, deleted in malignant brain tumors 1	CD163 antigen, ESTs, Highly similar to 138005 M130 antigen precursor, splice form 4 [H.sapiens], KIAA1822 protein, apoptosis inhibitory 6, crp-ductin, deleted in malignant brain tumors 1, lectin, galactoside-binding, soluble, 3 binding protein, macrophage scavenger receptor 2, peptidylprolyl isomerase C-associated protein
1813	127	NM_022855	h		EST, Weakly similar to KC13 RAT CASEIN KINASE I, GAMMA 3 ISOFORM [R.norvegicus], ESTs, Highly similar to KC13 RAT CASEIN KINASE I, GAMMA 3 ISOFORM [R.norvegicus], ESTs, Weakly similar to casein kinase [M.musculus], RIKEN cDNA 2610208K14 gene, RIKEN cDNA 3300002K07 gene, casein kinase 1, alpha 1, casein kinase 1, delta, casein kinase 1, epsilon, casein kinase 1, gamma 1, casein kinase 1, gamma 3
1814	152	NM_022858	j		ESTs, Highly similar to FXD3_HUMAN FORKHEAD BOX PROTEIN D3 [H.sapiens], ESTs, Weakly similar to FXD3_HUMAN FORKHEAD BOX PROTEIN D3 [H.sapiens], ESTs, Weakly similar to HEH1 RAT HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 [R.norvegicus], HNF-3/forkhead homolog 1 like, expressed sequence A1385632, forkhead box D1, forkhead box D2, forkhead box D3, winged helix/forkhead transcription factor
1816	18101	NM_022948	z		
1816	18103	NM_022948	u		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4:491-588WO Doc. No. 1708897.1
Seq. ID No.	Identified	GenBank/CCO Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1817	21491	NM_022951	w		CAT56 protein, EST, Highly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to A28996 proline-rich protein M14 precursor - mouse [M.musculus], EST, Weakly similar to E0291 FB19 protein [H.sapiens], collagen, type III, alpha 1 [Ehlers-Danlos syndrome type IV, autosomal dominant], procollagen, type III, alpha 1, proline rich protein, proline rich protein 2, protein phosphatase 1, regulatory subunit 10
1818	15742	NM_022958	y		ESTs, Moderately similar to S57219 phosphatidylinositol 3-kinase [H.sapiens], FK506 binding protein 12-rapamycin associated protein 1, Homo sapiens cDNA FLJ12591 fls, clone NT2RM4001313, moderately similar to PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137), Homo sapiens cDNA FLJ14331 fls, clone PLACE4000320, RIKEN cDNA 2410099E07 gene, phosphatidylinositol 3-kinase catalytic delta polypeptide, phosphatidylinositol 3-kinase, catalytic, beta polypeptide, phosphoinositide-3-kinase, class 3, rapamycin and FKBP12 target-1 protein
1819	9286	NM_023027	t,w		ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D), ESTs, Highly similar to HUD RAT PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG [R.norvegicus], ESTs, Moderately similar to HUD RAT PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG [R.norvegicus], ESTs, Moderately similar to POLYADENYLATE-BINDING PROTEIN 1 [M.musculus], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933407N23, full insert sequence, RIKEN cDNA 4932702K14 gene, poly A binding protein, cytoplasmic 1
1820	23215	NM_023102	z		RIKEN cDNA 261028K14 gene, VRK3 for vaccinia related kinase 3, casein kinase 1, alpha 1, casein kinase 1, delta, casein kinase 1, epsilon, casein kinase 1, gamma 2
1821	21238	NM_024125	cc,General	CCAAT/enhancer binding protein (C/EBP), beta	CCAAT/enhancer binding protein (C/EBP), beta
1821	21239	NM_024125	cc,General	CCAAT/enhancer binding protein (C/EBP), beta	CCAAT/enhancer binding protein (C/EBP), beta
1822	353	NM_024127	i,n,General	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-inducible, alpha

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Atyp. Deposit No. 44891-50896 Dep. No. 193887.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Gene	Homologous Gene Name	Homologous Cluster Name
1822	354	NM_024127	i, General	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-inducible, alpha
1822	352	NM_024127	h, General	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-inducible, alpha
1823	17227	NM_024131	x	O-dopachrome tautomerase	O-dopachrome tautomerase, expressed sequence C78855
1824	1598	NM_024134	i	DNA-damage inducible transcript 3, DNA-damage-inducible transcript 3	DNA-damage inducible transcript 3, EST, Moderately similar to GA15_HUMAN GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 [H.sapiens], myozenin
1825	1162	NM_024153	d		ferredoxin reductase
1826	7863	NM_024156	c		ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD, ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD, ESTs, Weakly similar to VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT [R.norvegicus], Mus musculus, Similar to ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD, clone MGC:5568 IMAGE:2812497, mRNA, complete cds
1827	22079	NM_024157	x		EST, Weakly similar to A29154 complement factor I [H.sapiens], I factor (complement), RIKEN cDNA 130008BA22 gene, complement component factor I, protease, serine, 7 (enterokinase), suppression of tumorigenicity 14 (colon carcinoma), transmembrane protease, serine 2
1828	16476	NM_024162	General	fatty acid binding protein 3, muscle and heart, fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	EST, Moderately similar to FABH MOUSE FATTY ACID-BINDING PROTEIN, HEART [M.musculus], ESTs, Highly similar to PCA011 fatty acid-binding protein - mouse [M.musculus], fatty acid binding protein 3, muscle and heart, fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor), fatty acid binding protein 3, pseudogene 2
1829	17765	NM_024351	b,s,v	heat shock 70kD protein 8	EST, Moderately similar to A27077 dnaK-type molecular chaperone [H.sapiens], EST, Weakly similar to A27077 dnaK-type molecular chaperone [H.sapiens], EST, Weakly similar to A45935 dnaK-type molecular chaperone hsc70 - mouse [M.musculus], heat shock 70kD protein 8, hypothetical protein MGC4859 similar to HSPA8

TABLE ON HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44971-5039WO Doc. No. 1998397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1830	8879	NM_024360	h		bHLH factor Hes4, basic helix-loop-helix domain containing, class B, 2, basic helix-loop-helix domain containing, class B, 3, hairy (Drosophila)-homolog, hairy and enhancer of split 1, (Drosophila), hairy and enhancer of split 6, (Drosophila), hairy/enhancer-of-split related with YRPW motif 1, hairy/enhancer-of-split related with YRPW motif 2, likely ortholog of mouse Hes6 neuronal differentiation gene
1831	20772	NM_024363	x	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2, heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae)	ANM1_HUMAN PROTEIN ARGININE N-METHYLTRANSFERASE 1 [H.sapiens], EST, Weakly similar to ANM1_HUMAN PROTEIN ARGININE N-METHYLTRANSFERASE 1 [H.sapiens], ESTs, Moderately similar to ANM1_MOUSE PROTEIN ARGININE N-METHYLTRANSFERASE 1 [M.musculus], HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2, HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 3, Homo sapiens cDNA: FLJ23133 fis, clone LNG08560, RIKEN cDNA 2410018A17 gene, coactivator-associated arginine methyltransferase-1, expressed sequence AW214366, heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae), heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae), related sequence, hypothetical protein FLJ10559
1832	2812	NM_024386	c		3-hydroxy-3-methylglutaryl-Coenzyme A lyase, 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria), Homo sapiens clone 24959 mRNA sequence, partial cds, hypothetical protein
1833	335	NM_024387	ly		RIKEN cDNA 2700048G17 gene, heme oxygenase (decycling) 2
1834	21	NM_024388	cc		nuclear receptor subfamily 4, group A, member 1
1834	22	NM_024388	cc		nuclear receptor subfamily 4, group A, member 1

TABLE OF HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44921-3083W Dns. No. 1733837.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1836	9929	NM_024392	f		Homo sapiens cDNA FLJ13261 fis, clone OVARC1000885, weakly similar to OXIDOREDUCTASE UCFA (EC 1.-.-). Human DNA sequence from clone 1068E13 on chromosome 20p11.21-12.3. Contains two putative novel genes, the gene for a novel protein similar to bovine SCP2 (Sterol Carrier Protein 2) and part of HSD17B4 (hydroxysteroid (17-beta) dehydrogenase 4), an EEF1A1 (eukaryotic translation elongation factor 1 alpha 1) pseudogene, ESTs, STSs and GSSs, RIKEN cDNA 1110029G07 gene, RIKEN cDNA 1700010M22 gene, RIKEN cDNA 1810026B04 gene, RIKEN cDNA 2810207116 gene, expressed sequence AW208803, hydroxysteroid (17-beta) dehydrogenase 4, hydroxysteroid 17-beta dehydrogenase 4, hypothetical protein MGCT0940, oxidoreductase UCFA, retinal short-chain dehydrogenase/reductase 1
1837	3582	NM_024396	aa		ATP-binding cassette, sub-family A (ABC1), member 2, ATP-binding cassette, sub-family A (ABC1), member 3, ATP-binding cassette, sub-family A (ABC1), member 4, ATP-binding cassette, sub-family A (ABC1), member 7, ATP-binding cassette, sub-family A (ABC1), member 8, ESTs, Weakly similar to ABC2 MOUSE ATP-BINDING CASSETTE TRANSPORTER 2 [M.musculus], Homo sapiens mRNA for KIAA1888 protein, partial cds, hypothetical protein FLJ14297, hypothetical protein PR02543
1838	19993	NM_024398	e,p,s,aa		DNA segment, Chr 9, ERATO Dcl 85, expressed, Homo sapiens aconitase precursor (ACON) mRNA, nuclear gene encoding mitochondrial protein, partial cds, RIKEN cDNA 5031409G22 gene, aconitase 1, aconitase 1, soluble, aconitase 2, mitochondrial, iron-responsive element-binding protein
1839	10789	NM_024399	o		Homo sapiens, RIKEN cDNA 0610006H10 gene, clone MGC:17267 IMAGE:4155233, mRNA, complete cds, Homo sapiens, Similar to RIKEN cDNA 0610006H10 gene, clone MGC:9740 IMAGE:3853707, mRNA, complete cds, asparinoylase (aminoacylase 2, Canavan disease)

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS				Any. Bucket No. 4494-5084C Doc. No. 1193857.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1840	22626	NM_024400	cc.General		ESTs, Weakly similar to T47158 hypothetical protein DKFZp762C1110.1 [H.sapiens], Mus musculus papilin mRNA, complete cds, Mus musculus, Similar to a disintegrin and metalloproteinase with thrombospondin motifs 1 (ADAMTS-1), clone IMAGE:3491991, mRNA, partial cds, RIKEN cDNA 6720426B09 gene, RIKEN cDNA A930008K15 gene, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 8, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9
1841	13633	NM_024403	g.General		EST, Weakly similar to ATF4_HUMAN CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-4 [H.sapiens], activating transcription factor 4 (tax-responsive enhancer element B67), activating transcription factor 5
1841	13634	NM_024403	g.General		EST, Weakly similar to ATF4_HUMAN CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-4 [H.sapiens], activating transcription factor 4 (tax-responsive enhancer element B67), activating transcription factor 5
1842	23387	NM_024404	b.General		ESTs, Moderately similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C [R.norvegicus], ESTs, Weakly similar to A44192 heterogeneous nuclear ribonucleoprotein C-like protein [H.sapiens], Mus musculus high-glycine/tyrosine protein type 1 E5 mRNA, complete cds, expressed sequence C85084, heterogeneous nuclear ribonucleoprotein A/B, heterogeneous nuclear ribonucleoprotein D, heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1, 37KD)
1843	21038	NM_024484	h	aminolevulinate, delta-, synthase 1, aminolevulinic acid synthase 1	EST, Weakly similar to SYHUAL 5-aminolevulinate synthase [H.sapiens], ESTs, Moderately similar to 5-AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC [R.norvegicus], aminolevulinate, delta-, synthase 1, aminolevulinic acid synthase 1, aminolevulinic acid synthase 2, erythroid, serine palmitoyltransferase, long chain base subunit 1, serine palmitoyltransferase, long chain base subunit 2

TABLE 3. HUMAN HOMOLOGUE NOTATIONS					Ally. Doc# No. 44924-36896 Doc. No. 179897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1844	1853	NM_030826	s	glutathione peroxidase 1	GSHG_MOUSE GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (GSHPX-GI) [M.musculus], ESTs, Weakly similar to GSHG_RAT GLUTATHIONE PEROXIDASE [R.norvegicus], glutathione peroxidase 1, glutathione peroxidase 2 (gastrointestinal)
1845	15111	NM_030827	e, General	low density lipoprotein receptor-related protein 2, low density lipoprotein-related protein 2	EST, Highly similar to LRP2 RAT LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR [R.norvegicus], EST, Moderately similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus], ESTs, Highly similar to S02392 alpha-2-macroglobulin receptor precursor [H.sapiens], ESTs, Highly similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus], ESTs, Weakly similar to I53413 calcium sensor protein [H.sapiens], expressed sequence C79313, low density lipoprotein receptor-related protein 1, low density lipoprotein receptor-related protein 2, low density lipoprotein-related protein 1B (deleted in tumors), low density lipoprotein-related protein 2
1845	15112	NM_030827	y, z	low density lipoprotein receptor-related protein 2, low density lipoprotein-related protein 2	EST, Highly similar to LRP2 RAT LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR [R.norvegicus], EST, Moderately similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus], ESTs, Highly similar to S02392 alpha-2-macroglobulin receptor precursor [H.sapiens], ESTs, Highly similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus], ESTs, Weakly similar to I53413 calcium sensor protein [H.sapiens], expressed sequence C79313, low density lipoprotein receptor-related protein 1, low density lipoprotein receptor-related protein 2, low density lipoprotein-related protein 1B (deleted in tumors), low density lipoprotein-related protein 2

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4924-3083WO Reg. No. 1798837.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
					EST. Highly similar to LRP2 RAT LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR [R.norvegicus]. EST. Moderately similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus]. ESTs. Highly similar to S02392 alpha-2-macroglobulin receptor precursor [H.sapiens]. ESTs. Highly similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus]. ESTs. Weakly similar to I53413 calcium sensor protein [H.sapiens], expressed sequence C79313, low density lipoprotein receptor-related protein 1, low density lipoprotein receptor-related protein 2, low density lipoprotein-related protein 1B (deleted in tumors), low density lipoprotein-related protein 2
1845	15110	NM_030827	General	low density lipoprotein receptor-related protein 2, low density lipoprotein-related protein 2	
					solute carrier family 21 (organic anion transporter), member 1, solute carrier family 21 (organic anion transporter), member 10, solute carrier family 21 (organic anion transporter), member 14, solute carrier family 21 (organic anion transporter), member 3, solute carrier family 21 (organic anion transporter), member 6
1846	808	NM_030837	k,m		
					ESTs. Weakly similar to I65309 autoantigen p69 - rat [R.norvegicus], Homo sapiens ALS2CR15 mRNA, partial cds, RIKEN cDNA 1700030B17 gene, islet cell autoantigen 1 (69kD), islet cell autoantigen 1, 89 kDa
1847	4057	NM_030844	k		
					GRO1 oncogene, GRO2 oncogene, Rattus norvegicus CXK chemokine RTCK1 (Rtck1) mRNA, complete cds, interleukin 8, platelet factor 4, pro-platelet basic protein, pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)
1848	1221	NM_030845	t		
					ESTs. Weakly similar to PERIPHERAL MYELIN PROTEIN 22 [R.norvegicus]. Peripheral myelin protein, epithelial membrane protein 3, peripheral myelin protein 22, peripheral myelin protein, 22 kDa
1849	21509	NM_030847	x		
					EST. Highly similar to PDK2 RAT [R.norvegicus], expressed sequence A1035637, pyruvate dehydrogenase 2, pyruvate dehydrogenase kinase, isoenzyme 2
1850	1928	NM_030872	v	pyruvate dehydrogenase 2, pyruvate dehydrogenase kinase, isoenzyme 2	
					EST. Weakly similar to A Chain A, Human Platelet Profilin Complexed With The L-Pro10 Peptide [SUB 3-140 [H.sapiens]. ESTs. Weakly similar to profilin [R.norvegicus], RIKEN cDNA 1700012P12 gene, profilin, profilin 1, profilin 2
1851	17342	NM_030873	u		

TABLE of HUMAN HOMOLOGUE ANNOTATIONS					Ally, Doclet No. 44921-5083WC Doc. No. 1795897.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1852	24648	NM_030985	u		G protein-coupled receptor 15, G-protein coupled receptor SALPR, somatostatin and angiotensin-like peptide receptor, angiotensin receptor 1, expressed sequence A1551199
1852	25453	NM_030985	General		
1853	21802	NM_030987	h		ESTs, Weakly similar to GBB1 RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)(Y)(S)(G)(T) BETA SUBUNIT 1 [R.norvegicus], Mus musculus, clone M3C.7534 IMAGE:3583848, mRNA, complete cds, RIKEN cDNA 593041SH02 gene, constitutive photomorphogenic protein 1 (Arabidopsis), guanine nucleotide binding protein (G protein), beta polypeptide 1, guanine nucleotide binding protein beta subunit 4, guanine nucleotide binding protein, beta 1, guanine nucleotide binding protein, beta 4, similar to constitutive photomorphogenic protein 1 (Arabidopsis)
1854	23109	NM_031000	f,s,z		EST, Weakly similar to ALCOHOL DEHYDROGENASE [R.norvegicus], RIKEN cDNA 231000SE10 gene, aldo-keto reductase family 1, member A1 (aldehyde reductase), aldo-keto reductase family 1, member A4 (aldehyde reductase), aldo-keto reductase family 1, member E1
1855	134	NM_031003	a,u		4-aminobutyrate aminotransferase, RIKEN cDNA 1300019H02 gene, RIKEN cDNA 2900006B13 gene, ornithine aminotransferase
1856	25461	NM_031009	o		
1857	1845	NM_031010	t		ARACHIDONATE 12-LIPOXYGENASE [R.norvegicus], arachidonate 12-lipoxygenase, arachidonate 12-lipoxygenase pseudogene 2, arachidonate 15-lipoxygenase, expressed sequence AW255591
1857	25517	NM_031010	c,t		ARACHIDONATE 12-LIPOXYGENASE [R.norvegicus], arachidonate 12-lipoxygenase, arachidonate 12-lipoxygenase pseudogene 2, arachidonate 15-lipoxygenase, expressed sequence AW255591
1858	16562	NM_031020	f		ESTs, Weakly similar to MK14 RAT MITOGEN-ACTIVATED PROTEIN KINASE 14 [R.norvegicus], mitogen-activated protein kinase 14, mitogen-activated protein kinase 11, mitogen-activated protein kinase 14
1859	1480	NM_031021	f		casein kinase 2, beta polypeptide, casein kinase II, beta subunit

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4:924-508W0	
					Doc. No.	Page 1
Seq. ID No.	Identifier	GenBank Acc. No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
1860	1719	NM_031024	n	drebrin 1	ESTs, Moderately similar to T30989 serine/threonine protein kinase NIK - mouse [M.musculus], RIKEN cDNA 1500031A17 gene, drebrin 1, drebrin-like, hypothetical protein FLJ13154, mitogen-activated protein kinase kinase kinase 4, mitogen-activated protein kinase kinase kinase 6, src homology 3 domain-containing protein HIP-55	
1861	1350	NM_031030	h		DnaJ (Hsp40) homolog, subfamily B, member 6, EST, Moderately similar to NEK1 MOUSE SERINE/THREONINE-PROTEIN KINASE NEK1 [M.musculus], EST, Moderately similar to T31096 cyclin G-associated kinase GAK - rat [R.norvegicus], EST, Weakly similar to T31096 cyclin G-associated kinase GAK - rat [R.norvegicus], ESTs, Moderately similar to NEK1 MOUSE SERINE/THREONINE-PROTEIN KINASE NEK1 [M.musculus], KIAA1048 protein, Mus musculus, Similar to cyclin G associated kinase, clone IMAGE:3487931, mRNA, partial cds, NIMA (never in mitosis gene a)-related expressed kinase 1, RIKEN cDNA 4632401F23 gene, cyclin G associated kinase, hypothetical protein DKFZp434P0116, serine/threonine kinase 16	
1862	16775	NM_031031	General		ESTs, Highly similar to GLYCINE AMIDINOTRANSFERASE PRECURSOR [R.norvegicus], RIKEN cDNA 1810003P21 gene, glycine amidinotransferase (L-arginine:glycine amidinotransferase)	
1863	691	NM_031034	w		ESTs, Highly similar to GB12 RAT GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-12 SUBUNIT [R.norvegicus], guanine nucleotide binding protein (G protein) alpha 12, guanine nucleotide binding protein (G protein), alpha 13, guanine nucleotide binding protein, alpha 12, guanine nucleotide binding protein, alpha 13	
1864	15886	NM_031035	z		guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2, guanine nucleotide binding protein, alpha inhibiting 2, guanine nucleotide binding protein, alpha inhibiting 3	
1866	3608	NM_031044	k, General		Homo sapiens, Similar to histamine N-methyltransferase, clone MGC:14500 IMAGE:4249496, mRNA, complete cds, expressed sequence A1788969, histamine N-methyltransferase	
1866	3610	NM_031044	d, General		Homo sapiens, Similar to histamine N-methyltransferase, clone MGC:14500 IMAGE:4249496, mRNA, complete cds, expressed sequence A1788969, histamine N-methyltransferase	

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Order No. 4493-4083WG Doc. No. 199897.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
1867	15137	NM_031051	s		EST, Highly similar to C Chain C, Macrophage Migration Inhibitory Factor [H.sapiens], EST, Moderately similar to C Chain C, Macrophage Migration Inhibitory Factor [H.sapiens], EST, Moderately similar to MIF RAT MACROPHAGE MIGRATION INHIBITORY FACTOR [R.norvegicus], macrophage migration inhibitory factor, macrophage migration inhibitory factor (glycosylation-inhibiting factor)	
1868	514	NM_031056	General		matrix metalloproteinase 14 (membrane-inserted), matrix metalloproteinase 19, vitronectin	
1869	17269	NM_031057	General		RIKEN cDNA 1110038105 gene, aldehyde dehydrogenase family 1, subfamily A4, expressed sequence A1427784, hypothetical protein FLJ23189, methylmalonate-semialdehyde dehydrogenase	
1870	11849	NM_031065	a		EST, Moderately similar to R10A MOUSE 60S RIBOSOMAL PROTEIN L10A [M.musculus], EST, Weakly similar to 60S RIBOSOMAL PROTEIN L10A [R.norvegicus], ESTs, Highly similar to R10A, HUMAN 60S RIBOSOMAL PROTEIN L10A [H.sapiens], ribosomal protein L10A, ribosomal protein L10a	
1871	1855	NM_031074	h	nucleoporin 98, nucleoporin 98kD	EST, Highly similar to NU98 RAT NUCLEAR PORE COMPLEX PROTEIN NUP98 [R.norvegicus], ESTs, Weakly similar to NU98 RAT NUCLEAR PORE COMPLEX PROTEIN NUP98 [R.norvegicus], RIKEN cDNA 0610038H21 gene, RIKEN cDNA 4930432K09 gene, RIKEN cDNA 5430432N15 gene, melanoma antigen, family D, 3, nucleoporin 98kD, plasma membrane associated protein, S3-12, trophinin	
1872	4683	NM_031083	d		phosphatidylinositol 3-kinase, catalytic, alpha polypeptide, phosphatidylinositol 4-kinase, catalytic, beta polypeptide, phosphoinositide-3-kinase, catalytic, gamma polypeptide	
1873	15202	NM_031093	a		EST, Weakly similar to RALA MOUSE RAS-RELATED PROTEIN RAL-A [M.musculus], Homo sapiens cDNA: FLJ23197 fs, clone REC00917, RIKEN cDNA 1110065D03 gene, v-ral simian leukemia viral oncogene homolog A (ras related), v-ral simian leukemia viral oncogene homolog B (ras related)	
1873	15201	NM_031093	a,n		EST, Weakly similar to RALA MOUSE RAS-RELATED PROTEIN RAL-A [M.musculus], Homo sapiens cDNA: FLJ23197 fs, clone REC00917, RIKEN cDNA 1110065D03 gene, v-ral simian leukemia viral oncogene homolog A (ras related), v-ral simian leukemia viral oncogene homolog B (ras related)	

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doctmt No. 43371-504W0 Doc. No. 3729393.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1874	12639	NM_031099	aa		ESTs, Weakly similar to S55912 ribosomal protein L5, cytosolic [H.sapiens], ribosomal protein L5
					EST, Moderately similar to 60S RIBOSOMAL PROTEIN L10 [M.musculus], EST, Moderately similar to 60S RIBOSOMAL PROTEIN L10 [R.norvegicus], ESTs, Highly similar to A42735 ribosomal protein L10, cytosolic [H.sapiens], Homo sapiens, Similar to ribosomal protein L10, clone MGC:22834 IMAGE:3935452, mRNA, complete cds, Human DNA sequence from clone RP3-334F4 on chromosome 6 Contains ESTs, STSs and GSSs, Contains a LAMR1 (laminin receptor 1, ribosomal protein SA) pseudogene and an RPL10 (ribosomal protein L10) pseudogene, Mouse 24.6 kda protein mRNA, complete cds, ribosomal protein L10
1875	20812	NM_031100	a		ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L19 [R.norvegicus], Homo sapiens mRNA; cDNA DKFZp434D115 (from clone DKFZp434D115), ribosomal protein L19
1876	16938	NM_031103	w		ESTs, Highly similar to JC2120 heparin-binding protein 15 [H.sapiens], ESTs, Moderately similar to RL22 RAT 60S RIBOSOMAL PROTEIN L22 [R.norvegicus], Homo sapiens mRNA; cDNA DKFZp586E0524 (from clone DKFZp586E0524), Human DNA sequence from clone 581F12 on chromosome Xq21, Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes, Contains ESTs, RIKEN cDNA 2700038K18 gene, RIKEN cDNA 3110001N18 gene, expressed sequence AU041196, ribosomal protein L22
1877	19268	NM_031104	q		EST, Weakly similar to RS9 RAT 40S RIBOSOMAL PROTEIN S9 [R.norvegicus], EST, Weakly similar to S55917 ribosomal protein S9, cytosolic [H.sapiens], Homo sapiens, clone IMAGE:4500773, mRNA, partial cds, RIKEN cDNA 301003SP07 gene, expressed sequence AL022771, expressed sequence AL022885, mitochondrial ribosomal protein S4, ribosomal protein S9
1878	16929	NM_031108	q		EST, Weakly similar to 40S RIBOSOMAL PROTEIN S11 [R.norvegicus], Homo sapiens mRNA; cDNA DKFZp434A0326 (from clone DKFZp434A0326), Human DNA sequence from clone RP5-1050K6 on chromosome 20p12.1-13, Contains an RPS11 (40S ribosomal protein S11) pseudogene, ESTs, STSs and GSSs, RAD21 homolog (S. pombe), ribosomal protein S11
1879	10878	NM_031110	q.bb		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Ally, Patent No. 4,924-509,926 Doc. No. 179,997.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1880	19162	NM_031111	a,a		EST, Moderately similar to 40S RIBOSOMAL PROTEIN S21 [R.norvegicus], Human DNA sequence from clone RP5-1116H23 on chromosome 20 Contains a novel gene, a 40S ribosomal protein S21 pseudogene, 2 CpG islands, ESTs, STSs and GSSs, RIKEN cDNA 1810049N11 gene, RIKEN cDNA 2410030A14 gene, ribosomal protein S21
1880	19161	NM_031111	a,bb		EST, Moderately similar to 40S RIBOSOMAL PROTEIN S21 [R.norvegicus], Human DNA sequence from clone RP5-1116H23 on chromosome 20 Contains a novel gene, a 40S ribosomal protein S21 pseudogene, 2 CpG islands, ESTs, STSs and GSSs, RIKEN cDNA 1810049N11 gene, RIKEN cDNA 2410030A14 gene, ribosomal protein S21
1881	24615	NM_031112	a,y		EST, Highly similar to 40S RIBOSOMAL PROTEIN S24 [R.norvegicus], EST, Weakly similar to JH0213 ribosomal protein S24, cytosolic [H.sapiens], EST, Weakly similar to RS24_HUMAN 40S RIBOSOMAL PROTEIN S24 [M.musculus], ESTs, Highly similar to JH0213 ribosomal protein S24, cytosolic [H.sapiens], ESTs, Weakly similar to RS24_HUMAN 40S RIBOSOMAL PROTEIN S24 [H.sapiens], ribosomal protein S24
1882	20839	NM_031113	a,q		EST, Moderately similar to S12583 polyubiquitin 4 - mouse [M.musculus], EST, Moderately similar to ubiquitin / ribosomal protein S27a [R.norvegicus], EST, Weakly similar to R27A_HUMAN 40S RIBOSOMAL PROTEIN S27A [SUB 77-156 [H.sapiens], Homo sapiens cDNA FLJ11603 fs, clone HEMBA1003926, RIKEN cDNA 061006J14 gene, expressed sequence A132487, ribosomal protein S27a, ubiquitin C
1883	19040	NM_031114	l,m,General	S100 calcium binding protein A10 (calgizarin), S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))	EST, Moderately similar to A Chain A, P11 [H.sapiens], EST, Moderately similar to CALPACTIN I LIGHT CHAIN [R.norvegicus], S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)), calcium binding protein A11 (calgizarin)
1884	16349	NM_031115	u		ESTs, Highly similar to 2111411A secretin receptor [H.sapiens], ESTs, Weakly similar to vasoactive intestinal polypeptide 1 [M.musculus], adenylylate cyclase activating polypeptide 1 receptor 1, secretin receptor, vasoactive intestinal peptide receptor 1

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Ally, DocId: No. 4494-56PVC Doc. No. 1798897.1
Seq. ID No.	Ident. ID	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologue Gene Name	Homologue Cluster Name
1885	14970	NM_031127	General		ESTs, Highly similar to SUOX RAT SULFITE OXIDASE PRECURSOR [R.norvegicus], RIKEN cDNA 0610009N12 gene, RIKEN cDNA 1810044O22 gene, RIKEN cDNA 2810034J18 gene, fatty acid desaturase 2, sulfite oxidase
1886	1814	NM_031134	n,q	thyroid hormone receptor alpha, thyroid hormone receptor, alpha (avian erythroblastic leukemia viral (v-erb-a) oncogene homology)	EST, Weekly similar to A30893 thyroid hormone receptor alpha, splice form 2 [H.sapiens], expressed sequence AW259572, expressed sequence R75201, thyroid hormone receptor, alpha (avian erythroblastic leukemia viral (v-erb-a) oncogene homology)
1887	13359	NM_031135	General		Kruppel-like factor 15 (kidney), Kruppel like factor 9, RIKEN cDNA 4930480i16 gene, TGFB inducible early growth response, basic transcription element binding protein 1, trans-acting transcription factor 3, trans-acting transcription factor 8
1888	15052	NM_031136	a		ESTs, Highly similar to A38682 thymosin beta-4 [H.sapiens], ESTs, Highly similar to TYB4 MOUSE THYMOSIN BETA-4 [M.musculus], ESTs, Highly similar to TYB4_HUMAN THYMOSIN BETA-4 [H.sapiens], Human interferon-inducible mRNA (cDNA 5-25), expressed sequence AW544206, thymosin, beta 10, thymosin, beta 4, X chromosome, thymosin, beta 4, Y chromosome
1888	19359	NM_031136	e		
1889	15185	NM_031140	General		EST, Moderately similar to A25074 vimentin [H.sapiens], EST, Weekly similar to A25074 vimentin [H.sapiens], ESTs, Moderately similar to VIME RAT VIMENTIN [R.norvegicus], ESTs, Weakly similar to A25074 vimentin [H.sapiens], ESTs, Weekly similar to VIME RAT VIMENTIN [R.norvegicus], vimentin
1890	21625	NM_031144	a,e		EST, Weakly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1 [R.norvegicus], ESTs, Highly similar to ATHUB actin beta [H.sapiens], ESTs, Weakly similar to ACTB_HUMAN ACTIN, CYTOPLASMIC 1 [R.norvegicus], Homo sapiens FKSG30 (FKSG30) mRNA, complete cds, RIKEN cDNA 1700052K15 gene, RIKEN cDNA 1700061J02 gene, actin, beta, actin-like 7a, actin-related protein 3-beta, melanoma X-actin
1891	238	NM_031152	bb		CATX-8 protein, ESTs, Weakly similar to R11A_HUMAN RAS-RELATED PROTEIN RAB-11A [R.norvegicus], RAB, member of RAS oncogene family like 2A, RAB11A, member RAS oncogene family, RAB11a, member RAS oncogene family, RAB25, member RAS oncogene family, RIKEN cDNA 2700023P08 gene

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS				Any. DocRef No. 43931-5081W6 Doc. No. 1799397	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Modif. Code	Homologous Gene Name	Homologous Cluster Name
1891	240	NM_031152	bb		CATX-8 protein, ESTs. Weakly similar to R11A_HUMAN RAS-RELATED PROTEIN RAB-11A [R.norvegicus]. RAB, member of RAS oncogene family like 2A, RAB11A, member RAS oncogene family, RAB11a, member RAS oncogene family, RAB25, member RAS oncogene family, RIKEN cDNA 2700023P08 gene
1892	15277	NM_031237	g		EST, Moderately similar to UBSB_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 [R.norvegicus], ESTs, Moderately similar to I59365 ubiquitin conjugating enzyme [H.sapiens], ESTs, Moderately similar to UBSB_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 [M.musculus], RIKEN cDNA 1100001F19 gene, RIKEN cDNA 160002817 gene, RIKEN cDNA 2700084L22 gene, Rattus norvegicus clone ubc2e ubiquitin conjugating enzyme (E217kB) mRNA, complete cds, expressed sequence AL022654, ubiquitin-conjugating enzyme E2D 1 (homologous to yeast UBC4/5), ubiquitin-conjugating enzyme E2D 2, ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC4/5), ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
1893	18083	NM_031315	q		ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens], Mus musculus, Similar to cytosolic acyl-CoA thioesterase 1, clone MGC-27572 IMAGE:4485973, mRNA, complete cds

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc# No. 44931-5683W0
Seq. ID No.	Identifier	Gene/Ref. Seq. ID No.	Modif. Code	Homologous Gene Name	Homologous Cluster Name
1893	1858	NM_031315	q	cytosolic acyl-CoA thioesterase 1, peroxisomal long-chain acyl-CoA thioesterase	PTE2_HUMAN PEROXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], ESTs, Moderately similar to JE0267 long-chain fatty-acyl-CoA hydrolase (EC 3.1.2.-) peroxisome proliferator-inducible - rat [R.norvegicus], ESTs, Moderately similar to PTE2_HUMAN PEROXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], ESTs, Weakly similar to PTE2_HUMAN PEROXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens], Mus musculus, Similar to cytosolic acyl-CoA thioesterase 1, clone MGC:27572 IMAGE4485973, mRNA, complete cds, RIKEN cDNA 463240BAC20 gene, cytosolic acyl-CoA thioesterase 1, expressed sequence AW108394, peroxisomal long-chain acyl-CoA
1894	15663	NM_031318	General		I-complex testis expressed 1, I-complex-associated-testis-expressed 1 like 1
1895	1422	NM_031324	bb,General		ESTs, Moderately similar to I38134 prylol oligopeptidase [H.sapiens], prylol endopeptidase
1896	18597	NM_031325	g,bb		UDP-glucose dehydrogenase
1897	11259	NM_031327	i,cc,General		ESTs, Moderately similar to CYR6 MOUSE CYR61 PROTEIN PRECURSOR [M.musculus], cysteine rich protein 61, cysteine-rich, angiogenic inducer, 61
1898	4235	NM_031330	General	heterogeneous nuclear ribonucleoprotein A/B	ESTs, Highly similar to WZHURS argininosuccinate lyase [H.sapiens], ESTs, Weakly similar to 1601424A argininosuccinate lyase [R.norvegicus], Homo sapiens cDNA FLJ14312 lis, clone PLACE3000322, Musashi-1 homolog (Drosophila), RIKEN cDNA 251006M18 gene, RIKEN cDNA 4933434H11 gene, argininosuccinate lyase, heterogeneous nuclear ribonucleoprotein A/B, heterogeneous nuclear ribonucleoprotein D-like
1899	18375	NM_031331	i,m		EST, Weakly similar to PSD4_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S5A [H.sapiens], ESTs, Moderately similar to PSD4_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S5A [H.sapiens], proteasome (prosome, macropain) 26S subunit, non-ATPase, 4

TABLE 3: EST WITH HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4:991-5081WC Doc. No. 1793897.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model/Code	Homologous Gene Name	Homologous Cluster Name	
1900	3519	NM_031334	cc	cadherin 1, cadherin 1, type 1, E-cadherin (epithelial)	ESTs, Weakly similar to I49556 cadherin-11 - mouse [M.musculus], RIKEN cDNA 2610005.07 gene, cadherin 1, type 1, E-cadherin (epithelial), cadherin 6, cadherin 6, type 2, K-cadherin (fetal kidney)	
1901	20698	NM_031357	b			
1903	634	NM_031509	n		EST, Moderately similar to GTC MOUSE GLUTATHIONE S-TRANSFERASE YC [M.musculus], glutathione S-transferase A3, glutathione S-transferase, alpha 3	
1903	25625	NM_031509	n			
1903	25069	NM_031509	b,n,w			
1903	635	NM_031509	z		EST, Moderately similar to GTC MOUSE GLUTATHIONE S-TRANSFERASE YC [M.musculus], glutathione S-transferase A3, glutathione S-transferase, alpha 3	
1904	848	NM_031517	t	met proto-oncogene, met proto-oncogene (hepatocyte growth factor receptor)	EST, Highly similar to RIKEN HUMAN MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR [H.sapiens], ESTs, Highly similar to TVHUME hepatocyte growth factor receptor precursor [H.sapiens], Mus musculus D88 mRNA, complete cds, Rattus norvegicus ryk mRNA for tyrosine kinase-related protein, partial cds, macrophage stimulating 1 receptor (c-met-related tyrosine kinase), met proto-oncogene, met proto-oncogene (hepatocyte growth factor receptor)	
1905	1872	NM_031523	a		RIKEN cDNA 0610007D04 gene, kallikrein 1, renal/pancreas/salivary, kallikrein 5, kallikrein 9, nerve growth factor, alpha, nerve growth factor, gamma	
1905	16245	NM_031523	a,d,u		EST, Moderately similar to epidermal growth factor binding protein type 1 [M.musculus], EST, Weakly similar to pre-pro-protein for kallikrein [H.sapiens]	
1905	16244	NM_031523	a		EST, Moderately similar to epidermal growth factor binding protein type 1 [M.musculus], EST, Weakly similar to pre-pro-protein for kallikrein [H.sapiens]	
1906	9370	NM_031527	w	protein phosphatase 1, catalytic subunit, alpha isoform	EST, Weakly similar to JN0723 phosphoprotein phosphatase [H.sapiens], protein phosphatase 1, catalytic subunit, alpha isoform	
1907	20448	NM_031530	General	small inducible cytokine A2, small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je)	EST, Weakly similar to SY02 RAT SMALL INDUCIBLE CYTOKINE A2 PRECURSOR [R.norvegicus], expressed sequence A1323594, expressed sequence AW987545, small inducible cytokine A2, small inducible cytokine A24, small inducible cytokine A7 (monocyte chemotactic protein 3), small inducible cytokine subfamily A (Cys-Cys), member 17	

TABLE 1: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc# No. 44924-5030WC Doc. No. 1998857.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Modif. Code	Homologous Gene Name	Homologous Cluster Name
1907	20449	NM_031530	General	small inducible cytokine A2, small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-1e)	EST, Weakly similar to SY02 RAT SMALL INDUCIBLE CYTOKINE A2 PRECURSOR [R.novegius], expressed sequence A1323594, expressed sequence AW987545, small inducible cytokine A2, small inducible cytokine A24, small inducible cytokine A7 (monocyte chemotactic protein 3), small inducible cytokine subfamily A (Cys-Cys), member 17
1908	14633	NM_031533	u		ESTs, Moderately similar to UDP-GLUCURONOSYLTRANSFERASE 2B5 PRECURSOR, MICROSOMAL [M.musculus], ESTs, Weakly similar to UDB7_HUMAN UDP-GLUCURONOSYLTRANSFERASE 2B7 PRECURSOR, MICROSOMAL [H.sapiens], ESTs, Weakly similar to UDBH_HUMAN UDP-GLUCURONOSYLTRANSFERASE 2B17 PRECURSOR, MICROSOMAL [H.sapiens], RIKEN cDNA 0610033E06 gene, UDP glycosyltransferase 2 family, polypeptide B17, UDP-glucuronosyltransferase 2 family, member 5, expressed sequence AA988709
1909	16048	NM_031541	f	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1, scavenger receptor class B1	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1, CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2, ESTs, Weakly similar to JC5533 scavenger receptor class B type I precursor - rat [R.novegius], Homo sapiens scavenger receptor class B type III SR-BIII mRNA, partial cds, scavenger receptor class B1
1910	4011	NM_031543	c,q	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)
1910	4010	NM_031543	c,q	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)
1910	4012	NM_031543	q	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)
1911	28	NM_031546	General	regucalcin, regucalcin (senescence marker protein-30)	regucalcin, regucalcin (senescence marker protein-30)
1912	24640	NM_031548	h,cc	sodium channel, nonvoltage-gated 1 alpha, sodium channel, nonvoltage-gated, type I, alpha polypeptide	expressed sequence AW742291, sodium channel, nonvoltage-gated 1 alpha, sodium channel, nonvoltage-gated 1, delta, sodium channel, nonvoltage-gated, type I, alpha polypeptide
1913	17149	NM_031549	x	transgelin	transgelin
1913	17151	NM_031549	x	transgelin	transgelin

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc#ot No. 4924-888WE Doc. No. 193837-1
Seq. ID No.	Accession Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1914	13105	NM_031552	w	adducin 3 (gamma)	ESTs, Moderately similar to ADDG_MOUSE GAMMA ADDUCIN (ADDUCIN-LIKE PROTEIN 70) [M.musculus], adducin 3 (gamma)
1915	15411	NM_031559	d,r	camitine palmityltransferase 1, liver, camitine palmityltransferase 1, liver	ESTs, Weakly similar to CPT1_MOUSE CARNITINE O- PALMITOYLTRANSFERASE 1, MITOCHONDRIAL LIVER ISOFORM [M.musculus], ESTs, Weakly similar to 159351 camitine O- palmityltransferase [H.sapiens], ESTs, Weakly similar to MITOCHONDRIAL CARNITINE O- PALMITOYLTRANSFERASE 1, LIVER ISOFORM [R.norvegicus], camitine palmityltransferase 1, liver, camitine palmityltransferase 1, muscle, camitine palmityltransferase 1, liver
1916	16164	NM_031563	a,y	Y box protein 1, nuclease sensitive element binding protein 1	ESTs, Highly similar to 130362 Y box- binding protein 1 - human [H.sapiens], RIKEN cDNA 1700102N10 gene
1917	9621	NM_031570	bb	ribosomal protein S7	EST, Moderately similar to 40S RIBOSOMAL PROTEIN S7 [R.norvegicus], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S7 [R.norvegicus], EST, Weakly similar to R57_HUMAN 40S RIBOSOMAL PROTEIN S7 [M.musculus], ESTs, Highly similar to Jc4388 ribosomal protein S7, cytosolic [H.sapiens], ESTs, Highly similar to R57_HUMAN 40S RIBOSOMAL PROTEIN S7 [H.sapiens], nuclear factor of kappa light polypeptide gene enhancer in B- cells inhibitor-like 2, ribosomal protein S7
1917	9620	NM_031570	w,bb	ribosomal protein S7	EST, Moderately similar to 40S RIBOSOMAL PROTEIN S7 [R.norvegicus], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S7 [R.norvegicus], EST, Weakly similar to R57_HUMAN 40S RIBOSOMAL PROTEIN S7 [M.musculus], ESTs, Highly similar to Jc4388 ribosomal protein S7, cytosolic [H.sapiens], ESTs, Highly similar to R57_HUMAN 40S RIBOSOMAL PROTEIN S7 [H.sapiens], nuclear factor of kappa light polypeptide gene enhancer in B- cells inhibitor-like 2, ribosomal protein S7
1918	546	NM_031573	f	phosphorylase kinase gamma, phosphorylase kinase, gamma 1 (muscle)	ESTs, Moderately similar to KPBG_HUMAN PHOSPHORYLASE B KINASE GAMMA CATALYTIC CHAIN, SKELETAL MUSCLE ISOFORM [H.sapiens], ESTs, Moderately similar to PHOSPHORYLASE B KINASE GAMMA CATALYTIC CHAIN, SKELETAL MUSCLE ISOFORM [R.norvegicus], RIKEN cDNA 1500017102 gene, endoplasmic reticulum (ER) to nucleus signalling 2, phosphorylase kinase gamma, phosphorylase kinase, gamma 1 (muscle)

HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc# No. 44891-6881W3 Reg. No. 1793817.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Protein/Polypeptide Name
1919	1921	NM_031576	f	P450 (cytochrome) oxidoreductase	ESTs, Highly similar to A Chain A, Crystal Structure Of The Fmn-Binding Domain Of Human Cytochrome P450 Reductase At 1.93a Resolution (SUB 61-241 [H.sapiens], NADPH-dependent FMN and FAD containing oxidoreductase, P450 (cytochrome) oxidoreductase, RIKEN cDNA 4930447P04 gene, hypothetical protein FLJ10900
1919	1920	NM_031576	r	P450 (cytochrome) oxidoreductase	ESTs, Highly similar to A Chain A, Crystal Structure Of The Fmn-Binding Domain Of Human Cytochrome P450 Reductase At 1.93a Resolution (SUB 61-241 [H.sapiens], NADPH-dependent FMN and FAD containing oxidoreductase, P450 (cytochrome) oxidoreductase, RIKEN cDNA 4930447P04 gene, hypothetical protein FLJ10900
1920	24219	NM_031579	l,General	protein tyrosine phosphatase 4a1, protein tyrosine phosphatase type IVA, member 1	protein tyrosine phosphatase 4a1, protein tyrosine phosphatase type IVA, member 2, protein tyrosine phosphatase type IVA, member 3
1921	770	NM_031584	k,x	solute carrier family 22 (organic cation transporter), member 2	EST, Moderately similar to JC4884 organic cation transporter protein 2 - rat [R.norvegicus], EST, Weakly similar to OCN2 MOUSE ORGANIC CATION/CARNITINE TRANSPORTER 2 [M.musculus], ESTs, Highly similar to OCN2_HUMAN ORGANIC CATION/CARNITINE TRANSPORTER 2 [H.sapiens], ESTs, Highly similar to organic cation transporter [H.sapiens], organic cation transporter-like 1, solute carrier family 22 (organic cation transporter), member 1, solute carrier family 22 (organic cation transporter), member 4, solute carrier family 22 (organic cation transporter), member 5, solute carrier family 22 (organic cation transporter), member 9, solute carrier family 22, member 3
1922	18008	NM_031588	cc		ESTs, Highly similar to NRG2_MOUSE PRO-NEUREGULIN-2 PRECURSOR (PRO-NRG2) [CONTAINS: NEUREGULIN-2 (NRG-2) (DIVERGENT OF NEUREGULIN 1) (DON-1)] [M.musculus], ESTs, Weakly similar to NRG2_MOUSE PRO-NEUREGULIN-2 PRECURSOR (PRO-NRG2) [CONTAINS: NEUREGULIN-2 (NRG-2) (DIVERGENT OF NEUREGULIN 1) (DON-1)] [M.musculus], neuregulin 1

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atyp. Doclet No. 44941-SubOWO Doc. No. 1793897.1
Seq. ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Cluster Name
1922	18005	NM_031588	h		ESTs, Highly similar to NRG2_MOUSE PRO-NEUREGULIN-2 PRECURSOR (PRO-NRG2) [CONTAINS: NEUREGULIN-2 (NRG-2) (DIVERGENT OF NEUREGULIN 1) (DON-1)] [M.musculus], ESTs, Weakly similar to NRG2_MOUSE PRO-NEUREGULIN-2 PRECURSOR (PRO-NRG2) [CONTAINS: NEUREGULIN-2 (NRG-2) (DIVERGENT OF NEUREGULIN 1) (DON-1)] [M.musculus], neuregulin 1
1922	18011	NM_031588	cc.General		ESTs, Highly similar to NRG2_MOUSE PRO-NEUREGULIN-2 PRECURSOR (PRO-NRG2) [CONTAINS: NEUREGULIN-2 (NRG-2) (DIVERGENT OF NEUREGULIN 1) (DON-1)] [M.musculus], ESTs, Weakly similar to NRG2_MOUSE PRO-NEUREGULIN-2 PRECURSOR (PRO-NRG2) [CONTAINS: NEUREGULIN-2 (NRG-2) (DIVERGENT OF NEUREGULIN 1) (DON-1)] [M.musculus], neuregulin 1
1923	1584	NM_031595	k	proteasome (prosome, macropain) 26S subunit, ATPase 3, proteasome (prosome, macropain) 26S subunit, ATPase, 3	EST, Moderately similar to PRSA RAT 26S PROTEASE REGULATORY SUBUNIT 6A [R.norvegicus], EST, Weakly similar to PRSA MOUSE 26S PROTEASE REGULATORY SUBUNIT 4 [M.musculus], EST, Weakly similar to PRSA RAT 26S PROTEASE REGULATORY SUBUNIT 6A [R.norvegicus], ESTs, Moderately similar to PRSA RAT 26S PROTEASE REGULATORY SUBUNIT 6A [R.norvegicus], expressed sequence A1325227, protease (prosome, macropain) 26S subunit, ATPase 1, proteasome (prosome, macropain) 26S subunit, ATPase 3, proteasome (prosome, macropain) 26S subunit, ATPase, 3
1924	24235	NM_031614	v	thioredoxin reductase 1	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010001F03, full insert sequence, glutathione reductase 1, thioredoxin reductase 1, thioredoxin reductase 2, thioredoxin reductase beta
1924	24234	NM_031614	General	thioredoxin reductase 1	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010001F03, full insert sequence, glutathione reductase 1, thioredoxin reductase 1, thioredoxin reductase 2, thioredoxin reductase beta
1925	1639	NM_031627	jj,v	nuclear receptor subfamily 1, group H, member 3	EST, Moderately similar to A56043 steroid hormone receptor-like protein RLD-1 - rat [R.norvegicus], expressed sequence AU018371, nuclear receptor subfamily 1, group H, member 3, nuclear receptor subfamily 1, group H, member 4

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS				Ally, DocId:344921-5083WC Doc. No. 1763837.1	
Seq. ID No.	Identifier	GenBank Acc/ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Automatic Status Name
1926	1727	NM_031642	m.General	core promoter element binding protein	EST, Moderately similar to CPBP RAT CORE PROMOTER ELEMENT-BINDING PROTEIN [R.norvegicus], ESTs, Moderately similar to CPBP RAT CORE PROMOTER ELEMENT-BINDING PROTEIN [R.norvegicus], Kruppel-like factor 3 (basic), Kruppel-like factor 5, Kruppel-like factor 7 (ubiquitous), core promoter element binding protein
1927	20766	NM_031643	y	mitogen activated protein kinase kinase 2, mitogen-activated protein kinase kinase 2	ESTs, Highly similar to MPK1 MOUSE DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE 1 [M.musculus], ESTs, Moderately similar to MPK1_HUMAN DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE 1 [H.sapiens], Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3000002B10, full insert sequence, mitogen activated protein kinase kinase 1, mitogen activated protein kinase kinase 3, mitogen activated protein kinase kinase 7, mitogen-activated protein kinase kinase 1, mitogen-activated protein kinase kinase 7
1929	1993	NM_031655	k,l,m.General	latexin, latexin protein	latexin, latexin protein, retinoic acid receptor responder (tazarotene induced) 1
1930	2057	NM_031660	e		Human DNA sequence from clone RP5-822J19 on chromosome 20. Contains an alpha-endosulfine pseudogene, STSs and GSSs, cyclic AMP phosphoprotein, 19 kD, cyclic AMP phosphoprotein, 19kD, endosulfine alpha
1931	15039	NM_031672	k.General	solute carrier family 15 (H+/peptide transporter), member 2	EST, Moderately similar to PET2 RAT OLIGOPEPTIDE TRANSPORTER, KIDNEY ISOFORM [R.norvegicus], EST, Moderately similar to PET2_HUMAN OLIGOPEPTIDE TRANSPORTER, KIDNEY ISOFORM [H.sapiens], expressed sequence C78862, solute carrier family 15 (H+/peptide transporter), member 2
1932	15175	NM_031682	bb		2-4-dienoyl-Coenzyme A reductase 2, peroxisomal, ESTs, Weakly similar to HCD2 RAT 3-HYDROXYACYL-COA DEHYDROGENASE TYPE II [R.norvegicus], H2K region expressed gene 6, hydroxyacyl-Coenzyme A dehydrogenase, type II, hydroxyprostaglandin dehydrogenase 15 (NAD), hydroxysteroid (17-beta) dehydrogenase 10, hypothetical protein FLJ14431, retinal short-chain dehydrogenase/reductase reISDR3
1933	1004	NM_031685	v	golgi SNAP receptor complex member 2	golgi SNAP receptor complex member 2

TABLE W. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4381-5088WG	Doc. No. 17936974
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name	
1934	19727	NM_031687	a,q,s	ubiquitin A-52 residue ribosomal protein fusion product 1	EST, Moderately similar to I65237 ubiquitin/ribosomal protein L40 - rat [R.norvegicus], Homo sapiens ubiquitin-like fusion protein mRNA, complete cds, RIKEN cDNA 061006J14 gene, Rattus norvegicus RSD-7 mRNA, complete cds, ubiquitin A-52 residue ribosomal protein fusion product 1	
1935	20404	NM_031700	i,r,y	claudin 3	ESTs, Weakly similar to A39484 androgen-withdrawal apoptosis protein RVP1, prostatic - rat [R.norvegicus], claudin 12, claudin 3, expressed sequence AI182374	
1935	20405	NM_031700	o,r	claudin 3	ESTs, Weakly similar to A39484 androgen-withdrawal apoptosis protein RVP1, prostatic - rat [R.norvegicus], claudin 12, claudin 3, expressed sequence AI182374	
1936	811	NM_031705	General	dihydropyrimidinase	PRO0195 protein, collapsin response mediator protein 5, collapsin response mediator protein-5; CRMP3-associated molecule, dihydropyrimidinase, dihydropyrimidinase-like 2, dihydropyrimidinase-related protein	
1936	812	NM_031705	o,v,bb,General	dihydropyrimidinase	PRO0195 protein, collapsin response mediator protein 5, collapsin response mediator protein-5; CRMP3-associated molecule, dihydropyrimidinase, dihydropyrimidinase-like 2, dihydropyrimidinase-related protein	
1937	16204	NM_031706	q,bb		EST, Moderately similar to RS8_HUMAN 40S RIBOSOMAL PROTEIN S [H.sapiens], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S8 [M.musculus], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S8 [R.norvegicus], ESTs, Moderately similar to RS8_HUMAN 40S RIBOSOMAL PROTEIN S [H.sapiens], RIKEN cDNA 1110008P08 gene, ribosomal protein S8	
1937	16205	NM_031706	a,y		EST, Moderately similar to RS8_HUMAN 40S RIBOSOMAL PROTEIN S [H.sapiens], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S8 [M.musculus], EST, Weakly similar to 40S RIBOSOMAL PROTEIN S8 [R.norvegicus], ESTs, Moderately similar to RS8_HUMAN 40S RIBOSOMAL PROTEIN S [H.sapiens], RIKEN cDNA 1110008P08 gene, ribosomal protein S8	
1938	24081	NM_031708	m		ESTs, Weakly similar to G100_HUMAN 110 KDA CELL MEMBRANE GLYCOPROTEIN [H.sapiens], cell membrane glycoprotein, 110000M(r) (surface antigen)	
1939	16918	NM_031709	a,q		ESTs, Highly similar to R3HU12 ribosomal protein S12, cytosolic [H.sapiens], mitochondrial ribosomal protein L50, ribosomal protein S12	

TABLE 1. HUMAN HOMOLOGUE ANNOTATIONS				Atyp. Grant No. 44921-508WG Doc. No. 178387.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Modif. Code	Homologous Gene Name	Homologous Cluster Name
1940	1081	NM_031712	General	PDZ domain containing 1	ESTs, Weakly similar to T30259 multiple PDZ domain protein - mouse [M.musculus], ESTs, Weakly similar to T46612 multi PDZ domain protein 1 - rat [R.norvegicus], PDZ domain containing 1, channel-interacting PDZ domain protein, hypothetical protein FLJ22756, multiple PDZ domain protein, semaF cytoplasmic domain associated protein 3, solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1, solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 2, syntaxin binding protein 4
1941	1340	NM_031715	b,n,u,cc,General	phosphofructokinase, muscle	ESTs, Highly similar to S71429 phosphofructokinase, muscle - rat [R.norvegicus], Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210403E17, full insert sequence, expressed sequence AA407869, phosphofructokinase, liver, B-type, phosphofructokinase, muscle
1942	23884	NM_031731	j,s	aldehyde dehydrogenase 3 family, member A2, aldehyde dehydrogenase family 3, subfamily A2	ESTs, Weakly similar to DH44 RAT FATTY ALDEHYDE DEHYDROGENASE [R.norvegicus], RIKEN cDNA 1700001N19 gene, RIKEN cDNA 1700055N04 gene, aldehyde dehydrogenase 3 family, member A2, aldehyde dehydrogenase family 3, subfamily A2, expressed sequence AU48554
1943	10241	NM_031740	d	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6, UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	ESTs, Weakly similar to N-ACETYLLACTOSAMINE SYNTHASE [M.musculus], UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1, UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2, UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3, UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4, UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5, UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6, UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3
1944	1214	NM_031741	r	solute carrier family 2 (facilitated glucose transporter), member 5, solute carrier family 2 (facilitated glucose/fructose transporter), member 5	Mus musculus, clone MGC:8298 IMAGE:3593581, mRNA, complete cds, glucose transporter protein 11, solute carrier family 2 (facilitated glucose transporter), member 5, solute carrier family 2 (facilitated glucose transporter), member 9, solute carrier family 2 (facilitated glucose/fructose transporter), member 5

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Alt. Doc# No. 43921-3686WO
					Doc. No. 179397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1944	1215	NM_031741	r	solute carrier family 2 (facilitated glucose transporter), member 5, solute carrier family 2 (facilitated glucose/fructose transporter), member 5	Mus musculus, clone MGC:8298 IMAGE:3593581, mRNA, complete cds, glucose transporter protein 11, solute carrier family 2 (facilitated glucose transporter), member 5, solute carrier family 2 (facilitated glucose transporter), member 9, solute carrier family 2 (facilitated glucose/fructose transporter), member 5
1945	20724	NM_031753	h		ESTs, Highly similar to C166_HUMAN CD166 ANTIGEN PRECURSOR [H.sapiens], Lutheran blood group (Aubergier b antigen included), activated leucocyte cell adhesion molecule, activated leukocyte cell adhesion molecule, advanced glycosylation end product-specific receptor, melanoma cell adhesion molecule
1946	20753	NM_031763	h		EST, Weakly similar to LIS1 MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus], ESTs, Weakly similar to LIS1 MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus], ESTs, Weakly similar to LIS1_HUMAN PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [H.sapiens], F-box protein FBW7, KIAA0007 protein, U3 snRNP-associated 55-kDa protein, F-box and WD-40 domain protein 2, platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit, platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD)
1946	20752	NM_031763	y		EST, Weakly similar to LIS1 MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus], ESTs, Weakly similar to LIS1 MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus], ESTs, Weakly similar to LIS1_HUMAN PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [H.sapiens], F-box protein FBW7, KIAA0007 protein, U3 snRNP-associated 55-kDa protein, F-box and WD-40 domain protein 2, platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit, platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD)
1947	14953	NM_031774	p	Rab acceptor 1 (prenylated)	
1948	14184	NM_031776	t,General		guanine deaminase
1948	14185	NM_031776	d,c,t,General		guanine deaminase

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Aty. Doc# No. 4494 5084WO Doc. No. 179397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1949	1169	NM_031789	c		ESTs, Highly similar to NFL2 RAT NUCLEAR FACTOR ERYTHROID 2 RELATED FACTOR 2 [R.norvegicus], ESTs, Weakly similar to NFL2 RAT NUCLEAR FACTOR ERYTHROID 2 RELATED FACTOR 2 [R.norvegicus], nuclear factor (erythroid-derived 2)-like 2, nuclear, factor, erythroid derived 2, like 2
1950	16155	NM_031810	d,z		defensin beta 1, defensin beta 2, defensin, beta 1
1950	16156	NM_031810	d		defensin beta 1, defensin beta 2, defensin, beta 1
1951	17194	NM_031814	z	G protein-coupled receptor kinase-interactor 1	EST, Weakly similar to T42627 ADP-ribosylation factor-directed GTPase activating protein, isoform a - mouse [M.musculus], ESTs, Highly similar to T42627 ADP-ribosylation factor-directed GTPase activating protein, isoform a - mouse [M.musculus], G protein-coupled receptor kinase-interactor 1, G protein-coupled receptor kinase-interactor 2, Homo sapiens p95 paxillin-kinase linker mRNA, complete cds, RIKEN cDNA 1700030C10 gene, development and differentiation enhancing
1952	17535	NM_031816	bb		ESTs, Weakly similar to GBLP_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 [R.norvegicus], Homo sapiens cDNA: FLJ21913 fs, clone HEP03888, Homo sapiens, clone IMAGE:3502107, mRNA, partial cds, RAE1 (RNA export 1, S.pombe) homolog, WD repeat domain 10, expressed sequence A1173248, expressed sequence A1504353, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1, retinoblastoma binding protein 7, retinoblastoma-binding protein 7, transducin (beta)-like 2
1953	2655	NM_031821	i,l,m,aa	serum-inducible kinase	ESTs, Highly similar to A57286 probable serine/threonine protein kinase [M.musculus], ESTs, Highly similar to SNK_RAT SERINE/THREONINE-PROTEIN KINASE SNK (SERUM INDUCIBLE KINASE) [R.norvegicus], ESTs, Weakly similar to SNK_RAT SERINE/THREONINE-PROTEIN KINASE SNK (SERUM INDUCIBLE KINASE) [R.norvegicus], cytokine-inducible kinase, serine/threonine kinase 18, serum-inducible kinase, tousel-like kinase 2 (Arabidopsis)
1954	10167	NM_031830	i		flotillin 1, flotillin 2
1955	22321	NM_031832	o,l,u,General	lectin, galactose binding, soluble 3, lectin, galactoside-binding, soluble, 3 (galectin 3)	EST, Weakly similar to X-Ray Crystal Structure Of The Human Galectin-3 Carbohydrate Recognition Domain [H.sapiens], galectin-related inter-fiber protein

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4-924-5383WC Doc. No. 179387 v.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1956	4748	NM_031834	e,l		expressed sequence A1266890, expressed sequence A1853643, sulfotransferase family 1A, phenol-prefering, member 1, sulfotransferase family 4A, member 1, sulfotransferase family, cytosolic, 1A, phenol-prefering, member 1, sulfotransferase family, cytosolic, 1A, phenol-prefering, member 2, sulfotransferase family, cytosolic, 1A, phenol-prefering, member 3
1956	4749	NM_031834	e,l		expressed sequence A1266890, expressed sequence A1853643, sulfotransferase family 1A, phenol-prefering, member 1, sulfotransferase family 4A, member 1, sulfotransferase family, cytosolic, 1A, phenol-prefering, member 1, sulfotransferase family, cytosolic, 1A, phenol-prefering, member 2, sulfotransferase family, cytosolic, 1A, phenol-prefering, member 3
1957	7914	NM_031835	e		ESTs, Weakly similar to AGT2 RAT ALANINE-GLYOXYLATE AMINOTRANSFERASE 2 PRECURSOR [R.norvegicus], RIKEN cDNA 1300019H02 gene, RIKEN cDNA 2900006B13 gene, alanine-glyoxylate aminotransferase 2, alanine-glyoxylate aminotransferase 2-like 1, ornithine aminotransferase
1958	8385	NM_031836	h		c-fos induced growth factor (vascular endothelial growth factor D), vascular endothelial growth factor, vascular endothelial growth factor B
1958	8384	NM_031836	h		c-fos induced growth factor (vascular endothelial growth factor D), vascular endothelial growth factor, vascular endothelial growth factor B
1959	10268	NM_031838	a		EST, Highly similar to 40S RIBOSOMAL PROTEIN S2 [M.musculus], EST, Highly similar to 40S RIBOSOMAL PROTEIN S2 [R.norvegicus], EST, Moderately similar to S08228 ribosomal protein S2, cytosolic [H.sapiens], EST, Weakly similar to S08228 ribosomal protein S2, cytosolic [H.sapiens], ESTs, Highly similar to RS2_HUMAN 40S RIBOSOMAL PROTEIN S2 [H.sapiens], ESTs, Moderately similar to 40S RIBOSOMAL PROTEIN S2 [M.musculus], repeat family 3 gene, ribosomal protein S2

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS				Ally, DocId: No. 43924-5669WC Doc. No. 179367-1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1959	10269	NM_031838	aa		EST, Highly similar to 40S RIBOSOMAL PROTEIN S2 [M.musculus], EST, Highly similar to 40S RIBOSOMAL PROTEIN S2 [R.norvegicus], EST, Moderately similar to S08228 ribosomal protein S2, cytosolic [H.sapiens], EST, Weakly similar to S08228 ribosomal protein S2, cytosolic [H.sapiens], ESTs, Highly similar to RS2_HUMAN 40S RIBOSOMAL PROTEIN S2 [H.sapiens], ESTs, Moderately similar to 40S RIBOSOMAL PROTEIN S2 [M.musculus], repeat family 3 gene, ribosomal protein S2
1959	10287	NM_031838	n,aa		EST, Highly similar to 40S RIBOSOMAL PROTEIN S2 [M.musculus], EST, Highly similar to 40S RIBOSOMAL PROTEIN S2 [R.norvegicus], EST, Moderately similar to S08228 ribosomal protein S2, cytosolic [H.sapiens], EST, Weakly similar to S08228 ribosomal protein S2, cytosolic [H.sapiens], ESTs, Highly similar to RS2_HUMAN 40S RIBOSOMAL PROTEIN S2 [H.sapiens], ESTs, Moderately similar to 40S RIBOSOMAL PROTEIN S2 [M.musculus], repeat family 3 gene, ribosomal protein S2
1960	15077	NM_031841	b		expressed sequence AU022220, hypothetical protein FLJ21032, stearoyl-CoA desaturase (delta-9-desaturase), stearoyl-Coenzyme A desaturase 1, stearoyl-Coenzyme A desaturase 2, stearoyl-coenzyme A desaturase 3
1961	16726	NM_031855	x	ketoheokinase, ketoheokinase (fructokinase)	ketoheokinase, ketoheokinase (fructokinase)
1962	25802	NM_031969	a	calmodulin 1, calmodulin 1 (phosphorylase kinase, delta)	Calmodulin III, ESTs, Highly similar to A Chain A, Calmodulin Complexed With Calmodulin-Binding Peptide From Smooth Muscle Myosin Light Chain Kinase (SUB 2-148 [H.sapiens], R.norvegicus CaMII retropseudogene (clone lambda SC27), RIKEN cDNA 2310068C22 gene, calmodulin, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3
1962	19191	NM_031969	c	calmodulin 1, calmodulin 1 (phosphorylase kinase, delta)	

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4-924-5087WC Reg. No. 1793877.1	
Seq. ID No.	Identifier	Source Ref. Seq. ID No.	Accession ID No.	Model Code	Homologous Gene	Homologous Cluster Name
1962	19195	NM_031969	r		calmodulin 1, calmodulin 1 (phosphorylase kinase, delta)	Calmodulin III, ESTs, Highly similar to A Chain A, Calmodulin Complexed With Calmodulin-Binding Peptide From Smooth Muscle Myosin Light Chain Kinase (SUB 2-148 [H.sapiens], R.norvegicus CaMII retrospseudogene (clone lambda SC27), RIKEN cDNA 2310068O22 gene, calmodulin, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3
1962	19190	NM_031969	p		calmodulin 1, calmodulin 1 (phosphorylase kinase, delta)	Calmodulin III, ESTs, Highly similar to A Chain A, Calmodulin Complexed With Calmodulin-Binding Peptide From Smooth Muscle Myosin Light Chain Kinase (SUB 2-148 [H.sapiens], R.norvegicus CaMII retrospseudogene (clone lambda SC27), RIKEN cDNA 2310068O22 gene, calmodulin, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3
1963	17734	NM_031970	v, General			EST, Weakly similar to HHU27 heat shock protein 27 [H.sapiens], ESTs, Moderately similar to HHU27 heat shock protein 27 [H.sapiens], crystallin, alpha C, heat shock 27kD protein 1, heat shock 27kD protein 3
1964	1475	NM_031971	v		heat shock 70kD protein 1B, heat shock protein, 70 kDa 1	ESTs, Weakly similar to BCHUA S-100 protein alpha chain [H.sapiens], ESTs, Weakly similar to S10A MOUSE S-100 PROTEIN, ALPHA CHAIN [M.musculus], Homo sapiens cDNA FLJ10018 fis, clone HEMBA1000531, RIKEN cDNA B230217N24 gene, S100 calcium binding protein A1, S100 calcium binding protein A11, S100 calcium-binding protein A11 (calgizzarin), S100 calcium-binding protein P, expressed sequence A1265795, heat shock 70kD protein 1A, heat shock 70kD protein 1B
1965	15470	NM_031978	f			proleasome (prosome, macropain) 26S subunit, non-ATPase, 1
1966	18502	NM_031984	c		calbindin 1, (28kD), calbindin-28K	ESTs, Moderately similar to CALBINDIN [M.musculus], calbindin 1, (28kD), calbindin-28K

TABLE 3. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4294-3087WG Pub. No. 179897.1
Seq. ID No.	Identifier	GenBank Accession Ref. Seq. ID No.	Model/Order	Homologous Gene Name	Homologous Cluster Name
1967	19768	NM_031986	v.a.a.General		ESTs, Highly similar to APB1 RAT AMYLOID BETA A4 PRECURSOR PROTEIN-BINDING FAMILY A MEMBER 1 [R.norvegicus], Mus musculus, Similar to hypothetical protein, clone MGC:11704 IMAGE:3964815, mRNA, complete cds, RIKEN cDNA 2310008D10 gene, amyloid beta (A4) precursor protein-binding, family A, APBA1: amyloid beta (A4) precursor protein-binding, family A, member 1 (X11), amyloid beta (A4) precursor protein-binding, family A, member 1 (X11), amyloid beta (A4) precursor protein-binding, family A, member 3, syndecan binding protein, syndecan binding protein (syntenin), syntenin-2 protein
1968	723	NM_032084	n		ESTs, Weakly similar to T42724 p190-B protein - mouse [M.musculus], PTPL1-associated RhoGAP 1, RIKEN cDNA 1700026N20 gene, RIKEN cDNA 1700112L09 gene, chimerin (chimaerin) 2, minor histocompatibility antigen HA-1, oligophrenin 1, rho GTPase activating protein 6
1969	17935	NM_032615	a	membrane interacting protein of RGS16	hypothetical protein FLJ20207, membrane interacting protein of RGS16
1970	16831	NM_033095	n		
1971	25468	NM_033234	c.z		
1971	25469	NM_033234	c		
1971	17832	NM_033234	c.p	hemoglobin beta chain complex, hemoglobin, beta	
1971	17829	NM_033234	c.z	hemoglobin beta chain complex, hemoglobin, beta	
1972	4723	NM_033235	z		ESTs, Highly similar to LDH HUMAN L-LACTATE DEHYDROGENASE H CHAIN [H.sapiens], Lactate dehydrogenase B, RIKEN cDNA 1700124B08 gene, lactate dehydrogenase 2, B chain, lactate dehydrogenase B, malate dehydrogenase 1, NAD (soluble), malate dehydrogenase, soluble
1973	1409	NM_033349	p.General	glyoxylase 2, hydroxyacyl glutathione hydrolase	Mus musculus, Similar to hydroxyacyl glutathione hydrolase, clone MGC:6697 IMAGE:3583919, mRNA, complete cds, RIKEN cDNA 1500017E18 gene, RIKEN cDNA 2810014I23 gene, RIKEN cDNA C330022E15 gene, hydroxyacyl glutathione hydrolase, hypothetical protein MGC2605, protein expressed in thyroid

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Any. Docet. No. 4-921-5033WG Doc. No. 179387 v.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1974	19998	NM_033352	General	PDZ domain containing 1	ESTs, Weakly similar to T30259 multiple PDZ domain protein - mouse [M.musculus], ESTs, Weakly similar to T46612 multi PDZ domain protein 1 - rat [R.norvegicus], PDZ domain containing 1, channel-interacting PDZ domain protein, hypothetical protein FLJ22756, multiple PDZ domain protein, semaF cytoplasmic domain associated protein 3, solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1, solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 2, syntaxin binding protein 4
1975	1410	NM_052798	d	zinc finger protein 354A	ESTs, Moderately similar to S47073 finger protein HZF2, Krueppel-related [H.sapiens], ESTs, Moderately similar to T12489 hypothetical protein DKFZp572P0920.1 [H.sapiens], ESTs, Weakly similar to TC17 MOUSE TRANSCRIPTION FACTOR 17 [M.musculus], ESTs, Weakly similar to Z184_HUMAN ZINC FINGER PROTEIN 184 [H.sapiens], expressed sequence A1875089, transcription factor 17, transcription factor 17-like 1, transcription factor 17-like 2
1976	15028	NM_052809	f	cysteine dioxygenase 1, cytosolic, cysteine dioxygenase, type I	RIKEN cDNA 2900002E17 gene, cysteine dioxygenase 1, cytosolic, cysteine dioxygenase, type I
1977	5176	NM_053297	u	pyruvate kinase 3, pyruvate kinase, muscle	
1978	7660	NM_053299	i	diubiquitin, ubiquitin D	EST, Moderately similar to S12583 polyubiquitin 4 - mouse [M.musculus], Homo sapiens UBBP2 pseudogene for ubiquitin UBB, RIKEN cDNA 2700054C04 gene, diubiquitin, expressed sequence A194771, expressed sequence AL033289, ubiquitin B, ubiquitin C
1979	5117	NM_053310	p	dynein, cytoplasmic, light chain 1, dynein, cytoplasmic, light polypeptide	CAT56 protein, EST, Weakly similar to A28996 proline-rich protein M14 precursor - mouse [M.musculus], EST, Weakly similar to JE0291 FB19 protein [H.sapiens], Homer, neuronal immediate early gene, 1B, RuvB-like protein 1, homer, neuronal immediate early gene, 1, homer, neuronal immediate early gene, 2, proline rich protein, proline rich protein 2, protein phosphatase 1, regulatory subunit 10
1981	17473	NM_053319	a,v	insulin-like growth factor binding protein, acid labile subunit	ESTs, Moderately similar to protein inhibitor of nitric oxide synthase [M.musculus], RIKEN cDNA 6720463E02 gene, Retrus norvegicus dynein light chain-2 (Dlc2) mRNA, complete cds, dynein, cytoplasmic, light chain 1, dynein, cytoplasmic, light polypeptide
1982	25480	NM_053329	g		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 43924-008WG Doc. No. 1728887.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1982	21977	NM_053329	y	insulin-like growth factor binding protein, acid labile subunit	ESTs, Weakly similar to ALS RAT INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to JC6128 insulin-like growth factor binding complex acid labile chain - mouse [M.musculus], ESTs, Weakly similar to membrane glycoprotein [M.musculus], KIAA0644 gene product, glycoprotein 1a, alpha polypeptide, hypothetical protein FLJ20156, insulin-like growth factor binding protein, acid labile subunit, nogo receptor, reticulon 4 receptor, toll-like receptor 6, tumor endothelial marker 5 precursor
1983	14926	NM_053330	f	ribosomal protein L21	EST, Moderately similar to 21132008 ribosomal protein L21 [H.sapiens], EST, Moderately similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], EST, Weakly similar to 21132008 ribosomal protein L21 [H.sapiens], EST, Weakly similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], EST, Weakly similar to RL21_HUMAN 60S RIBOSOMAL PROTEIN L21 [H.sapiens], ESTs, Moderately similar to RL21 RAT 60S RIBOSOMAL PROTEIN L21 [R.norvegicus], RIKEN cDNA 2700085M18 gene, ribosomal protein L21
1983	14929	NM_053330	e.General	ribosomal protein L21	EST, Moderately similar to 21132008 ribosomal protein L21 [H.sapiens], EST, Moderately similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], EST, Weakly similar to 21132008 ribosomal protein L21 [H.sapiens], EST, Weakly similar to RL21 MOUSE 60S RIBOSOMAL PROTEIN L21 [M.musculus], EST, Weakly similar to RL21_HUMAN 60S RIBOSOMAL PROTEIN L21 [H.sapiens], ESTs, Moderately similar to RL21 RAT 60S RIBOSOMAL PROTEIN L21 [R.norvegicus], RIKEN cDNA 2700085M18 gene, ribosomal protein L21
1984	16407	NM_053332	c.e	cubilin (intrinsic factor-cobalamin receptor)	DNA segment, Chr 2, Wayne State University 88, expressed, EST, Weakly similar to T09456 intrinsic factor-B12 receptor Cubilin precursor [H.sapiens], ESTs, Moderately similar to T09456 intrinsic factor-B12 receptor Cubilin precursor [H.sapiens], Homo sapiens cDNA FLJ12558 fis, clone NT2RM4000787, bone morphogenetic protein 1, cubilin (intrinsic factor-cobalamin receptor), expressed sequence AL022750, platelet-derived growth factor, C polypeptide, toll-like, toll-like 2, tumor necrosis factor induced protein 6, tumor necrosis factor, alpha-induced protein 6

TABLE B: HUMAN HOMOLOGUE ANNOTATIONS					Ally DocId: No. 41921-5433WG Doc. No. 175877.1
Seq. ID No.	Accession	Genbank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
1985	15790	NM_053341	jx	chromosome 19 open reading frame 3, regulator of G-protein signaling 19 interacting protein 1	chromosome 19 open reading frame 3, hypothetical protein FLJ20075
1986	6154	NM_053356	p	collagen, type I, alpha 2, procollagen, type I, alpha 2	ESTs, Weakly similar to CGHU2S collagen alpha 2(I) chain precursor [H.sapiens], KIAA1026 protein, RIKEN cDNA 1110030G05 gene, RIKEN cDNA 9030409G11 gene, collagen, type I, alpha 1, collagen, type I, alpha 2, collagen, type II, alpha 1 (primary osteoarthritis, spondylophyseal dysplasia, congenital), hypothetical protein FLJ20654, nischarin, procollagen, type I, alpha 1, procollagen, type I, alpha 2, procollagen, type II, alpha 1
1987	8215	NM_053374	i	interleukin 18 binding protein	ESTs, Weakly similar to NPT2 RAT RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [R.norvegicus], ESTs, Weakly similar to NPT2_HUMAN RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 [H.sapiens], Homo sapiens, Similar to solute carrier family 34 (sodium phosphate), member 1, clone MGC:18179 IMAGE:4155326, mRNA, complete cds, Rattus norvegicus mRNA for NaPi-2 alpha, complete cds, Solute carrier family 17 (sodium/hydrogen exchanger), member 2, expressed sequence A1649385, solute carrier family 34 (sodium phosphate), member 1, solute carrier family 34 (sodium phosphate), member 2
1988	6416	NM_053380	General	small muscle protein, X-linked	small muscle protein, X-linked
1989	19113	NM_053395	a	small muscle protein, X-linked	ESTs, Highly similar to FMO3_HUMAN DIMETHYLANILINE MONOOXYGENASE [H.sapiens], Flavin-containing monooxygenase 1, Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSs, flavin containing monooxygenase 1, flavin containing monooxygenase 2, flavin containing monooxygenase 3, hypothetical protein PRO1257
1990	2242	NM_053433	n,General		RIKEN cDNA 1700055B19 gene, RIKEN cDNA 5730408C10 gene, zinc finger protein 103, zinc finger protein homologous to Zfp103 in mouse
1991	5561	NM_053438	y		

TABLE OF HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4:99-508PWO Doc. No. 1993197.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Modif. Code	Homologous Gene Name	Homologous Cluster Name
1992	14670	NM_053439	n, General		ESTs, Highly similar to RAB7 RAT RAS-RELATED PROTEIN RAB-7 [R.norvegicus], RAB7, member RAS oncogene family, RAN, member RAS oncogene family, RIKEN cDNA 1700009N14 gene
1993	17102	NM_053440	w	stathmin-like 2, superiorcervical ganglia, neural specific 10	stathmin-like 2, stathmin-like 4, superiorcervical ganglia, neural specific 10
1994	24762	NM_053442	General		ESTs, Weakly similar to 1615347A ras p21 GTPase activating protein [M.musculus], KIAA1938 protein, Mus musculus, Similar to RAS p21 protein activator, clone MGC:7759 [IMAGE:3498774, mRNA, complete cds, RAS protein activator like 2, Rattus norvegicus DCC2/DAB2 interactive protein mRNA, complete cds, expressed sequence BB079060, hypothetical protein FLJ21438
1995	8085	NM_053453	General		ESTs, Moderately similar to RGS8 RAT REGULATOR OF G-PROTEIN SIGNALING 8 [R.norvegicus], regulator of G-protein signaling 16, regulator of G-protein signaling 2, regulator of G-protein signaling 8, regulator of G-protein signalling 13, regulator of G-protein signalling 2, 24kD, regulator of G-protein signalling 8
1996	4622	NM_053463	d		NEFA precursor, expressed sequence A1807785, nucleobindin, nucleobindin 1, nucleobindin 2
1997	21866	NM_053472	p	cytochrome c oxidase subunit IV isoform 2, cytochrome c oxidase, subunit IVb	EST, Weakly similar to COX4, HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR [H.sapiens], cytochrome c oxidase subunit IV, cytochrome c oxidase subunit IV isoform 2, cytochrome c oxidase, subunit IV, cytochrome c oxidase, subunit IVa, cytochrome c oxidase, subunit IVb, expressed sequence AL024441
1998	9573	NM_053475	h		protein tyrosine phosphatase 4a1, protein tyrosine phosphatase 4a2, protein tyrosine phosphatase type IVA, member 1, protein tyrosine phosphatase type IVA, member 2, protein tyrosine phosphatase type IVA, member 3
1999	16137	NM_053480	k		DNA polymerase alpha 2, 68 kDa, Mus musculus, Similar to DNA polymerase alpha 2, 68 kDa, clone MGC:11533 [IMAGE:3602559, mRNA, complete cds, expressed sequence A1573378, polymerase (DNA-directed), alpha (70kD)
2000	15556	NM_053483	y		ESTs, Weakly similar to A Chain A, Importin Alpha, Mouse [M.musculus], expressed sequence AW146299, karyopherin (importin) alpha 2, karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
2001	16394	NM_053485	General		EST, Moderately similar to CALCYCLIN [R.norvegicus], S100 calcium-binding protein A6 (calcyclin), calcium binding protein A6 (calcyclin)

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS				Atyp. Doc# No. 44924-50397/2 Doc. No. 1783397-1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Gene Cluster Name
2002	4290	NM_053487	jy		peroxisomal biogenesis factor 11A, peroxisomal biogenesis factor 11B
					EST, Moderately similar to Y025_HUMAN HYPOTHETICAL PROTEIN KIAA0025 [H.sapiens], RIKEN cDNA 5031400M07 gene, homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1, hypothetical protein FLJ22313
2004	18826	NM_053523	d		DEADH (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome, DNA segment, Chr 1, Pasteur Institute 1, ESTs, Moderately similar to DDX1_HUMAN DEAD BOX PROTEIN 3, Y-CHROMOSOMAL [H.sapiens], KIAA0801 gene product, RNA helicase, Rattus norvegicus RNA helicase with arginine-serine-rich domain mRNA, complete cds, expressed sequence A1324246, expressed sequence A1325430, expressed sequence C86129
2005	7764	NM_053525	aa		Lysosomal-associated multispinning membrane protein-5, lysosomal-associated protein transmembrane 5
2006	14199	NM_053536	c		
2007	1058	NM_053539	c,d		
					DNA segment, Chr 17, human D6S81E 1, EST, Weakly similar to HE47 RAT PROBABLE ATP-DEPENDENT RNA HELICASE P47 [R.norvegicus], HLA-B associated transcript 1, KIAA0111 gene product, Mus musculus, clone MCC.664 IMAGE:3498954, mRNA, complete cds, RIKEN cDNA 2610307C23 gene, eukaryotic translation initiation factor 4A, isoform 2, eukaryotic translation initiation factor 4A1, eukaryotic translation initiation factor 4A2, nuclear RNA helicase, DECD variant of DEAD box family
2008	4327	NM_053563	General		ESTs, Weakly similar to JE0096 myocilin - mouse [M.musculus], Homo sapiens NOE3-4 (NOE3) mRNA, complete cds, alternatively spliced, expressed sequence AW742568, olfactomedin related ER localized protein
2009	1342	NM_053573	h		ESTs, Moderately similar to AOP2_HUMAN ANTIOXIDANT PROTEIN 2 [H.sapiens], anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5
2010	19254	NM_053576	h,s	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5	ESTs, Moderately similar to AOP2_HUMAN ANTIOXIDANT PROTEIN 2 [H.sapiens], anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5
2010	19253	NM_053576	h	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5	ESTs, Moderately similar to AOP2_HUMAN ANTIOXIDANT PROTEIN 2 [H.sapiens], anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5

TABLE OF HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc. No. 4-021-3039W Doc. No. 1183897-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
2011	3049	NM_053582	p.cc.General		ESTs, Highly similar to JC7189 tubulointerstitial nephritis antigen [H.sapiens], P3ECSL, cathepsin B, lipocalin 7, tubulointerstitial nephritis antigen
2011	3050	NM_053582	o.General		ESTs, Highly similar to JC7189 tubulointerstitial nephritis antigen [H.sapiens], P3ECSL, cathepsin B, lipocalin 7, tubulointerstitial nephritis antigen
2012	21423	NM_053586	s.v		EST, Moderately similar to CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR [R.norvegicus], cytochrome c oxidase subunit Vb, cytochrome c oxidase, subunit Vb
2013	21445	NM_053587	lv		
2014	20871	NM_053591	lj		ESTs, Weakly similar to MDP1 MOUSE MICROSOMAL DIPEPTIDASE PRECURSOR [M.musculus], ESTs, Weakly similar to S33757 membrane dipeptidase [M.musculus], RIKEN cDNA 1700018F16 gene, dipeptidase 1 (renal), putative dipeptidase, putative metallopeptidase (family M19)
2014	20870	NM_053591	li		ESTs, Weakly similar to MDP1 MOUSE MICROSOMAL DIPEPTIDASE PRECURSOR [M.musculus], ESTs, Weakly similar to S33757 membrane dipeptidase [M.musculus], RIKEN cDNA 1700018F16 gene, dipeptidase 1 (renal), putative dipeptidase, putative metallopeptidase (family M19)
2015	21044	NM_053594	ld		protein tyrosine phosphatase, receptor type, R
2016	21709	NM_053596	lk		KIAA0604 gene product, endothelin converting enzyme 1, endothelin converting enzyme-like 1, expressed sequence AW322500, expressed sequence BB127715, mel transforming oncogene-like 1, membrane metallo endopeptidase
2016	21708	NM_053596	lz		KIAA0604 gene product, endothelin converting enzyme 1, endothelin converting enzyme-like 1, expressed sequence AW322500, expressed sequence BB127715, mel transforming oncogene-like 1, membrane metallo endopeptidase
2017	1597	NM_053611	lt	nuclear protein 1, p8 protein (candidate of metastasis 1)	ESTs, Weakly similar to Gene product with similarity to Rat P8 [H.sapiens]
2018	5565	NM_053618	General	Bardet-Biedl syndrome 2, Bardet-Biedl syndrome 2 (human)	
				fatty acid-Coenzyme A ligase, long chain 4, fatty acid-Coenzyme A ligase, long-chain 4	
2019	13004	NM_053623	lt		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Aty. Pocket No. 44944-60696 Doc. No. 179349
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
2020	1127	NM_053626	g		D-amino acid oxidase, D-amino-acid oxidase, D-aspartate oxidase, EST, Weakly similar to OXDA RAT D-AMINO ACID OXIDASE [R.norvegicus], ESTs, Highly similar to OXDA RAT D-AMINO ACID OXIDASE [R.norvegicus], RIKEN cDNA 5330420D20 gene, RIKEN cDNA 5730402C02 gene
2021	18644	NM_053648	n	beta-carotene 15, 15'-dioxygenase, beta-carotene 15, 15'-dioxygenase	EST, Moderately similar to 0806162D protein COH [M.musculus], EST, Weakly similar to 81024D cytochrome oxidase II [H.sapiens]
2022	21637	NM_053653	p		c-fos induced growth factor, c-fos induced growth factor (vascular endothelial growth factor D), vascular endothelial growth factor, vascular endothelial growth factor B, vascular endothelial growth factor C
2023	3454	NM_053662	cc		ESTs, Highly similar to CG1C RAT G1/S-SPECIFIC CYCLIN C [R.norvegicus], Homo sapiens, clone IMAGE:3537447, mRNA, partial cds, RIKEN cDNA 1810009O10 gene, cyclin C, cyclin K, cyclin L, cyclin L anti-6s, cyclin T2
2024	16121	NM_053698	h,j,z		with Glu/Asp-rich carboxy-terminal domain, 2, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4, ESTs, Weakly similar to MRG1_HUMAN MSG-RELATED PROTEIN 1 [H.sapiens], expressed sequence AW742964
2024	16122	NM_053698	h,j,z		with Glu/Asp-rich carboxy-terminal domain, 2, Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4, ESTs, Weakly similar to MRG1_HUMAN MSG-RELATED PROTEIN 1 [H.sapiens], expressed sequence AW742964
2025	25379	NM_053713	General		ESTs, Moderately similar to CPBP RAT CORE PROMOTER ELEMENT-BINDING PROTEIN [R.norvegicus], Kruppel-like factor 4 (gut), RIKEN cDNA 7420700M05 gene, core promoter element binding protein
2025	13622	NM_053713	General		
2026	15376	NM_053747	h	ubiquitin 1	expressed sequence C86324, hypothetical protein FLJ23590
2027	1218	NM_053748	b		cytochrome P450, 40 (25-hydroxyvitamin D3 1 alpha-hydroxylase), cytochrome P450, subfamily XXVIIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1
2028	1137	NM_053763	y		MKP-1 like protein tyrosine phosphatase, dual specificity phosphatase 1, dual specificity phosphatase 13, dual specificity phosphatase 14, dual specificity phosphatase 2, expressed sequence BB104621, protein tyrosine phosphatase, non-receptor type 16
2029	15996	NM_053769	cc	dual specificity phosphatase 1, protein tyrosine phosphatase, non-receptor type 16	

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44121-Sub W6 Seq. No. 1493357.1
Seq. ID No.	Identifier	GenBank Acc./Ref. Seq. ID No.	Model Code	Protein Name	Homologous Cluster Name
2030	8652	NM_053774	g	ubiquitin specific protease 2	KAA1453 protein, RIKEN cDNA 4630511O11 gene, expressed sequence AA405661, ubiquitin specific protease 2, ubiquitin specific protease 8
2031	14664	NM_053806	General		
2032	4361	NM_053812	k		B cell lymphoma 2 like, BCL2-antagonist/killer 1, BCL2-like 1, Bcl-w protein, Bcl2-like, Mus musculus N-BAK1 (Bak1) mRNA, complete cds, alternatively spliced, RIKEN cDNA 0610031G08 gene
2034	15002	NM_053819	b,x,bb,General		EST, Moderately similar to TIM1 RAT METALLOPROTEINASE INHIBITOR 1 PRECURSOR [R.norvegicus], EST, Weakly similar to TIM1 RAT METALLOPROTEINASE INHIBITOR 1 PRECURSOR [R.norvegicus], tissue inhibitor of metalloproteinase, tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
2034	15003	NM_053819	b,l,x,bb,General		EST, Moderately similar to TIM1 RAT METALLOPROTEINASE INHIBITOR 1 PRECURSOR [R.norvegicus], EST, Weakly similar to TIM1 RAT METALLOPROTEINASE INHIBITOR 1 PRECURSOR [R.norvegicus], tissue inhibitor of metalloproteinase, tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
2035	16173	NM_053822	i		
2036	17154	NM_053836	j		
2037	20868	NM_053843	i		
2037	20869	NM_053843	i		
2040	714	NM_053863	y		ESTs, Highly similar to CNT1_HUMAN SODIUM/NUCLEOSIDE COTRANSPORTER 1 [H.sapiens], ESTs, Moderately similar to A54892 Na+-dependent nucleoside transport protein CNT1 - rat [R.norvegicus]
2041	19781	NM_053883	b		ESTs, Moderately similar to DUS6 RAT DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 [R.norvegicus], ESTs, Weakly similar to DUS6 RAT DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 [R.norvegicus], dual specificity phosphatase 10, dual specificity phosphatase 13, dual specificity phosphatase 14, dual specificity phosphatase 6, dual specificity phosphatase 9, expressed sequence BB104621, mitogen-activated protein kinase phosphatase x, protein tyrosine phosphatase, non-receptor type 16

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS				Atty. Docket No. 4924-3889WG Doc. No. 109387-1	
Seq. ID No.	Identifier	SimBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
					ESTs, Moderately similar to DUS6 RAT DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 [R.norvegicus], ESTs, Weakly similar to DUS6 RAT DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 [R.norvegicus], dual specificity phosphatase 10, dual specificity phosphatase 13, dual specificity phosphatase 14, dual specificity phosphatase 5, dual specificity phosphatase 9, expressed sequence BB104621, mitogen-activated protein kinase phosphatase x, protein tyrosine phosphatase, non-receptor type 15
2041	19780	NM_053883	b		
2042	1454	NM_053887	General		
					ESTs, Moderately similar to CD5R MOUSE CYCLIN-DEPENDENT KINASE 5 ACTIVATOR 1 PRECURSOR [R.norvegicus], cyclin-dependent kinase 5, regulatory subunit (p35), cyclin-dependent kinase 5, regulatory subunit 1 (p35), cyclin-dependent kinase 5, regulatory subunit 2 (p39)
2043	1660	NM_053891	g		
2044	712	NM_053895	k		
					coagulation factor II (thrombin) receptor-like 1, coagulation factor II (thrombin) receptor-like 2
2045	753	NM_053897	k		
					RIKEN cDNA 4432411A05 gene, kynureninase (L-kynurenine hydrolase)
2046	794	NM_053902	General		
					ESTs, Weakly similar to ARNO_HUMAN ARF NUCLEOTIDE-BINDING SITE OPENER [H.sapiens]
2047	17937	NM_053911	f		
					DNA segment, Chr 10, ERATO D01 398, expressed, ESTs, Weakly similar to PTNL RAT PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 21 [R.norvegicus], Homo sapiens, Similar to erythrocyte membrane protein band 4.1-like 3, clone MGC:12343 IMAGE:4044866, mRNA, complete cds, Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330430110, full insert sequence, Rattus norvegicus protein tyrosine phosphatase 2E (PTP2E) mRNA, complete cds, erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked), erythrocyte membrane protein band 4.1-like 1, erythrocyte membrane protein band 4.1-like 3, erythrocyte protein band 4.1-like 1, erythrocyte protein band 4.1-like 3, protein tyrosine phosphatase, non-receptor type 21
2048	8188	NM_053927	General		

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					Ally, Docm No. 44991-6081WO Doc No. 179997.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologue Name	Homologue Cluster Name
2050	1628	NM_053936	h		endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor 4, endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor 7, endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2, endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4, endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7, putative G-protein-coupled receptor anGPCR32
2051	13954	NM_053955	General		ESTs, Highly similar to B46290 mu-crystallin [H.sapiens], crystallin, mu
2052	408	NM_053961	General		
2052	19991	NM_053961	a		DNA segment, Chr 9, ERATO D01 85, expressed, Homo sapiens aconitase precursor (ACON) mRNA, nuclear gene encoding mitochondrial protein, partial cds, RIKEN cDNA 5031409G22 gene, aconitase 1, aconitase 1, soluble, aconitase 2, mitochondrial, iron-responsive element-binding protein
2052	16190	NM_053961	g		Homo sapiens hepatocellular carcinoma-associated antigen 64 (HCA64) mRNA, complete cds, RIKEN cDNA 1300014E15 gene, RIKEN cDNA 1300017C12 gene, RIKEN cDNA 1810022C23 gene, RIKEN cDNA 2610009M20 gene, RIKEN cDNA 4933417A18 gene, enoyl Coenzyme A hydratase, short chain, 1, mitochondrial, peroxisomal D3,D2-enoyl-CoA isomerase, peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase
2052	21355	NM_053961	i,l,y,z		
2055	15136	NM_053971	aa		EST, Moderately similar to I51803 TAXREB107 [H.sapiens], ESTs, Highly similar to I51803 TAXREB107 [H.sapiens], ribosomal protein L6
2055	15135	NM_053971	d		EST, Moderately similar to I51803 TAXREB107 [H.sapiens], ESTs, Highly similar to I51803 TAXREB107 [H.sapiens], ribosomal protein L6
2056	1764	NM_053974	h		ESTs, Highly similar to A26411 translation initiation factor eIF-4E [H.sapiens], RIKEN cDNA 2700069E09 gene, eukaryotic translation initiation factor 4E
2057	1292	NM_053980	i		ADP-ribosylation factor related protein 1, RIKEN cDNA 1500006I01 gene
2058	15468	NM_053982	q		EST, Highly similar to 40S RIBOSOMAL PROTEIN S15A [R.norvegicus], EST, Weakly similar to RS1A_HUMAN 40S RIBOSOMAL PROTEIN S15A [R.norvegicus], ESTs, Weakly similar to RS1A_HUMAN 40S RIBOSOMAL PROTEIN S15A [H.sapiens]
2059	15642	NM_053985	General		ESTs, Highly similar to HISTONE H3.3 [R.norvegicus], H3 histone, family 3A, H3 histone, family 3B, H3 histone, family 3B (H3.3B)

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS				Atty. Docket No. 4:191-5385WG Case No. 02-23327-1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Group Name	Homologous Cluster Name
2060	21066	NM_054001	t		CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II), EST, Moderately similar to LYII_HUMAN LYOSOSOME MEMBRANE PROTEIN II [H.sapiens]
2061	17326	NM_054008	o		RGC32 protein, RIKEN cDNA 1190002H23 gene
2061	17327	NM_054008	cc		RGC32 protein, RIKEN cDNA 1190002H23 gene
2061	17329	NM_054008	g.o.cc		RGC32 protein, RIKEN cDNA 1190002H23 gene
2062	25253	NM_057099	J.l.m.p.z	proteasome (prosome, macropain) subunit, beta type 6, proteasome (prosome, macropain) subunit, beta type, 6	EST, Weakly similar to S17522 multicatalytic endopeptidase complex [H.sapiens], ESTs, Weakly similar to PROTEASOME DELTA CHAIN PRECURSOR [R.norvegicus], proteasome (prosome, macropain) subunit, beta type 6, proteasome (prosome, macropain) subunit, beta type, 7
2062	22849	NM_057099	j.l	proteasome (prosome, macropain) subunit, beta type 6, proteasome (prosome, macropain) subunit, beta type, 6	EST, Weakly similar to S17522 multicatalytic endopeptidase complex [H.sapiens], ESTs, Weakly similar to PROTEASOME DELTA CHAIN PRECURSOR [R.norvegicus], proteasome (prosome, macropain) subunit, beta type 6, proteasome (prosome, macropain) subunit, beta type, 5, proteasome (prosome, macropain) subunit, beta type, 7
2063	19657	NM_057103	b.cc	A kinase (PRKA) anchor protein (gravin) 12	
2064	5492	NM_057105	w	UDP glycosyltransferase 1 family, polypeptide A cluster, UDP glycosyltransferase 1 family, polypeptide A6, UDP-glucuronosyltransferase 1 family, member 1	
2064	15126	NM_057105	r	UDP glycosyltransferase 1 family, polypeptide A cluster, UDP glycosyltransferase 1 family, polypeptide A6, UDP-glucuronosyltransferase 1 family, member 1	
2064	15125	NM_057105	s	UDP glycosyltransferase 1 family, polypeptide A cluster, UDP-glucuronosyltransferase 1 family, member 1	
2066	15381	NM_057114	n		EST, Moderately similar to TDX2_HUMAN THIOREDIXIN PEROXIDASE 2 [H.sapiens], EST, Weakly similar to TDX2_HUMAN THIOREDIXIN PEROXIDASE 2 [H.sapiens], peroxiredoxin 1

TABLE 8: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44931-3188WG Doc. No. 1793897.1
Seq. ID No.	Identifier	GenBank/ Acc# Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
2067	727	NM_057123	m		BCS1 (yeast homolog)-like, ESTs, Highly similar to PRS4_HUMAN 26S PROTEASE REGULATORY SUBUNIT 4 [H.sapiens], ESTs, Weakly similar to A44468 26S proteasome regulatory chain 4 [H.sapiens], expressed sequence A1325227, protease (prosome, macropain) 26S subunit, ATPase 1, proteasome (prosome, macropain) 26S subunit, ATPase, 1
2068	915	NM_057124	s		ESTs, Weakly similar to P2UR MOUSE P2U PURINOCEPTOR 1 [M.musculus], G protein-coupled receptor 35, purinergic receptor P2Y, G-protein coupled 2, pyrimidinergic receptor P2Y, G-protein coupled, 4, pyrimidinergic receptor P2Y, G-protein coupled, 6
2069	15151	NM_057131	k		
2070	1892	NM_057144	b		cysteine and glycine-rich protein 3 (cardiac LIM protein), cysteine rich protein, cysteine-rich protein 2, cysteine-rich protein 3, thymus LIM protein
2071	12333	NM_057155	r		
2071	12331	NM_057155	v.General		
2071	12332	NM_057155	f.General		
2072	17477	NM_057194	a.General		EST, Weakly similar to B36298 proline-rich protein PRB3S [H.sapiens], EST, Weakly similar to CGHU3B collagen alpha 3(IV) chain precursor, long splice form [H.sapiens], EST, Weakly similar to D40750 proline-rich protein PRB1/2S [H.sapiens], EST, Weakly similar to J62284 htm-1 cell derived transplantability-associated protein 1b [H.sapiens], galectin-related inter-fiber protein, murine leukemia viral (bmi-1) oncogene homolog, phospholipid scramblase 1, phospholipid scramblase 2, phospholipid scramblase 3
2073	15408	NM_057197	p.t		2,4-dienoyl CoA reductase 1, mitochondrial, 2,4-dienoyl CoA reductase 2, peroxisomal, peroxisomal trans 2-enoyl CoA reductase, putative short chain alcohol dehydrogenase
2073	15409	NM_057197	t		2,4-dienoyl CoA reductase 1, mitochondrial, 2,4-dienoyl CoA reductase 2, peroxisomal, peroxisomal trans 2-enoyl CoA reductase, putative short chain alcohol dehydrogenase
2074	7866	NM_057198	h		ESTs, Highly similar to PUR1_HUMAN AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR [H.sapiens], ESTs, Moderately similar to PUR1_HUMAN AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR [H.sapiens], RIKEN cDNA 5730454C12 gene, expressed sequence A6875351, expressed sequence C79645, glutamine fructose-6-phosphate transaminase 2, glutamine-fructose-6-phosphate transaminase 2, phosphoribosyl pyrophosphate amidotransferase

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS						Atty. Docket No. 44924-3000W
						Doc. No. 449332/1
Seq. ID No.	Identif.	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Annotation, etc. Cluster Name	
2075	14125	NM_057208	h.j.y.z		ESTs, Highly similar to A25530	
2076	1743	NM_057210	k.s		Tropomyosin, fibroblast [H.sapiens]	
					EST, Moderately similar to RS23_HUMAN 40S RIBOSOMAL PROTEIN S2 [R.norvegicus], EST, Weakly similar to RS23_HUMAN 40S RIBOSOMAL PROTEIN S2 [R.norvegicus], ESTs, Weakly similar to RS23_HUMAN 40S RIBOSOMAL PROTEIN S2 [R.norvegicus], Mus musculus, Similar to mitochondrial ribosomal protein S12, clone MGC:13892 IMAGE:4209358, mRNA, complete cds, RIKEN cDNA 2410044J15 gene, expressed sequence A1327385, mitochondrial ribosomal protein S12, ribosomal protein S23	
2077	10458	NM_078617	a			
2078	8820	NM_080399	n			
					ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (multiple drug resistance-associated protein), ATP-binding cassette, sub-family C (CFTR/MRP), member 1a, ATP-binding cassette, sub-family C (CFTR/MRP), member 1b, ATP-binding cassette, sub-family C (CFTR/MRP), member 2, ATP-binding cassette, sub-family C (CFTR/MRP), member 3, ATP-binding cassette, sub-family C (CFTR/MRP), member 6, ESTs, Moderately similar to JE0336 canalicular multispecific organic anion transporter [H.sapiens], RIKEN cDNA 1700019L09 gene	
2079	15701	NM_080581	j.m.y.z			
2079	20105	NM_080581	aa			
2080	16109	NM_080585	c			
2081	1757	NM_080766	d			
					ESTs, Highly similar to COT2 RAT COUP TRANSCRIPTION FACTOR 2 [R.norvegicus], Homo sapiens cDNA: FLJ22186 fs, clone HRC01043, RIKEN cDNA 2700033K02 gene, nuclear receptor subfamily 2, group E, member 3, nuclear receptor subfamily 2, group F, member 2	
2082	7108	NM_080778	y			
					cyclin-dependent kinase inhibitor 1A (P21), cyclin-dependent kinase inhibitor 1A (p21, Cip1), cyclin-dependent kinase inhibitor 1B (p27, kip1), cyclin-dependent kinase inhibitor 1B (p27, Kip1)	
2083	132	NM_080782	k			
					cyclin-dependent kinase inhibitor 1A (P21), cyclin-dependent kinase inhibitor 1A (p21, Cip1), cyclin-dependent kinase inhibitor 1B (p27, kip1), cyclin-dependent kinase inhibitor 1B (p27, Kip1)	
2083	133	NM_080782	l			
					HT014, Homo sapiens thioredoxin delta 3 (TXN delta 3) mRNA, partial cds, RIKEN cDNA 4930429J24 gene, expressed sequence AU021712, thioredoxin, thioredoxin domain-containing 2 (spermatozo), thioredoxin-like (32kD), thioredoxin-like, 32kD	
2084	20122	NM_080887	General			

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44291-5000/02 Doc. No. 199387.4
Seq. ID No.	Gene/Link/Accession	Ref. Seq. ID No.	Muscle Source	Homologous Gene Name	Homologous Gene Name
2085	6143	NM_080892	e		Human sapiens, Similar to selenium binding protein 1, clone MGC-17268 [IMAGE:4155236, mRNA, complete cds, selenium binding protein 1, selenium binding protein 2]
2086	9952	NM_080902	h		
2087	17546	NM_130401	b		epithelial protein up-regulated in carcinoma, membrane associated protein 17
2088	21695	NM_130411	c,x		ESTs, Weakly similar to CO1A, MOUSE CORONIN-LIKE PROTEIN P57 (CORONIN 1A) [M.musculus], coronin, actin binding protein 1A, coronin, actin binding protein 1B, coronin, actin binding protein 1C, coronin, actin-binding protein, 1A, hypothetical protein DKFZp782166
2089	21391	NM_130416	x,General		annexin VII, long form [H.sapiens], ESTs, Moderately similar to ANX4 MOUSE ANNEXIN IV [M.musculus], ZAP 36/annexin IV, annexin A4, annexin A7
2090	20694	NM_130430	General		
2090	19818	NM_130430	cc		
2090	18810	NM_130430	e,s		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle, EST, Moderately similar to ATPase ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR [R.norvegicus], expressed sequence AL022851, expressed sequence AL023067
2091	18293	NM_130433	q		
2092	25064	S45392	a,n		
2093	3244	S63519	u		
2094	25501	S63521	q		
2095	18248	S68135	h		
2096	18647	S69316	q		EST, Weakly similar to ENPL_HUMAN ENDOPLASMIN PRECURSOR [H.sapiens], ESTs, Highly similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus], ESTs, Weakly similar to ENPL_HUMAN ENDOPLASMIN PRECURSOR [H.sapiens], Homo sapiens mRNA; cDNA DKFZp584F053 (from clone DKFZp584F053), RIKEN cDNA 1810014B01 gene, RIKEN cDNA 2410002K23 gene, expressed sequence C81438, heat shock 90kD protein 1, beta, heat shock protein, 84 kDa 1, tumor rejection antigen (gp96) 1, tumor rejection antigen gp96
2097	24351	S74257	v		ATP-binding cassette, sub-family D (ALD), member 4, ESTs, Highly similar to JC5604 ABC-transporting peroxisomal membrane protein 69 [H.sapiens], ESTs, Moderately similar to JC5604 ABC-transporting peroxisomal membrane protein 69 [H.sapiens]
2098	25066	S75280	d		

TABLE 8. HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc# No. 44921-5031 VO Doc. No. 749337-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
2099	1460	S76054	j,m,x,y.General		DNA segment, Chr 15, Wayne State University 77, expressed, EST, Moderately similar to K2C8 RAT KERATIN, TYPE II CYTOSKELETAL 8 [R.norvegicus], EST, Weakly similar to I37982 Keratin 8 [H.sapiens], ESTs, Moderately similar to I37982 Keratin 8 [H.sapiens], ESTs, Weakly similar to I37982 Keratin 8 [H.sapiens], Homo sapiens mRNA: cDNA DKFZp434C107 (from clone DKFZp434C107), RIKEN cDNA 1200016G03 gene, expressed sequence AU019895, keratin 8, keratin complex 2, basic, gene 8
2100	25339	S76742	v		
2101	16400	S76779	c		
2102	24469	S77858	n		EST, Weakly similar to MOHURN myosin alkali light chain 6, nonmuscle form [H.sapiens], myosin light chain, alkali, nonmuscle, myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
2103	25545	S77900	k,s		
2103	21583	S77900	k		EST, Weakly similar to MOHULP myosin regulatory light chain, placental [H.sapiens], ESTs, Moderately similar to MOHULP myosin regulatory light chain, placental [H.sapiens], myosin regulatory light chain, myosin, light polypeptide, regulatory, non-sarcomeric (20kD)
2104	10260	S81497	s	lipase A, lysosomal acid, cholesterol esterase (Wolman disease), lysosomal acid lipase 1	
2105	3609	S82579	k		Homo sapiens, Similar to histamine N-methyltransferase, clone MGC:14500 IMAGE:4249496, mRNA, complete cds, expressed sequence AI788969, histamine N-methyltransferase
2106	111	U02506	u		
2107	14959	U03390	a,q.General		EST, Moderately similar to GBLP_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 [R.norvegicus], EST, Weakly similar to B33928 GTP-binding protein beta chain homolog [H.sapiens], ESTs, Weakly similar to A36986 activated protein kinase C receptor RACK1 - rat [R.norvegicus], Homo sapiens cDNA: FLJ21913 fls, clone HEP03888, Homo sapiens, Similar to guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, clone MGC:17239 IMAGE:4155303, mRNA, complete cds, expressed sequence AW544865, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doct. No. 4391-5836W3 Doc. No. 1123337.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
2109	2010	U05675	b.x.bb		EST, Weakly similar to beta-fibrinogen precursor [H.sapiens], ESTs, Moderately similar to AF125176 1 angiotensin-related protein-2 [M.musculus], ESTs, Weakly similar to FIBB RAT FIBRINOGEN BETA CHAIN PRECURSOR [R.norvegicus], expressed sequence AI256424, fibrinogen, B beta polypeptide
2110	15452	U06230	d		
2112	1583	U07201	s,General	asparagine synthetase	
2113	627	U09229	h		ESTs, Highly similar to CDP HUMAN CCAAT DISPLACEMENT PROTEIN [H.sapiens], Hepatocyte nuclear factor 6, Human chromosome 17q21 mRNA clone 1046:1-1, KIAA0293 protein, cut (Drosophila)-like 1, cut (Drosophila)-like 1 (CCAAT displacement protein), cut (Drosophila)-like 2, one cut domain, family member 1
2114	809	U17035	General		
2115	16675	U17565	k.x.bb	mini chromosome maintenance deficient 6 (S. cerevisiae), minichromosome maintenance deficient (mis5, S. pombe) 6	mini chromosome maintenance deficient 6 (S. cerevisiae), minichromosome maintenance deficient (mis5, S. pombe) 6
2116	25587	U20110	r		
2117	90	U20796	r		Mus musculus, Similar to nuclear receptor subfamily 1, group D, member 1, clone MGC:6402 IMAGE:3585478, mRNA, complete cds, nuclear receptor subfamily 1, group D, member 2, thyroid hormone receptor alpha
2118	25589	U21718	h,ea		
2119	22196	U21719	h		
2120	17118	U25746	s		DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide 5, ESTs, Moderately similar to A57514 RNA helicase HEL117 - rat [R.norvegicus], KIAA0801 gene product, RIKEN cDNA 2610007K22 gene, RIKEN cDNA 4921506D17 gene, RIKEN cDNA 9130430L19 gene, RNA helicase, expressed sequence AI325430
2121	1537	U27518	g,h,n		
2122	1558	U28504	bb		EST, Weakly similar to NPT1 RAT RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 1 [R.norvegicus], ESTs, Weakly similar to NPT1 MOUSE RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 1 [M.musculus], expressed sequence AW261723, solute carrier family 17 (sodium phosphate), member 1, solute carrier family 17 (sodium phosphate), member 3, solute carrier family 17 (sodium phosphate), member 4, solute carrier family 17 (sodium/hydrogen exchanger), member 1

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4391-508W	Doc. No. 199997-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Gene	Homologous Gene Name	Homologous Cluster Name	
2123	16193	U30831	n		B/K protein, EST, Moderately similar to S68895 B/K protein - rat [R.norvegicus], Mus musculus B/K mRNA for B/K protein, complete cds, strain: BALB/c, RIKEN cDNA C030008b15 gene, synaptotagmin 1, synaptotagmin 5	
2124	17480	U31596	z			
2125	18302	U33560	General			
2126	25599	U34897	y			
2127	1394	U37099	h		Homo sapiens, clone MGC:4711 IMAGE:3534915, mRNA, complete cds, RAB23, member RAS oncogene family, RAB3A, member RAS oncogene family, RAB3C, member RAS oncogene family, expressed sequence A185088	
2128	244	U38376	n		ESTs, Highly similar to FGD1_HUMAN PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [H.sapiens], ESTs, Weakly similar to B39898 phospholipase A2 [M.musculus], ESTs, Weakly similar to FGD1 MOUSE PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [M.musculus], ESTs, Weakly similar to FGD1_HUMAN PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR [H.sapiens], FGD1 family, member 3, RIKEN cDNA 5830461L01 gene, faciogenital dysplasia (Aarskog-Scott syndrome), faciogenital dysplasia homolog, faciogenital dysplasia homolog 2 (human)	
2129	1623	U41164	h		ESTs, Weakly similar to AF167320 1 zinc finger protein ZFP113 [M.musculus], ESTs, Weakly similar to Z135_HUMAN ZINC FINGER PROTEIN 13 [H.sapiens], ESTs, Weakly similar to ZF29 MOUSE ZINC FINGER PROTEIN 29 [M.musculus], RIKEN cDNA 2310040I01 gene, expressed sequence A1835008	
2130	15851	U42719	f,l,x,General	complement component 4 (within H-2S), complement component 4B	EST, Weakly similar to complement component C4A [H.sapiens]	
2131	17886	U47315	s,z			
2132	21654	U63184	l,l,General			
2133	1439	U57391	w			
2134	725	U62316	bb		expressed sequence AW146050, monocarboxylate transporter, solute carrier family 16 (monocarboxylic acid transporters), member 3, solute carrier family 16 (monocarboxylic acid transporters), member 7	
2137	2153	U79404	b,cc,General	A kinase (PRKA) anchor protein (gravin) 12		
2139	4956	U76714	y			
2140	4477	U77829	l,m			
2141	21703	U82591	z		expressed sequence C76683, putative c-Myc-responsive	

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 4924-5037WC Doc. No. 779337.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
2142	977	U89744	s		KIAA1683 protein, KIAA1802 protein, expressed sequence AA407558, lymphocyte antigen 64, polymerase (RNA) II (DNA directed) polypeptide A (220kD), suppressor of Ty (S.cerevisiae) 5 homolog
2143	23282	U90725	h		high density lipoprotein binding protein (vigilin)
2144	22005	U96490	m		
2146	819	X02284	j,z		
2147	818	X02291	e,j,z	aldolase 2, B isoform, aldolase B, fructose-bisphosphate	
2148	20818	X02904	n,q		
2149	16401	X04979	c		
2150	20513	X05684	o,r	pyruvate kinase liver and red blood cell, pyruvate kinase, liver and RBC	
2151	25084	X06769	cc		
2152	672	X13722	h		
2153	25675	X14181	n		
2153	20810	X14181	n,q,w		EST, Moderately similar to RL1X_HUMAN 60S RIBOSOMAL PROTEIN L18A [H.sapiens], EST, Weakly similar to RL1X_HUMAN 60S RIBOSOMAL PROTEIN L18A [H.sapiens], EST, Weakly similar to S47353 ribosomal protein L18a, cytosolic [H.sapiens], ESTs, Highly similar to RL1X_HUMAN 60S RIBOSOMAL PROTEIN L18A [H.sapiens], RIKEN cDNA 2510019J09 gene, ribosomal protein L18a
2154	18541	X14671	y		ESTs, Highly similar to RL26_HUMAN 60S RIBOSOMAL PROTEIN L26 [H.sapiens], ESTs, Highly similar to S33713 ribosomal protein L26, cytosolic [H.sapiens], ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L26 [R.norvegicus], ribosomal protein L26, ribosomal protein L26 pseudogene 1
2155	25679	X15013	q		EST, Weakly similar to 60S RIBOSOMAL PROTEIN L7A [M.musculus], ESTs, Highly similar to R5H7A ribosomal protein L7e, cytosolic [H.sapiens], Homo sapiens rpl7a pseudogene, clone 3a, Human DNA sequence from clone RP1-189G13 on chromosome 20. Contains an RPL7A (60S ribosomal protein L7A) (SURF3) pseudogene, an RPS4 (40S ribosomal protein S4) pseudogene, ESTs, STSs and GSSs, RIKEN cDNA 4632404N19 gene, ribosomal protein L7a
2155	19244	X15013	c,q,w		EST A1317031, EST, Weakly similar to R3HU16 ribosomal protein S16, cytosolic [H.sapiens], expressed sequence AA420385, ribosomal protein S16
2156	15626	X17665	a		
2157	1893	X51529	i	phospholipase A2, group IIA (platelets, synovial fluid)	
2158	25686	X51536	bb		

TABLE 32: HUMAN HOMOLOGUE ANNOTATIONS					Ally, Pocket No. 44974-000WC Doc. No. 199807.1
Seq. ID No.	Seq. Identifier	GenBank Acc./Ref. Seq. ID No.	Model Code	Homologous Gene	Transcript Cluster Name
2158	10819	X51536	aa.bb		EST, Moderately similar to R3RT3 ribosomal protein S3 - rat [R.norvegicus], EST, Weakly similar to R3RT3 ribosomal protein S3 - rat [R.norvegicus], hypothetical protein FLJ23059, ribosomal protein S3
2159	18250	X51706	a,q,w	ribosomal protein L9	EST, Weakly similar to 60S RIBOSOMAL PROTEIN L9 [R.norvegicus], EST, Weakly similar to S42106 ribosomal protein L9 homolog [H.sapiens], ESTs, Highly similar to S42106 ribosomal protein L9 homolog [H.sapiens], ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L9 [R.norvegicus], RIKEN cDNA 4930401B11 gene, ribosomal protein L9
2160	20872	X51707	a	ribosomal protein S19	EST, Moderately similar to 40S RIBOSOMAL PROTEIN S19 [R.norvegicus], EST, Weakly similar to RS19_HUMAN 40S RIBOSOMAL PROTEIN S19 [H.sapiens], ribosomal protein S19
2161	516	X52711	c		myxovirus (influenza virus) resistance 1, myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78)
2162	25689	X52815	g		
2163	20427	X53378	w		ESTs, Highly similar to RS13_HUMAN 40S RIBOSOMAL PROTEIN S13 [H.sapiens], ESTs, Moderately similar to RS13_HUMAN 40S RIBOSOMAL PROTEIN S13 [H.sapiens]
2164	18606	X53504	General		EST, Moderately similar to S35531 ribosomal protein L12, cytosolic [H.sapiens], EST, Weakly similar to 60S RIBOSOMAL PROTEIN L12 [R.norvegicus], hypothetical protein, ribosomal protein L12
2165	1463	X54467	d,u,General		
2166	24577	X55153	a,v		EST, Weakly similar to 60S ACIDIC RIBOSOMAL PROTEIN P2 [R.norvegicus], EST, Weakly similar to RSHLP2 acidic ribosomal protein P2, cytosolic [H.sapiens], ESTs, Highly similar to 60S ACIDIC RIBOSOMAL PROTEIN P2 [R.norvegicus], ESTs, Highly similar to MTJ1 MOUSE DNAJ PROTEIN HOMOLOG MTJ1 [M.musculus], Human DNA sequence from clone RP3-408B20 on chromosome 6 Contains ESTs, STSs and GSSs. Contains a gene and two pseudogenes for novel 7 transmembrane receptors (olfactory family) and a gene for a novel protein similar to 60S acidic ribosomal protein P2 (RPLP2), RIKEN cDNA 2700049P22 gene, ribosomal protein, large P2, ribosomal protein, large, P1

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Doc# No. 4199-3301W3 Sec. No. 116387-1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
2167	10344	X57405	j,m	Notch (Drosophila) homolog 1 (translocation-associated), Notch gene homolog 1, (Drosophila)	EST, Highly similar to A40043 notch protein homolog TAN-1 precursor [H.sapiens], EST, Weakly similar to A40043 notch protein homolog TAN-1 precursor [H.sapiens], ESTs, Weakly similar to NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR [M.musculus], Homo sapiens mRNA, cDNA DKFZp761G02121 (from clone DKFZp761G02121), partial cds, Notch (Drosophila) homolog 1 (translocation-associated), Notch (Drosophila) homolog 2, Notch (Drosophila) homolog 3, Notch gene homolog 1, (Drosophila), Notch gene homolog 3, (Drosophila), Jagged 1
2168	15106	X57529	g,n,q		EST, Weakly similar to S30393 ribosomal protein S18, cytosolic [H.sapiens], ESTs, Highly similar to S30393 ribosomal protein S18, cytosolic [H.sapiens], ribosomal protein S18
2169	9567	X56200	q,bb	ribosomal protein L23	EST, Moderately similar to 60S RIBOSOMAL PROTEIN L23 [R.norvegicus], EST, Weakly similar to S65784 ribosomal protein L29, cytosolic [H.sapiens], ESTs, Highly similar to S65784 ribosomal protein L29, cytosolic [H.sapiens], ESTs, Weakly similar to 60S RIBOSOMAL PROTEIN L29 [M.musculus], Human DNA sequence from clone RP4-595K12 on chromosome 1p31.2-31.3 Contains a pseudogene similar to 60S RPL29 (ribosomal protein L29 (cell surface heparin binding protein HBP)), a chromosome 1 specific mRNA (KIAA0499), a novel mRNA (KIAA0433), ESTs, STSs, GSSs and a CpG Island, ribosomal protein L29
2169	18611	X58200	a,v	ribosomal protein L29	EST, Moderately similar to RL17_HUMAN 60S RIBOSOMAL PROTEIN L17 [H.sapiens], EST, Weakly similar to RL17_RAT 60S RIBOSOMAL PROTEIN L17 [R.norvegicus], EST, Weakly similar to RL17_HUMAN 60S RIBOSOMAL PROTEIN L17 [H.sapiens], ESTs, Weakly similar to RSHU22 ribosomal protein L17, cytosolic [H.sapiens]
2170	17175	X58389	w		EST, Moderately similar to 40S RIBOSOMAL PROTEIN S5 [R.norvegicus], ESTs, Weakly similar to S55916 ribosomal protein S5, cytosolic [H.sapiens], ribosomal protein S5
2171	25702	X58465	w	ribosomal protein S5	EST, Moderately similar to 40S RIBOSOMAL PROTEIN S5 [R.norvegicus], ESTs, Weakly similar to S55916 ribosomal protein S5, cytosolic [H.sapiens], ribosomal protein S5
2171	10109	X58465	c,g	ribosomal protein S5	
2172	25705	X59375	c,aa,General		

TABLE 2: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Board No. 41924-5088WO
					Doc. No. 1795837.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Gene Name
				creatine kinase, mitochondrial 1 (ubiquitous), creatine kinase, mitochondrial 1, ubiquitous	
2173	25709	X59737	u		
2174	18354	X59859	General	decorin	ESTs, Moderately similar to dJ63G5.3 [H.sapiens], RIKEN cDNA 1700034K16 gene, RIKEN cDNA 5530600M07 gene, decorin
2174	18355	X59859	t	decorin	ESTs, Moderately similar to dJ63G5.3 [H.sapiens], RIKEN cDNA 1700034K16 gene, RIKEN cDNA 5530600M07 gene, decorin
2175	21657	X61381	General		ESTs, Moderately similar to S17182 Interferon-induced protein 1-8U [H.sapiens], ESTs, Weakly similar to putative haemopoietic membrane protein [M.musculus], Human DNA sequence from clone RP4-781L3 on chromosome 1p34.3-38.11 Contains a pseudogene similar to IFITM3 (Interferon Induced transmembrane protein 3 (1-8U)), STSs and GSSs, RIKEN cDNA 1110004C05 gene, Interferon induced transmembrane protein 3 (1-8U), Interferon induced transmembrane protein 3-like, Interferon-inducible protein 16
2176	25718	X62145	bb, General		
2176	15875	X62145	s,q,v		EST, Highly similar to 60S RIBOSOMAL PROTEIN L8 [R.norvegicus], EST, Moderately similar to 60S RIBOSOMAL PROTEIN L8 [R.norvegicus], EST, Weakly similar to JN0923 ribosomal protein L8, cytosolic [H.sapiens], ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L8 [R.norvegicus], ESTs, Highly similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus], ESTs, Moderately similar to RL8_HUMAN 60S RIBOSOMAL PROTEIN L [M.musculus], expressed sequence AL024098, ribosomal protein L8
2177	13646	X62166	bb		EST, Weakly similar to 60S RIBOSOMAL PROTEIN L3 [R.norvegicus], EST, Weakly similar to I84501 ribosomal protein L3 [H.sapiens], ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L3 [R.norvegicus], ESTs, Moderately similar to I84501 ribosomal protein L3 [H.sapiens], ESTs, Weakly similar to RL3 MOUSE 60S RIBOSOMAL PROTEIN L3 [M.musculus], RIKEN cDNA 1110057H16 gene, ribosomal protein L3, ribosomal protein L3-like
2178	25721	X62325	p		
2179	16012	X62875	m,s,z		high mobility group AT-hook 1, high-mobility group (nonhistone chromosomal) protein isoforms I and Y
2180	25730	X63369	cc		
2181	25089	X63594	General		
2181	25090	X63594	cc, General		

TABLE 2. HUMAN HOMOLOGUE ANNOTATIONS					Any Doc No. 4491-5081WO Doc. No. 179397.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
2182	20844	X65228	n_w		EST, Highly similar to 60S RIBOSOMAL PROTEIN L23A [R.norvegicus], ESTs, Highly similar to RL2B_HUMAN 60S RIBOSOMAL PROTEIN L23A [H.sapiens], ribosomal protein L23a
2183	20879	X65296	l_y		EST, Weakly similar to JC5408 carboxylesterase [H.sapiens], ESTs, Moderately similar to ES22 MOUSE LIVER CARBOXYLESTERASE Z2 PRECURSOR [M.musculus], T-complex expressed gene 5, carboxylesterase 1, carboxylesterase 1 (monocyte/macrophage serine esterase 1), carboxylesterase 3, carboxylesterase 3 (brain)
2184	25735	X68782	c		EST, Highly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Moderately similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens], ESTs, Highly similar to CA21_HUMAN COLLAGEN ALPHA 2(I) CHAIN PRECURSOR [H.sapiens], collagen type V, alpha 2, collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), macrophage receptor with collagenous structure, procollagen, type III, alpha 1
2185	16426	X70369	c	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1	ESTs, Highly similar to A34789 T-plastin [H.sapiens], ESTs, Highly similar to PLS1_HUMAN I-PLASTIN [H.sapiens], expressed sequence A115446, expressed sequence A1427122, expressed sequence AL024105, plastin 2, L
2186	16300	X70706	u		B-cell CLL/lymphoma 1, EST, Moderately similar to COD1 RAT G1/S-SPECIFIC CYCLIN D1 [R.norvegicus], ESTs, Weakly similar to 1709356A cyclin PRAD1 [H.sapiens], cyclin D1, cyclin D1 (PRAD1: parathyroid adenomatosis 1), expressed sequence A1327039
2187	24232	X75207	c		ESTs, Highly similar to alpha-albumin protein [H.musculus], Mus musculus mRNA for alpha-albumin protein, albumin
2188	16272	X76456	n_p		
2189	25741	X76489	u		
2190	23302	X78949	h		ESTs, Weakly similar to DAHUA1 procollagen-proline dioxygenase [H.sapiens], expressed sequence A1853847, expressed sequence C76437, procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide, procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I, procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II

TABLE 3: HUMAN HOMOLOGUE ANNOTATION					Any, DocId: No. 64921-5030.W3 Doc. No. 1123337.1
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Cluster Name
2191	25747	X81448	General		EST, Weakly similar to KERATIN, TYPE I CYTOSKELETAL 19 [M.musculus], ESTs, Moderately similar to K1C-J HUMAN KERATIN, TYPE I CYTOSKELETAL 10 [H.sapiens], ESTs, Weakly similar to S30433 keratin 17, type I, cytoskeletal [H.sapiens], Homo sapiens mRNA for keratin 19, partial cds, isolate K19-141, keratin 19, keratin complex 1, acidic, gene 19, type I intermediate filament cytokeratin
2192	24115	X81449	u		
2193	25754	X89696	g		
2194	25097	X90642	y,z		
2195	12976	X86437	cc,General		immediate early response 3
2197	4594	Y07704	c		
2198	25777	Y08355	g,p,General		
2199	15986	Y09945	bb,General		EST, Weakly similar to OCN2 MOUSE ORGANIC CATION/CARNITINE TRANSPORTER 2 [M.musculus], ESTs, Highly similar to OCN2_HUMAN ORGANIC CATION/CARNITINE TRANSPORTER 2 [H.sapiens], ESTs, Weakly similar to JED346 high-affinity carnitine transporter, CT1 - rat [R.norvegicus], ion transporter protein, solute carrier family 22 (organic cation transporter), member 1, solute carrier family 22 (organic cation transporter), member 4, solute carrier family 22 (organic cation transporter), member 5, solute carrier family 22 (organic cation transporter), member 9
2200	20890	Y13275	k		CD9 antigen, RIKEN cDNA 6330415F13 gene, RIKEN cDNA B230119D02 gene, expressed sequence C76990, transmembrane 4 superfamily member 3
2201	21914	Y13336	d		ESTs, Weakly similar to DAD1_HUMAN DEFENDER AGAINST CELL DEATH 1 [R.norvegicus], defender against cell death 1, expressed sequence A1323713
2202	406	Z11995	o,General		
2203	16352	Z12298	t	decorin	ESTs, Moderately similar to dJ53G5.3 [H.sapiens], RIKEN cDNA 1700034K16 gene, RIKEN cDNA 5530600M07 gene, decorin
2204	17481	Z49761	k		ESTs, Highly similar to T17342 hypothetical protein DKFZp596K1924.1 [H.sapiens], ESTs, Moderately similar to T17342 hypothetical protein DKFZp596K1924.1 [H.sapiens]
2205	8664	Z75029	r,v		
2206	2459	AA964755	cc		
2207	23830	AA956636	aa		
2208	6100	X73524	x		

TABLE 3: HUMAN HOMOLOGUE ANNOTATIONS					Atty. Docket No. 44374-5089WO Doc. No. 1768397.1	
Seq. ID No.	Identifier	GenBank Acc./ Ref. Seq. ID No.	Model Code	Homologous Gene Name	Homologous Gene	Cluster Name
2209	439	Z22607	w	bone morphogenetic protein 4	bone morphogenetic protein 15, bone morphogenetic protein 4, endometrial bleeding associated factor, endometrial bleeding associated factor (left-right determination, factor A), transforming growth factor beta superfamily), growth differentiation factor 2, growth differentiation factor 5, hypothetical protein FLJ10314 ESTs, Highly similar to T17342 hypothetical protein DKFZp586K1924.1 [H.sapiens]. ESTs, Moderately similar to T17342 hypothetical protein DKFZp586K1924.1 [H.sapiens]	
2210	8665	AI071965	v		CD163 antigen, ESTs, Highly similar to I38005 M130 antigen precursor, splice form 4 [H.sapiens], KIAA1822 protein, apoptosis inhibitory 8, crp-ductin, deleted in malignant brain tumors 1, lectin, galactoside-binding, soluble, 3 binding protein, macrophage scavenger receptor 2, peptidylprolyl isomerase C-associated protein	
2211	155	U32681	t	crp-ductin, deleted in malignant brain tumors 1	ESTs, Moderately similar to AOP2_HUMAN ANTIOXIDANT PROTEIN 2 [H.sapiens], anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5	
2212	19252	AA892041	s	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5		
2213	15582	AI232320	q			
2214	17541	M26125	n	epoxide hydrolase 1, microsomal, epoxide hydrolase 1, microsomal (xenobiotic)	EST, Moderately similar to HYPEP_HUMAN EPOXIDE HYDROLASE 1 [H.sapiens], ESTs, Highly similar to HYPEP_HUMAN EPOXIDE HYDROLASE 1 [H.sapiens], epoxide hydrolase 1, microsomal, epoxide hydrolase 1, microsomal (xenobiotic)	
2215	18609	M30689	i			
2216	6262	AI177125	g			
2217	23859	AI072161	f			
2218	21011	H32189	e	glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2	ESTs, Moderately similar to GLUTATHIONE S-TRANSFERASE YB1 [R.norvegicus], glutathione S-transferase M1, glutathione S-transferase, mu 1	
2220	2572	AI177143	b			
2221	25419	M22922	a			

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TABLE 4: CODE KEY			Atty. Docket No. 44921-5039WO	
			Doc. No. 1793397.1	
	Time (hrs)	Code		
GENERAL TOXICITY		General		
ACYCLOVIR	24, 168	a		
ACYCLOVIR	6	b		
ADR	120, 168	c		
AY	360	d		
BEA	6, 24	e		
CAPTOPRIL	336	f		
CARBOPLATIN	6	g		
CEPHALORIDINE	6, 24	h		
CIDOFOVIR	120	i		
CISPANcombined	6, 24	j		
CISPLATIN	168	k		
CISPLATIN	6, 24	l		
CISPLATIN	6, 24, 168	m		
CITRININ	6, 24	n		
COLCHICINE	6, 24, 48	o		
CYCLOPHOSPHAMIDE	6	p		
DIFLUNISAL	24	q		
HYDRALAZINE	6	r		
IFOSFAMIDE	6, 24, 48, 144	s		
INDOMETHACIN	48, 72	t		
LITHIUMCHLORIDE	120	u		
MERCURICCHLORIDE	3, 6, 24	v		
PAMIDRONATE	24	w		
PAN	168	x		
PAN	6, 24	y		
PAN	6, 24, 168	z		
SEMUSTINE	168	aa		
SULFADIAZINE	24	bb		
SULFADIAZINE	3, 6	cc		

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TABLE 5: GENERAL					
Atty. Docket No. 44921-5089WO					
Doc. No. 1793397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
12979	326.05	98.48	729.13	345.15	83.46
23314	-7.57	63.50	480.54	528.59	83.43
5461	161.65	48.19	368.42	210.09	82.70
9583	40.60	17.67	158.01	127.01	82.56
16982	59.51	36.53	506.74	577.57	81.34
1809	5.28	13.85	191.53	265.23	81.21
19184	59.98	26.06	191.02	128.18	81.04
24200	382.07	78.91	618.97	199.18	80.18
15003	13.42	14.74	154.63	217.73	79.83
2629	18.92	8.93	58.17	43.50	79.72
22321	82.69	25.99	192.94	130.47	79.58
15301	20.84	20.65	124.72	132.03	79.47
15032	280.18	50.93	183.93	78.32	79.33
7489	89.81	28.30	47.02	25.94	79.28
2242	2431.04	453.24	1658.86	711.96	79.26
3050	77.80	26.29	166.37	91.49	79.22
22681	170.38	56.88	497.37	377.15	79.20
24042	4.31	9.28	112.52	198.98	79.06
14425	191.57	51.38	315.84	117.32	79.05
15300	104.10	41.29	305.26	261.16	79.01
23651	487.82	171.51	1473.41	1227.36	78.44
15964	1274.63	262.79	824.24	343.96	78.27
16312	44.81	17.42	107.40	60.46	78.21
16168	305.21	53.33	588.32	425.68	78.12
5384	28.68	24.27	102.33	70.63	78.08
12978	92.29	28.22	178.30	79.32	77.90
21654	332.77	53.62	518.29	196.63	77.78
3874	934.64	159.07	672.84	188.60	77.60
3049	176.71	56.69	334.05	163.05	77.39
16314	33.02	22.70	103.37	64.81	77.39
23299	345.71	73.26	514.49	166.24	77.35
9166	13.09	10.08	40.42	28.18	77.33
14763	1.59	39.67	228.03	268.46	77.30
4479	133.60	62.59	233.57	86.27	77.27
15928	142.69	34.11	244.10	90.89	77.08
3941	229.39	59.58	325.62	88.12	76.99
28	540.29	128.18	342.30	188.50	76.94
14929	687.79	150.66	1358.82	807.54	76.87
22885	1229.56	342.00	1987.11	703.59	76.84
22765	15.12	10.37	52.20	40.27	76.68
19040	158.12	34.83	333.27	212.49	76.68
21239	98.57	31.29	190.62	93.31	76.57
2555	83.76	25.31	159.42	79.77	76.51
15051	558.01	156.42	953.70	424.38	76.38
22569	701.48	148.25	468.05	181.60	76.33
15299	73.40	22.15	164.49	121.44	76.17
20116	1.36	12.44	53.19	60.94	76.12
7299	141.75	59.67	363.99	279.53	75.86
11618	445.83	108.35	290.81	162.81	75.81
23868	113.35	64.90	514.43	654.54	75.65
812	164.76	29.18	118.06	38.83	75.63
23166	116.47	37.76	215.89	104.73	75.55
19723	63.30	24.96	147.23	109.39	75.53
2161	10.89	22.79	40.17	28.34	75.53
22592	195.01	88.25	453.16	291.73	75.50
21683	27.66	14.45	65.00	37.84	75.44

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TABLE 5: GENERAL						Atty. Docket No. 44921-5089WO	
						Doc. No. 1793397.1	
Identifier	NonTexMean	NonTexSD	TexMean	TexSD	LDAScore		
7540	135.61	39.51	269.18	167.73	75.42		
3121	1387.78	270.45	970.56	410.36	75.23		
17325	37.68	26.79	190.12	198.72	75.23		
4049	8.16	14.26	100.05	143.11	75.21		
24219	294.84	62.68	415.01	115.05	75.14		
7101	266.61	65.47	1024.56	1594.33	75.14		
21482	246.43	47.45	320.88	67.53	75.11		
21458	203.89	61.93	345.78	139.58	75.01		
1460	178.45	37.93	302.50	171.15	74.92		
23957	57.89	29.03	120.87	65.67	74.89		
12921	92.69	31.09	174.99	86.55	74.88		
24237	46.61	22.12	105.68	71.47	74.84		
20830	482.35	118.55	717.12	282.77	74.80		
14185	181.85	52.63	307.94	156.98	74.74		
3091	821.34	154.51	616.81	215.94	74.73		
6046	221.77	64.88	141.08	71.40	74.73		
10818	509.63	159.26	301.00	207.18	74.63		
18906	270.92	73.69	171.86	79.69	74.60		
17361	160.53	54.00	92.22	55.73	74.60		
574	297.07	48.04	543.78	340.56	74.58		
1529	305.18	51.69	224.24	69.41	74.56		
20161	30.38	21.73	80.33	56.50	74.54		
22152	-0.67	16.93	51.48	64.42	74.54		
21391	183.11	55.68	391.43	249.63	74.34		
20056	319.93	46.22	248.41	81.57	74.34		
5711	402.83	114.80	268.76	100.84	74.34		
16169	126.24	66.19	419.88	462.11	74.32		
7196	160.17	37.22	297.55	159.08	74.29		
13634	754.99	133.63	1123.83	475.68	74.29		
10659	111.21	36.66	239.07	166.99	74.28		
15089	162.94	57.42	271.19	109.36	74.26		
2628	8.82	14.55	37.93	39.15	74.22		
1521	7.84	37.91	80.00	74.26	74.20		
17524	1225.79	235.19	927.05	284.85	74.20		
14677	64.57	22.56	114.45	54.63	74.04		
17357	284.47	66.73	189.90	103.16	73.97		
15382	79.92	58.73	367.62	435.18	73.94		
1141	226.12	47.74	315.88	93.78	73.94		
3995	643.39	131.36	476.67	160.12	73.88		
6804	1354.29	374.19	830.60	415.24	73.82		
20694	1004.30	200.48	773.76	246.63	73.81		
8477	493.77	117.87	724.70	226.98	73.80		
13332	440.18	81.35	336.07	113.36	73.79		
2912	2775.27	619.46	2040.05	590.49	73.79		
8143	30.96	28.78	105.91	87.78	73.79		
8639	351.67	79.66	468.70	121.28	73.78		
354	191.57	43.15	335.31	175.98	73.77		
2702	261.10	53.61	363.77	115.07	73.74		
13411	857.90	304.76	508.64	242.77	73.71		
23261	1651.29	316.95	1185.07	374.72	73.69		
16775	1092.58	348.47	732.47	398.39	73.66		
10016	191.31	45.71	298.01	134.57	73.59		
353	154.16	43.72	275.53	149.36	73.59		
5295	199.26	56.55	318.50	126.31	73.55		
10015	215.25	41.54	323.40	147.43	73.54		

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**TABLE 5: GENERAL**      **Atty. Docket No. 44921-5089WO**  
**Doc. No. 1798897.1**

Identifier	NonToxMean	NonToxSD	ToxMean*	ToxSD	LDAScore
20458	377.19	83.99	263.38	95.28	73.52
23860	24.11	23.82	132.98	190.30	73.46
20848	474.69	80.77	708.43	261.80	73.46
9067	645.45	126.00	841.67	201.55	73.45
923	10.66	7.41	32.76	27.77	73.40
4291	317.92	87.25	202.30	99.83	73.38
18529	184.43	47.69	306.78	139.66	73.35
22626	66.24	25.65	191.03	161.08	73.32
3823	488.87	101.91	709.19	233.23	73.30
15663	179.56	40.22	269.94	97.24	73.29
22929	927.47	283.23	548.56	310.91	73.27
373	20.21	24.84	107.75	123.23	73.25
4952	97.10	31.18	160.25	66.14	73.23
2905	221.02	70.67	379.00	165.35	73.23
7127	301.01	84.77	195.82	87.14	73.22
20035	157.82	53.67	318.27	196.89	73.21
14424	40.56	38.11	216.48	294.45	73.19
1501	46.55	22.43	125.28	104.55	73.19
811	268.35	42.34	201.54	69.48	73.14
3610	1272.79	264.85	879.10	411.90	73.12
9053	249.79	41.36	182.96	58.86	73.09
23538	85.95	40.73	190.24	133.78	73.07
18337	1699.33	315.35	1238.46	390.84	73.06
15002	119.96	26.12	252.22	220.20	73.06
21147	365.33	62.56	285.83	76.45	73.05
8721	208.57	63.43	132.86	65.90	73.01
1462	364.98	75.98	659.63	429.84	73.01
11483	54.82	19.42	118.04	81.85	72.90
2348	545.81	197.73	349.07	201.06	72.86
1564	6.71	7.78	209.28	375.95	72.86
12467	60.46	20.47	103.84	48.93	72.85
6638	104.00	28.03	76.61	32.45	72.83
19031	50.08	27.00	116.79	84.17	72.83
1246	98.28	29.26	60.78	37.90	72.82
23872	30.55	27.67	146.46	207.24	72.80
19678	121.25	48.99	54.47	69.08	72.78
23512	1086.33	216.78	839.09	240.27	72.77
6321	458.69	127.59	644.50	219.13	72.75
22596	57.04	17.25	81.28	26.16	72.75
24431	50.52	15.50	151.16	210.56	72.73
15110	663.97	145.61	479.15	149.17	72.73
15892	12.32	15.49	44.12	34.64	72.71
14458	29.92	20.00	71.32	39.77	72.67
6641	402.83	66.65	309.63	82.93	72.53
1422	315.77	80.70	215.58	83.38	72.53
21443	90.69	31.63	155.73	92.87	72.53
8829	264.33	62.24	350.44	106.21	72.51
21632	27.74	33.70	87.38	68.91	72.48
24388	173.36	44.15	275.21	119.72	72.47
15851	171.96	68.96	332.47	267.49	72.38
15042	55.43	27.40	117.95	81.96	72.32
17908	49.38	21.99	125.62	121.11	72.32
15618	90.24	22.13	124.19	32.66	72.27
21318	41.50	23.94	72.71	32.13	72.27
6054	18.00	9.60	85.39	126.27	72.24

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TABLE 5: GENERAL					
Atty. Docket No. 44924-5089WO					
Doc. No. 1793397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	L.O.A.Score
1727	30.19	25.05	113.76	121.46	72.19
23202	169.96	36.51	126.76	36.17	72.16
22248	216.64	78.55	393.59	188.28	72.15
22612	487.17	110.76	359.48	126.14	72.14
17734	106.27	34.17	214.91	182.70	72.12
19235	1112.95	271.69	810.00	308.94	72.06
13618	96.22	26.36	137.92	45.79	72.04
19525	23.64	12.50	46.38	27.18	72.03
4584	76.41	22.50	109.66	36.31	71.98
22197	112.68	34.33	178.88	75.61	71.98
24762	1064.07	310.38	755.53	273.04	71.97
10985	1189.01	218.09	885.13	290.39	71.96
3145	466.94	133.08	330.71	144.92	71.93
20828	278.75	83.71	482.02	272.83	71.89
2395	172.58	47.67	175.81	100.28	71.86
13609	252.08	52.43	186.04	64.47	71.86
21339	29.51	15.60	53.28	32.70	71.78
3079	27.52	22.01	67.24	49.93	71.78
16321	219.91	42.72	273.17	55.96	71.77
4944	100.32	33.19	177.16	86.89	71.77
24568	162.64	51.57	105.85	46.68	71.75
3875	539.59	120.20	389.50	146.06	71.75
6382	117.04	33.24	171.65	55.00	71.73
3959	329.28	86.36	451.00	151.79	71.73
8795	14.06	10.71	26.30	13.30	71.72
17477	102.32	22.97	156.34	68.17	71.71
7700	74.32	20.26	138.95	92.87	71.68
17550	1380.51	319.12	1028.40	363.64	71.63
410	1155.16	215.31	918.14	252.51	71.63
17682	706.42	143.23	505.72	215.80	71.63
5897	20.54	16.83	45.41	23.66	71.63
4661	288.80	58.15	408.62	120.87	71.59
16521	266.79	60.39	378.60	127.02	71.59
13610	371.99	53.12	283.18	88.22	71.55
22554	565.54	122.08	428.04	154.62	71.49
11910	25.51	35.63	-5.43	31.38	71.47
15588	-4.65	25.14	33.98	37.77	71.42
5601	1014.34	210.01	731.23	341.39	71.42
5780	-23.15	27.07	32.19	62.08	71.38
21546	-79.60	43.55	44.91	170.38	71.38
15039	285.29	65.31	206.99	101.12	71.38
18300	483.67	133.71	307.50	148.77	71.38
14970	215.37	35.86	161.84	54.69	71.32
13151	635.29	173.43	1103.53	626.81	71.31
7197	180.11	57.15	296.88	139.25	71.28
21238	-24.44	33.42	22.20	43.34	71.27
25090	74.42	33.18	128.49	62.02	71.24
18564	225.23	44.60	181.56	58.17	71.23
1409	441.80	78.21	357.51	91.06	71.20
7903	526.91	184.33	331.16	186.75	71.18
24109	231.59	87.11	172.36	143.80	71.18
6416	108.18	41.02	234.59	190.53	71.17
2250	1462.04	256.17	1165.90	304.84	71.12
5867	157.83	35.87	210.76	63.63	71.11
17771	710.83	199.94	1089.58	460.00	71.09

TABLE 5: GENERAL					
Atty. Docket No. 44921-5089WO					
Doc. No. 1793397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
5494	62.28	23.39	104.89	53.79	71.08
18269	729.55	160.51	578.31	143.90	71.07
14996	459.09	95.27	332.24	132.64	71.03
24617	27.48	28.57	-0.27	26.14	71.02
23195	323.13	74.82	242.16	107.55	71.01
22656	113.29	44.19	184.20	80.34	70.99
8728	114.64	32.58	163.70	57.48	70.99
14664	56.90	24.89	82.06	31.36	70.98
22698	286.73	90.38	147.82	160.71	70.97
24053	35.17	15.83	56.32	29.72	70.97
8796	190.54	59.10	259.72	68.76	70.97
5474	783.73	210.50	556.59	211.13	70.96
22820	199.69	49.08	296.30	123.01	70.89
21796	666.75	117.72	898.08	374.38	70.88
25747	41.52	18.23	88.80	66.31	70.85
5443	12.36	13.98	34.29	27.55	70.84
12965	104.50	38.53	152.54	54.48	70.80
12332	602.96	147.89	428.95	204.34	70.77
3773	20.24	15.61	47.49	38.34	70.75
5990	310.53	65.78	375.84	76.70	70.73
18302	132.49	67.39	63.56	100.58	70.70
23964	9.67	12.94	24.20	18.71	70.68
9468	65.20	31.76	38.22	29.36	70.68
16631	14.50	12.00	57.40	80.51	70.66
21653	224.19	41.69	303.28	104.55	70.63
9097	272.42	76.73	194.27	78.59	70.61
11259	79.73	54.95	259.20	287.87	70.60
1081	515.94	100.86	394.77	126.28	70.58
18360	214.50	54.30	161.55	58.13	70.58
4789	35.91	18.80	60.76	25.85	70.56
1798	346.08	90.64	258.66	95.94	70.56
25089	69.92	34.04	119.62	57.66	70.55
24234	170.64	48.79	257.81	150.22	70.55
23270	197.31	46.26	264.06	80.46	70.54
8339	457.12	115.09	336.46	156.58	70.52
4119	104.13	29.50	142.73	41.65	70.50
18581	239.39	63.97	323.89	102.81	70.48
8188	429.99	130.68	311.19	123.41	70.46
17950	60.85	21.71	84.23	24.05	70.45
11967	1829.61	479.72	1293.20	638.27	70.45
5252	13.79	9.94	24.05	13.59	70.44
22928	235.05	79.02	162.79	64.64	70.38
16684	483.85	102.78	662.86	218.95	70.37
1463	562.00	123.95	959.70	610.46	70.36
8495	174.57	44.41	233.96	68.66	70.36
2195	94.72	37.50	60.02	37.89	70.35
3042	289.42	103.30	458.48	192.79	70.34
15330	96.55	24.69	69.31	26.59	70.32
12399	80.36	27.26	110.73	35.05	70.32
16351	67.79	22.25	109.53	54.61	70.27
3822	871.73	175.65	1184.82	469.53	70.26
21025	483.29	121.39	358.54	123.38	70.26
6548	93.61	35.75	138.74	52.86	70.23
12561	159.96	46.53	108.93	51.49	70.19
5481	36.03	51.29	102.88	72.89	70.19

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TABLE 5: GENERAL					
Atty. Docket No. 44921-5089WO					
Doc. No. 1793297.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
3430	414.54	95.45	587.65	251.37	70.17
26335	940.03	330.95	625.84	337.88	70.16
352	77.57	33.06	132.92	75.36	70.14
23044	213.44	34.48	253.69	53.74	70.13
17161	1069.69	220.67	1639.92	740.76	70.11
14352	179.82	26.18	211.25	38.48	70.10
21993	71.93	19.33	98.79	30.29	70.09
16756	165.09	40.66	231.09	68.53	70.09
7537	240.15	64.50	185.74	68.65	70.09
15986	336.87	70.00	240.73	102.05	70.07
17256	428.03	84.39	329.02	149.16	70.04
18151	1182.11	241.37	915.26	244.04	70.03
18354	372.44	129.56	548.59	224.71	70.03
19152	155.28	37.87	219.58	85.40	70.01
8314	44.66	24.23	401.40	1027.58	70.01
13222	132.87	25.87	162.46	38.58	69.99
3808	157.93	29.12	224.59	103.04	69.99
25705	432.30	81.33	560.17	181.12	69.98
4360	341.32	51.71	279.62	90.37	69.97
15904	48.14	15.72	70.45	28.37	69.96
3733	307.48	109.96	502.42	242.20	69.95
12349	248.84	51.51	206.79	57.13	69.94
6039	293.57	52.57	404.95	147.79	69.94
16394	529.95	207.80	998.31	642.96	69.92
1340	194.50	26.68	172.82	51.16	69.92
13393	68.65	39.60	120.92	67.73	69.91
28119	115.29	35.39	165.90	63.73	69.91
21471	-15.71	27.91	21.66	45.38	69.91
498	513.15	100.54	694.75	220.14	69.89
19	324.56	59.40	415.19	125.18	69.89
22599	40.60	18.16	65.55	34.14	69.84
7427	235.31	43.69	295.43	88.56	69.83
16520	82.42	40.09	151.39	91.91	69.83
15642	389.37	82.84	518.22	172.58	69.83
1430	171.08	83.75	102.96	99.73	69.82
7918	36.73	13.76	61.83	31.90	69.82
13633	276.86	77.72	463.55	259.47	69.80
7936	155.24	33.42	122.46	38.98	69.79
15004	132.61	42.50	344.40	385.03	69.78
15955	791.51	166.06	571.10	228.60	69.77
1478	366.90	66.96	278.05	99.94	69.75
7622	55.21	18.42	74.69	23.71	69.75
22796	7.01	12.41	21.99	21.24	69.73
17401	821.97	205.41	1398.10	790.55	69.73
7888	262.03	59.59	349.92	94.63	69.72
13392	181.47	36.33	245.35	76.20	69.70
22101	199.60	77.45	118.24	102.76	69.70
18	61.29	34.62	98.91	45.09	69.69
21657	407.16	79.73	529.18	177.19	69.69
20414	124.45	34.92	93.89	36.15	69.68
3852	40.90	23.02	60.54	43.90	69.64
12436	40.94	17.34	63.44	29.74	69.64
15011	90.81	29.75	122.02	40.98	69.63
3434	300.37	104.25	456.96	211.34	69.62
21444	10.25	27.61	65.55	77.70	69.62

**TABLE 5: GENERAL**      **Atty. Docket No. 44921-5089WO**  
**Doc. No. 1798897.1**

Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
3493	56.09	16.33	78.09	27.67	69.58
13727	133.95	45.99	86.22	54.51	65.58
17339	2512.73	596.97	1882.04	680.16	69.56
6518	108.28	26.66	143.55	38.12	69.55
14484	468.99	102.51	371.12	113.87	69.50
45	184.62	61.15	131.00	98.51	69.50
4235	383.35	65.78	479.39	109.87	69.47
2350	631.18	75.04	733.81	127.04	69.47
20816	359.20	71.33	589.66	361.06	69.47
20448	51.14	15.80	96.53	91.69	69.45
3608	354.31	96.17	240.45	122.08	69.45
20829	754.23	187.16	1139.64	525.74	69.43
14388	133.84	46.32	189.57	73.63	69.41
13974	269.51	60.19	455.96	331.84	69.41
13611	289.40	97.62	194.81	124.78	69.39
9452	109.85	33.54	243.69	304.19	69.39
19679	744.23	156.00	548.50	220.11	69.38
23471	80.62	27.27	134.19	61.98	69.38
15596	200.04	61.45	269.73	83.16	69.38
17159	662.06	139.21	916.50	373.05	69.37
9114	907.26	198.07	711.93	216.95	69.36
7690	188.30	76.58	286.44	101.61	69.30
4462	896.55	240.26	700.53	283.12	69.30
15146	117.66	45.74	219.43	151.19	69.28
4747	52.09	18.56	76.30	30.54	69.28
4463	171.78	48.48	116.71	64.25	69.26
21275	208.39	53.25	293.29	120.48	69.26
22537	314.16	116.85	217.64	134.70	69.24
21015	224.01	149.40	523.06	502.39	69.21
14184	104.95	35.03	152.30	77.88	69.21
16859	113.00	39.98	171.46	70.52	69.20
13359	18.79	19.20	41.55	29.30	69.17
24192	65.10	27.46	107.06	63.04	69.17
22357	537.91	143.42	683.30	219.11	69.15
22540	1928.78	500.80	1396.93	518.89	69.15
15111	1008.00	256.31	739.45	278.04	69.15
23128	629.03	117.68	522.92	126.85	69.13
9905	702.23	115.37	558.07	156.97	69.13
23387	23.75	24.01	57.01	48.92	69.12
21797	316.03	77.43	447.83	179.03	69.12
20457	401.15	78.89	312.93	100.71	69.12
13954	1425.24	337.03	1039.20	391.69	69.12
2059	134.19	33.99	173.66	52.56	69.11
21125	163.43	45.61	120.34	59.14	69.08
4048	-12.32	8.61	25.98	74.75	69.08
13349	122.00	33.87	171.03	54.95	69.08
20086	103.42	54.54	186.02	112.44	69.07
7414	177.49	39.38	246.64	72.25	69.07
4327	84.49	26.30	133.01	68.89	69.07
19011	389.45	84.42	492.01	130.94	69.04
6384	55.77	19.77	79.31	27.28	69.03
8221	192.95	91.60	123.84	72.63	69.02
11876	100.42	32.61	145.49	59.19	69.00
275	540.79	117.63	450.26	289.26	69.00
19940	19.25	13.33	32.95	17.53	68.99

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TABLE 5: GENERAL						Atty. Docket No. 449241-5089WO
						Doc. No. 1788897.1
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore	
21895	415.77	107.68	527.63	122.68	68.99	
6674	2569.26	592.43	1970.28	559.33	68.97	
4330	519.93	146.26	393.68	177.88	68.97	
1698	59.46	33.76	154.33	156.35	68.96	
6927	351.13	88.63	276.07	87.17	68.95	
15879	389.05	88.44	309.88	89.07	68.94	
17269	669.21	164.65	510.44	183.69	68.94	
809	38.57	18.55	73.18	50.10	68.93	
25567	429.75	132.83	636.76	280.62	68.91	
6711	46.47	22.83	68.95	25.01	68.91	
25777	370.17	112.15	585.45	351.28	68.90	
22801	1309.01	233.61	1102.68	241.27	68.88	
17447	912.03	226.33	708.62	297.79	68.88	
1603	652.04	149.41	516.80	165.06	68.85	
20460	363.41	114.33	257.61	112.54	68.84	
21145	216.97	60.61	173.14	61.10	68.83	
25453	225.18	45.75	181.00	63.32	68.81	
14670	1156.99	219.65	1505.97	540.37	68.80	
19623	56.27	29.98	87.15	39.31	68.80	
12716	167.13	43.68	133.50	41.78	68.80	
24236	75.95	22.54	104.28	32.01	68.79	
15617	18.52	33.89	39.26	21.38	68.79	
3925	498.78	107.84	390.92	113.69	68.77	
20449	39.97	25.35	119.71	151.16	68.76	
21390	89.77	28.23	115.10	33.69	68.76	
23514	434.32	164.14	307.02	151.33	68.74	
20849	259.38	58.40	370.11	145.72	68.74	
794	224.09	52.71	162.86	64.32	68.71	
4592	183.27	30.19	222.63	53.46	68.70	
13614	325.22	70.14	423.70	138.23	68.70	
12673	32.94	15.97	60.47	35.35	68.69	
3125	347.43	89.73	270.34	103.82	68.67	
4232	131.63	36.97	170.35	127.98	68.67	
1399	187.08	41.04	289.41	156.72	68.66	
13930	114.32	44.14	212.08	140.70	68.65	
5689	9.09	13.75	27.68	24.99	68.63	
2370	1158.46	172.59	949.24	224.94	68.63	
4933	93.92	113.34	358.13	386.59	68.63	
406	374.38	68.18	306.59	91.47	68.62	
22957	165.92	62.59	266.91	150.55	68.62	
2768	2026.25	370.26	1657.86	463.04	68.61	
24197	243.13	77.12	185.53	85.38	68.60	
16650	242.10	65.10	338.01	127.40	68.57	
8085	36.42	17.42	58.09	26.97	68.57	
1712	167.50	36.63	216.60	72.08	68.57	
5565	407.17	100.35	305.41	133.21	68.56	
16883	1543.18	301.38	1229.72	308.97	68.55	
13622	45.42	26.78	87.87	76.11	68.55	
17807	711.63	133.84	948.59	316.04	68.55	
8496	39.06	20.93	64.65	32.09	68.53	
11559	615.91	118.47	505.06	115.82	68.53	
19094	1013.42	192.17	1274.36	327.89	68.53	
7584	99.66	69.21	216.92	170.84	68.53	
457	268.02	49.06	378.26	164.79	68.53	
21105	323.39	54.03	270.87	64.06	68.52	

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**TABLE 5: GENERAL**      **Atty. Docket No. 44921-5089WO**  
**Doc. No. 1798997.1**

Identifier	NonTexMean	NonTexSD	TexMean	TexSD	LDAScore
18900	449.75	84.06	557.56	130.48	68.48
16709	858.46	172.57	709.82	176.49	68.46
1993	26.13	15.23	53.08	37.27	68.43
13348	116.50	39.71	170.35	84.06	68.43
11454	223.14	54.78	315.07	133.93	68.43
18606	608.53	116.39	789.92	267.15	68.43
2986	39.62	12.73	54.78	18.98	68.41
15644	1338.83	225.09	1588.45	345.24	68.39
22541	3613.59	853.73	2681.23	879.66	68.39
17905	902.96	243.00	654.49	232.60	68.38
408	201.66	67.43	144.70	78.36	68.37
21409	86.43	35.21	119.21	45.92	68.37
22543	721.16	195.27	540.47	258.13	68.36
3863	214.88	78.45	158.64	93.71	68.36
21596	100.77	27.25	132.16	47.14	68.33
1583	25.58	12.08	46.81	25.12	68.32
8917	41.59	14.82	56.19	17.88	68.31
17324	371.15	66.13	297.98	105.05	68.30
5199	641.61	169.29	484.54	199.84	68.29
11164	532.49	129.79	382.15	153.36	68.28
10887	76.37	24.73	54.29	25.72	68.28
15540	36.28	11.51	64.56	42.69	68.27
4949	1162.93	273.54	892.52	329.00	68.26
21024	596.29	101.41	489.27	121.68	68.26
19085	70.29	20.84	101.53	44.09	68.25
25718	380.48	63.33	465.71	138.80	68.25
3981	53.40	27.49	166.56	218.99	68.25
19939	176.96	53.69	235.92	70.52	68.24
21305	438.34	113.88	332.58	104.75	68.23
22833	431.45	106.61	540.94	147.67	68.23
13310	116.08	48.35	197.32	125.83	68.22
19187	102.48	30.70	135.61	50.44	68.21
18011	27.06	22.52	56.30	38.43	68.21
24895	78.92	42.28	60.83	59.54	68.21
11563	52.55	31.11	94.44	49.63	68.20
2506	78.97	20.73	98.29	25.44	68.20
10434	30.66	16.63	56.30	35.67	68.19
23546	749.61	138.38	631.19	195.15	68.19
17104	430.01	79.30	558.85	188.65	68.18
12587	236.86	55.30	189.70	64.51	68.17
17316	70.29	31.03	47.27	32.31	68.17
10464	136.34	32.97	104.50	38.05	68.15
15185	154.81	45.05	251.81	139.06	68.15
22689	44.68	18.28	64.87	29.10	68.14
5855	74.85	27.42	52.36	35.41	68.14
2140	160.37	40.29	131.23	57.33	68.11
1510	780.11	196.05	591.05	213.64	68.11
15313	6.84	9.54	24.57	23.36	68.10
8972	26.33	18.24	47.84	25.93	68.10
2888	2111.78	515.11	1569.20	595.26	68.10
23834	68.94	19.78	90.90	31.53	68.09
3082	244.35	47.01	302.78	72.37	68.09
3487	738.89	191.34	545.12	221.95	68.09
16476	738.64	159.14	630.49	196.22	68.09
5819	230.72	47.15	189.99	56.21	68.08

**TABLE 5: GENERAL** Atty. Docket No. 44921-5089WO  
Doc. No. 1798397.1

Identifier	NonTexMean	NonTexSD	TexMean	TexSD	LDAScore
1942	12.95	13.20	45.54	48.73	68.08
514	4.47	50.55	52.66	56.22	68.06
19768	683.61	138.87	883.43	263.72	68.06
5183	204.36	51.85	284.20	109.64	68.06
24375	107.65	26.73	157.63	66.73	68.05
6059	199.74	47.55	169.09	54.88	68.04
12937	20.23	21.04	62.89	58.77	68.04
3245	97.45	32.09	132.43	48.29	68.02
19469	376.00	72.62	300.86	98.78	68.02
22696	72.56	48.08	25.09	39.70	68.02
4355	116.49	44.14	163.32	82.62	68.01
21579	110.85	35.32	153.51	68.22	68.00
1431	521.93	166.42	374.89	194.57	67.99
9673	66.91	27.02	44.90	26.55	67.99
20257	137.10	42.30	102.53	48.53	67.99
12961	185.53	42.22	151.73	41.05	67.97
22538	338.12	80.15	255.39	90.87	67.97
7243	56.76	22.51	79.45	28.02	67.96
5634	64.78	29.00	96.85	47.59	67.96
17438	62.59	33.01	31.95	40.59	67.96
1581	70.58	17.49	93.61	30.37	67.96
25379	75.47	18.52	100.15	31.59	67.95
2153	153.35	49.73	361.58	346.41	67.94
7499	17.61	8.98	28.61	16.07	67.94
6102	150.29	40.49	187.75	46.70	67.94
3878	479.08	106.98	389.02	107.79	67.93
20122	174.65	39.83	214.44	52.37	67.93
6828	122.12	53.45	207.48	104.75	67.92
11455	106.22	31.64	162.96	86.72	67.92
16058	146.84	40.61	225.40	102.56	67.92
23567	42.81	36.02	114.42	124.08	67.90
19998	290.74	86.07	214.07	102.16	67.90
24054	25.17	14.49	39.46	20.61	67.89
22352	139.84	54.27	253.98	211.46	67.89
21146	119.46	36.34	92.66	39.95	67.89
11791	136.74	46.57	173.47	50.00	67.88
19086	102.38	32.93	153.92	65.34	67.87
13111	235.97	68.33	187.10	77.46	67.86
14959	595.43	107.90	761.75	241.85	67.86
22103	222.38	50.69	294.15	83.02	67.84
1454	110.82	42.51	160.57	70.87	67.83
1844	167.38	35.91	216.33	60.90	67.83
13023	110.03	149.11	607.48	946.55	67.81
22487	34.23	15.90	60.56	35.71	67.80
7543	268.34	96.90	185.92	86.13	67.80
3107	779.30	164.38	696.29	236.36	67.80
8975	102.89	42.50	68.46	48.06	67.80
825	59.44	21.82	42.35	25.50	67.80
4473	192.83	43.69	148.92	66.25	67.78
18109	15.28	14.01	39.23	36.39	67.78
2845	651.40	103.22	768.87	160.95	67.76
11974	247.17	76.60	176.82	86.10	67.73
3547	14.36	11.57	25.42	14.68	67.73
22931	87.38	47.83	52.96	42.09	67.72
7161	46.95	14.21	64.96	24.05	67.69

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TABLE 5: GENERAL			Atty. Docket No. 449241-5089WO Doc. No. 1793397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
9061	1135.34	236.25	942.16	326.87	67.69
12331	618.37	134.26	483.61	182.86	67.69
13962	523.52	110.90	438.13	148.62	67.68
24277	134.73	41.18	181.65	55.29	67.67
14790	176.36	78.47	102.86	72.99	67.67
18528	361.23	136.11	589.25	331.81	67.66
19665	81.08	33.19	142.12	76.68	67.66
14242	32.67	14.37	49.07	20.85	67.64
17407	1713.79	374.66	1443.40	337.67	67.64
6765	820.06	183.88	653.70	231.97	67.62
9514	675.01	129.64	570.37	132.48	67.62
22602	334.13	94.17	237.80	117.01	67.57
19822	1669.92	376.25	1281.37	430.75	67.56
9699	58.47	18.16	42.68	19.82	67.55
12812	99.34	33.83	74.64	38.83	67.55
24566	200.15	82.45	135.98	77.12	67.54
17499	24.56	23.09	55.11	35.51	67.53
18447	1233.88	274.38	958.23	329.75	67.53
21014	142.85	40.94	210.35	117.97	67.52
2536	406.73	114.26	323.04	150.73	67.51

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TABLE SA: AGYCLOVIR Timepoint(s): 24, 168 hrs						Atty. Docket No. 44921-5089WO Doc. No. 1793927.1	
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore		
25419	159.17	64.32	38.16	8.66	99.48		
25415	169.94	67.00	36.69	10.41	99.48		
1872	723.76	219.40	182.16	67.65	99.36		
17198	814.88	264.22	145.60	82.51	99.14		
17567	1172.88	345.04	2623.71	250.73	98.97		
14959	616.48	139.00	1288.62	137.24	98.84		
20945	896.18	242.10	1896.41	180.47	98.80		
16245	387.31	114.26	41.23	45.70	98.80		
10887	73.83	25.90	17.83	4.94	98.67		
4222	544.00	97.71	1042.92	176.22	98.67		
19161	1064.06	296.13	2360.57	327.19	98.63		
15626	1281.17	347.65	3250.17	648.92	98.58		
11849	701.03	165.94	1608.51	320.36	98.50		
20872	832.75	216.84	1896.38	376.01	98.50		
15875	1175.87	375.74	2630.93	347.24	98.45		
10498	1085.24	333.50	2568.66	334.73	98.45		
20884	639.33	257.31	46.55	54.58	98.37		
13151	702.17	319.88	2212.94	511.24	98.32		
18611	1409.99	440.83	2945.57	350.22	98.28		
20885	538.89	188.67	83.65	54.88	98.28		
16244	40.33	21.14	-0.26	5.01	98.24		
16918	1172.71	382.43	2977.59	742.16	98.15		
3027	1121.82	319.93	2267.04	262.71	98.15		
20056	309.42	59.71	118.77	41.29	98.11		
16205	932.31	252.05	1896.76	307.48	98.02		
20812	1107.00	305.73	2296.29	293.56	97.98		
14384	375.87	76.79	604.80	58.76	97.94		
24615	809.56	214.82	1799.64	368.34	97.94		
17524	1175.90	282.46	541.39	119.09	97.85		
20839	1037.63	274.92	2191.65	391.42	97.85		
18250	1088.85	307.06	2058.50	257.28	97.77		
22846	1492.71	284.92	855.87	120.77	97.68		
3026	512.85	99.35	933.31	159.19	97.64		
13647	864.69	256.24	2095.09	431.00	97.64		
17563	1195.18	331.95	2542.06	387.04	97.59		
17473	422.91	93.66	796.08	169.41	97.59		
20746	673.25	126.38	1181.14	211.43	97.59		
19359	1061.61	314.08	2336.47	601.88	97.51		
15201	1478.32	513.09	3558.35	808.75	97.47		
15052	1433.93	492.46	3597.61	980.31	97.42		
4490	76.73	73.42	270.49	135.30	97.42		
2696	773.00	225.06	1860.28	390.37	97.42		
22552	313.47	90.91	645.46	155.87	97.38		
1694	1139.80	326.74	2255.77	345.62	97.38		
19824	224.99	67.29	73.65	27.54	97.34		
16333	133.41	38.84	45.56	15.40	97.16		
16150	495.73	119.09	217.15	50.78	97.16		
15928	157.91	59.34	354.44	52.65	97.16		
15335	424.77	103.56	772.54	127.56	96.99		
15202	788.60	313.98	1866.58	266.92	96.99		
18749	116.41	42.26	34.59	11.87	96.95		
16164	1075.08	276.06	1925.19	293.15	96.86		
20088	384.13	78.71	185.57	40.67	96.78		
23989	1057.77	294.07	466.66	116.46	96.74		
24048	695.95	214.73	269.65	68.66	96.65		
4254	144.21	377.79	15.39	14.62	96.65		

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TABLE 5A: AGYCLOVIR					
Timepoint(s): 24, 168 hrs			Atty. Docket No. 44921-5089WC		
			Doc. No. 1793397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
24577	1170.09	364.08	2400.41	380.56	96.65

**TABLE 5B: ACYCLOVIR**      **Atty. Docket No. 44924-5083WO**  
**Timepoint(s): 6 hrs**      **Doc. No. 1798397.1**

Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
2572	1079.22	272.72	292.63	34.53	99.96
657	325.86	85.70	825.82	55.34	99.96
15174	582.65	154.01	1160.30	40.29	99.96
22060	120.39	46.22	489.85	39.32	99.87
21151	108.89	64.20	1068.35	133.62	99.87
17546	542.45	131.44	1300.18	82.92	99.83
8477	528.52	158.91	1301.77	46.70	99.83
16993	147.03	72.47	5.04	12.16	99.79
10667	41.39	38.71	-236.50	27.34	99.79
3822	915.99	266.90	2473.92	69.91	99.74
17157	50.71	97.99	182.37	23.19	99.70
4532	266.41	75.57	62.22	7.77	99.70
15004	160.24	140.85	1576.85	132.63	99.70
4832	149.39	47.92	32.65	11.70	99.70
11836	219.06	64.52	69.22	8.46	99.61
24390	165.64	111.19	-250.24	60.63	99.61
24200	421.04	138.48	1131.90	38.93	99.61
15002	137.74	85.32	904.65	69.55	99.61
3713	1141.71	271.69	457.32	36.48	99.57
6778	109.70	31.47	262.53	25.12	99.57
7936	149.06	36.24	49.64	5.41	99.57
13542	446.95	133.65	59.60	28.78	99.57
22385	107.82	53.29	22.50	3.64	99.57
20700	74.63	363.62	3153.73	549.12	99.57
15190	1801.09	1118.86	7715.59	404.27	99.53
20698	-0.10	63.70	407.01	114.99	99.53
9757	408.35	98.75	159.69	13.35	99.53
15077	87.92	41.66	6.25	3.82	99.53
12301	58.09	29.22	219.75	30.79	99.53
3304	881.73	218.32	247.94	48.65	99.53
24041	11.98	28.98	230.57	61.01	99.53
19780	47.97	40.89	251.97	31.79	99.53
12899	-9.55	17.51	146.15	30.06	99.49
23387	29.40	30.63	203.21	32.17	99.49
20699	86.60	192.11	2061.40	288.42	99.49
608	-48.26	30.91	77.22	17.44	99.49
8874	118.63	59.95	395.15	33.95	99.49
5475	445.78	146.14	115.95	22.16	99.49
985	21.00	43.98	281.44	50.96	99.49
24243	258.96	69.54	71.35	13.38	99.44
6057	104.47	44.96	358.76	52.20	99.44
1892	-6.30	35.30	58.25	24.52	99.40
275	519.62	162.35	80.95	30.90	99.40
2695	210.32	124.89	613.77	27.62	99.40
7804	1764.46	393.34	898.61	69.66	99.40
20701	32.96	54.09	404.95	132.78	99.40
12420	23.45	48.04	-131.74	28.29	99.36
15003	33.26	83.63	776.16	111.38	99.36
24564	568.95	174.41	66.56	19.02	99.36
24246	300.44	96.46	678.79	40.80	99.36
9423	939.03	252.01	2035.02	137.31	99.36
23151	380.64	125.08	82.73	15.55	99.36
9071	48.03	25.31	2.95	1.90	99.36
2905	244.95	103.58	780.68	56.20	99.36
20856	55.56	46.37	-5.93	3.53	99.36

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TABLE 5B: ACYCLOVIR			Atty. Docket No. 44921-5089WO		
Timepoint(s): 6 hrs			Doc. No. 1798397.1		
Identifier	NonTexMean	NonTexSD	TexMean	TexSD	LDAScore
5931	182.37	66.37	9.61	8.36	99.36
24042	18.74	67.93	772.42	198.67	99.36
17765	1285.78	452.80	2557.67	63.52	99.31
17470	102.21	54.04	410.26	61.20	99.31
2010	32.91	314.74	355.60	90.97	99.31
20848	510.27	150.82	1095.65	24.39	99.31
17591	385.36	90.04	744.25	62.21	99.27
1340	192.09	49.88	96.02	6.73	99.27
7806	51.84	19.09	122.32	8.65	99.27
7493	78.12	36.73	174.58	4.92	99.27
20035	180.04	101.54	817.96	80.03	99.23
19657	3.30	17.67	125.30	19.29	99.23
24563	309.99	99.44	4.82	17.01	99.23
22453	171.10	46.39	60.55	10.10	99.23
23995	161.66	57.89	380.58	31.88	99.23
15191	1989.62	1126.31	8988.79	1157.81	99.23
11326	332.40	95.69	94.87	14.33	99.23
7586	793.77	201.98	306.02	29.21	99.23
2392	154.00	87.41	1138.50	400.02	99.23
4205	222.66	72.63	591.81	54.59	99.23
8245	54.69	20.70	113.91	5.63	99.23
16324	194.65	61.24	42.04	11.21	99.23
12404	105.63	62.52	662.04	167.20	99.23
7639	753.14	166.01	339.14	44.82	99.23
20895	331.67	100.56	50.78	24.52	99.19
22018	158.66	41.98	360.67	50.74	99.19
3823	524.10	147.80	1250.81	97.60	99.14
6477	13.58	161.23	99.71	26.48	99.14
223	11.18	17.65	124.61	25.10	99.14
15146	130.31	69.77	744.71	139.52	99.14
25069	134.29	80.66	25.21	12.36	99.14
3431	1503.29	617.93	3867.63	202.46	99.14
3271	576.75	119.79	239.69	44.71	99.14
6054	26.29	47.50	386.77	134.53	99.14
20202	627.69	194.14	49.29	62.88	99.14
25546	473.74	139.13	145.65	40.29	99.14
19781	113.50	55.43	454.62	115.29	99.14
22488	58.52	53.30	334.10	50.62	99.10
10281	168.73	157.24	1702.50	591.27	99.10
9452	125.58	75.70	1560.61	720.48	99.10
2153	182.83	143.86	1201.51	175.46	99.10
13745	27.62	27.50	297.57	96.36	99.10
1218	198.28	37.55	92.30	12.70	99.10
15042	63.76	42.44	353.57	60.19	99.10
9521	95.05	24.96	222.10	33.80	99.10

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TABLE 5C: ADR Timepoint(s): 120, 168 hrs			Atty. Docket No. 44921-509WO Doc. No. 1793397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LPAScore
1688	5353.71	3830.70	26.75	39.23	99.44
25469	1577.10	747.53	25.91	13.98	99.44
1684	2831.22	1612.49	24.53	31.27	99.44
17829	2235.92	1102.19	58.14	58.70	99.44
25468	2186.32	1123.33	11.47	13.96	99.44
26150	783.82	532.35	-38.06	15.15	99.40
1687	1894.26	855.11	45.95	32.94	99.31
1685	9226.22	7079.05	58.61	94.83	99.31
1689	4411.94	2221.14	43.26	28.59	99.31
17832	1976.64	870.20	17.22	14.67	99.18
19358	792.56	328.04	6.04	46.93	98.71
18907	102.84	49.44	17.51	7.82	97.33
25467	636.86	169.13	1263.84	257.87	97.25
4011	457.30	195.33	953.88	244.47	96.78
14199	71.52	35.30	26.74	5.48	96.09
2852	49.29	27.79	19.72	2.87	95.92
21140	109.12	47.83	38.53	9.71	95.83
4594	63.32	30.73	22.33	5.88	95.44
7089	102.25	41.59	48.02	7.26	95.40
2984	582.52	185.78	258.99	70.15	95.27
1831	49.81	23.36	10.63	6.34	94.67
25705	455.64	115.95	612.52	59.36	94.45
16109	414.49	75.48	556.38	45.14	94.28
11165	529.31	155.75	250.39	51.44	93.98
19237	77.59	39.42	10.97	14.64	93.68
16401	1239.09	805.30	2322.72	497.80	93.68
109	547.11	293.37	1881.21	571.81	93.63
4312	77.34	39.04	127.17	10.27	93.51
16400	580.43	474.95	1090.34	298.55	93.42
18794	138.50	77.18	48.95	11.54	93.38
7489	81.80	32.11	25.62	12.02	93.34
2586	52.04	30.18	14.65	5.97	93.04
17742	1059.53	304.09	1669.92	253.17	92.99
956	54.64	39.22	1.90	10.80	92.78
17563	1201.38	349.79	1590.38	101.68	92.69
2125	78.10	82.13	-4.59	19.58	92.69
24844	32.09	22.37	8.57	2.19	92.65
16676	38.73	27.29	17.84	2.42	92.61
19189	60.60	62.41	14.86	7.74	92.61
16521	285.39	89.91	428.27	70.75	92.56
14430	34.74	32.18	3.43	3.27	92.48
1301	325.54	286.68	14.24	17.87	92.43
21006	55.98	36.26	16.33	6.58	92.39
23778	69.71	34.49	24.74	8.89	92.26
2812	193.71	46.19	284.99	38.81	92.22
16407	459.56	105.59	825.37	208.72	92.12
16426	280.85	109.78	118.35	49.48	91.79
24232	160.98	60.26	72.06	20.28	91.66
6059	193.61	50.50	116.52	21.50	91.40
17234	634.83	173.83	432.41	36.23	91.27
13025	335.88	84.38	224.82	24.51	91.23
20757	411.95	220.62	771.74	157.51	91.09
10076	105.84	50.96	140.17	10.04	91.06
4010	961.35	403.18	2024.17	546.67	91.05
22220	147.73	137.94	463.05	162.91	90.96
9644	-4.86	27.32	39.61	11.58	90.93

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TABLE 5C: ADR		Atty. Docket No. 449241-5089WO			
Timepoint(s): 120, 168 hrs		Doc. No. 1798397.1			
Identifier	NonTexMean	NonTexSD	TexMean	TexSD	LDAScore
8597	240.84	58.03	315.06	30.21	90.89
16582	56.67	19.30	29.31	5.28	90.89
1321	510.50	316.91	1496.60	371.84	90.88
14337	211.54	44.52	148.64	18.05	90.84
19191	1011.62	281.12	631.62	94.67	90.76
20716	652.51	142.58	1029.68	128.61	90.75
8017	188.58	76.89	406.11	152.05	90.68
18502	670.14	243.60	313.44	111.24	90.63
2782	214.23	97.42	522.66	132.70	90.62
13354	88.85	57.76	34.85	9.49	90.50
22896	62.39	50.49	-5.66	12.94	90.50
4242	749.55	193.32	1337.17	268.80	90.49
12660	71.28	22.64	44.42	5.74	90.46
15892	18.01	22.79	36.39	7.65	90.46
25517	39.47	33.13	2.75	7.99	90.41
22697	59.68	40.43	15.77	10.73	90.33
16448	129.58	38.04	43.90	19.88	90.32
1058	75.84	35.86	30.65	8.83	90.24
7863	1200.90	307.30	1386.51	55.05	90.24
11967	1725.17	550.50	1088.97	237.35	90.20
516	55.59	33.01	17.20	9.40	90.11
25736	24.77	16.54	7.84	4.16	89.98
6544	53.15	110.52	379.03	173.46	89.89
21651	32.42	26.38	7.38	3.39	89.85
16581	39.86	19.57	17.01	3.68	89.72
2607	218.90	50.79	175.06	11.54	89.55
15247	637.26	192.10	1113.60	210.08	89.41
6691	119.56	54.62	32.51	16.76	89.41
20702	300.67	70.50	198.62	33.60	89.38
10109	1044.97	289.50	1362.38	117.72	89.34
24040	557.97	233.98	196.88	87.97	89.29
1169	90.18	28.72	92.58	4.98	89.21
5421	279.85	96.20	162.53	31.31	89.21
19244	1224.80	382.60	1678.75	173.86	89.17
3015	2307.62	994.19	2930.38	184.09	89.12
21695	60.82	36.14	4.02	14.39	89.03
11218	102.70	37.49	47.65	19.31	88.95
21766	286.32	76.11	204.08	26.91	88.95
494	698.84	215.82	1186.69	207.80	88.86
24528	61.08	25.93	19.77	6.13	88.81

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TABLE 50: AY Att. Docket No. 44921-5039WO					
Timepoint(s): 360 hrs Doc. No. 1792397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
6360	7.76	5.80	30.12	3.08	99.36
18826	1069.51	321.45	473.21	31.01	99.32
24886	1264.06	371.77	2165.64	63.29	99.27
6517	233.00	158.96	437.46	12.19	99.19
16576	111.85	41.47	67.47	0.61	99.19
22846	1490.00	287.46	852.52	44.29	99.10
2708	383.37	87.00	425.82	1.07	98.97
14349	413.99	144.50	244.25	2.46	98.97
13023	187.03	420.15	-22.68	5.88	98.85
6585	653.17	368.20	239.73	12.54	98.76
15093	35.54	16.49	-7.39	3.34	98.76
25066	136.51	58.55	34.09	4.82	98.72
21796	696.51	210.24	1145.40	47.75	98.67
3610	1195.23	334.91	780.10	28.06	98.67
24236	80.80	27.74	39.65	1.30	98.67
16156	858.19	319.87	3220.95	1137.23	98.59
17672	2630.76	734.18	3325.88	12.22	98.59
472	658.60	175.52	1275.16	135.82	98.59
15462	86.01	35.25	28.41	2.70	98.55
10159	7.63	18.34	30.64	0.79	98.55
457	284.29	87.14	421.47	22.09	98.42
22093	-21.77	38.66	56.32	5.98	98.37
5212	189.25	67.72	0.93	13.47	98.33
11368	20.04	24.02	29.17	0.30	98.29
22731	24.04	24.97	9.37	0.65	98.29
23313	404.59	87.09	292.34	2.67	98.29
25178	4.72	6.91	30.15	9.22	98.25
11561	389.44	87.17	225.68	12.21	98.25
14120	740.64	221.38	1485.37	218.95	98.20
4622	608.46	110.69	956.12	79.60	98.20
12894	141.35	34.03	72.48	5.99	98.12
3447	33.98	17.04	11.74	0.97	98.03
1410	99.49	46.40	23.57	5.02	97.99
22103	235.14	64.79	449.04	43.64	97.99
14185	204.58	95.56	321.83	10.61	97.99
24770	233.44	86.68	44.57	16.38	97.95
21044	24.56	22.71	-11.37	2.16	97.95
24721	203.93	53.62	144.06	2.18	97.95
20184	11.29	9.18	20.17	0.35	97.95
6062	182.74	59.18	106.49	1.72	97.90
16172	467.00	120.07	308.58	10.28	97.86
19731	225.58	214.69	63.47	15.21	97.82
16155	1075.32	410.99	3024.24	951.97	97.82
5425	85.43	33.27	153.80	5.81	97.82
1463	620.25	296.25	1592.90	480.18	97.78
2696	777.90	238.27	1766.44	260.04	97.78
2126	223.21	75.66	478.73	56.24	97.78
16245	384.42	117.13	589.67	20.00	97.73
4683	211.56	40.44	323.17	13.38	97.73
11590	276.38	78.94	238.32	1.35	97.69
556	82.41	35.72	33.35	5.40	97.69
10241	67.50	27.73	4.65	11.47	97.69
275	516.42	162.40	1038.56	193.69	97.65
10784	24.89	30.12	-21.79	6.29	97.65
6523	30.10	14.87	8.53	1.41	97.60
4467	656.82	156.93	1236.28	198.60	97.60

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TABLE 5D: AY		Atty. Docket No. 44921-5089WO				
Timepoint(s): 360 hrs		Doc. No. 1798397.1				
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore	
24042	21.86	84.61	58.64	10.50	97.56	
15135	706.76	182.37	1034.39	31.17	97.52	
6790	63.12	24.62	19.35	3.71	97.52	
6743	1405.82	280.92	2262.37	206.08	97.52	
6351	45.29	26.36	88.65	2.94	97.48	
18942	-11.45	10.37	24.19	16.98	97.43	
6726	393.51	104.57	242.70	10.50	97.43	
9808	30.77	14.74	50.69	1.63	97.39	
21078	567.53	143.04	363.30	11.51	97.39	
22619	371.47	90.93	316.17	2.78	97.39	
1058	75.62	35.90	24.89	3.27	97.39	
22692	209.08	63.65	106.95	5.50	97.39	
21914	404.11	71.79	635.41	66.12	97.39	
22063	68.58	25.03	47.50	0.52	97.35	
1162	10.60	37.16	138.81	40.04	97.35	
15224	689.92	152.18	1138.23	103.80	97.35	
24178	2.75	9.42	20.42	4.02	97.31	
20891	140.77	49.29	78.20	3.12	97.31	
17393	145.61	59.87	87.56	1.63	97.31	
17061	557.85	95.17	904.28	161.35	97.22	
21656	54.49	25.08	22.60	1.43	97.18	
23651	656.34	623.55	2317.09	936.44	97.18	
2357	76.01	23.05	69.48	0.72	97.13	
18130	378.79	74.65	591.90	50.88	97.13	
23898	10.17	6.54	30.37	7.27	97.13	
9363	89.83	29.45	184.93	13.77	97.09	
2920	78.42	29.88	124.28	3.10	97.09	
21930	587.55	127.69	1108.70	256.19	97.05	
12770	600.59	229.99	230.85	29.99	97.05	
23799	146.92	43.68	75.83	5.19	97.05	
1757	23.41	13.46	-0.34	3.13	97.05	
18419	1317.37	373.39	2669.33	536.46	97.05	
7023	364.44	77.23	413.76	3.42	97.01	
5811	35.76	18.86	52.44	0.86	97.01	
1529	290.79	62.32	164.72	18.30	97.01	
15259	227.54	56.59	163.79	2.45	97.01	
14095	379.89	98.99	246.75	8.11	97.01	
17107	2200.10	722.73	4177.24	487.81	96.96	
13393	76.83	46.83	166.60	16.98	96.96	
15411	305.14	91.59	162.75	9.40	96.96	

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TABLE 53: BEA			Atty. Docket No. 44924-5089WC		
Timepoint(s): 6, 24 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
21011	154.85	315.31	689.68	175.67	98.32
21015	271.80	338.52	933.97	202.57	97.98
21013	214.58	340.35	710.95	153.21	97.68
22057	349.60	55.08	477.85	22.42	97.33
8477	529.15	184.21	878.58	49.54	97.03
23849	285.73	136.63	521.70	61.30	96.65
15969	339.58	71.02	574.34	94.47	96.47
5901	92.67	50.17	176.54	31.37	96.43
17034	885.84	144.51	1193.98	93.26	95.36
23140	172.19	53.17	288.43	107.64	94.67
6143	560.24	135.28	861.03	122.25	94.20
22931	79.76	48.36	19.97	4.03	94.15
13608	21.70	23.78	64.61	13.40	94.07
3167	308.80	70.69	438.24	41.83	94.07
17771	769.01	307.47	1086.30	71.95	93.98
10477	87.73	37.06	137.33	14.74	93.42
17563	1206.59	350.63	917.80	32.07	92.99
3551	440.44	98.71	307.06	31.45	92.69
22885	1347.43	493.33	2161.55	380.96	92.61
8515	262.49	109.22	415.39	29.53	92.52
20745	471.03	70.08	354.88	30.48	92.30
4748	110.75	127.98	202.78	32.60	92.18
8839	368.78	99.86	530.10	59.33	91.92
14874	50.39	17.11	78.62	12.99	91.86
21625	2492.78	1106.79	1805.41	173.96	91.53
2729	638.00	170.57	841.33	45.73	91.53
6844	124.24	58.33	32.11	26.05	91.53
19993	2317.82	568.48	3182.90	249.42	91.36
10742	62.40	27.77	27.67	6.47	91.32
8205	398.00	113.24	583.05	83.76	91.23
17400	121.53	78.34	254.55	53.39	91.23
1698	73.83	75.94	197.90	43.39	91.22
3557	107.65	39.24	177.58	40.40	91.14
18905	1365.13	302.42	1751.48	71.12	91.06
7276	72.89	27.71	30.30	10.38	91.01
15111	954.53	281.39	581.40	91.29	90.97
14929	800.42	430.77	1096.37	215.26	90.80
18077	2820.17	1190.40	1912.67	180.40	90.28
14862	181.12	72.28	270.61	28.36	90.28
10636	369.25	95.44	241.19	39.11	90.24
2057	291.01	74.63	398.13	39.83	90.15
21014	155.16	80.93	268.20	58.44	90.15
4232	137.37	62.35	64.91	22.20	90.07
5687	189.73	55.56	278.09	42.24	90.03
13614	342.46	95.82	447.07	32.82	90.03
11805	98.56	37.96	208.10	79.38	89.97
17107	2202.25	730.97	2581.41	115.51	89.72
14069	29.03	14.66	50.58	9.56	89.68
16407	463.39	111.03	329.66	41.65	89.68
3014	29.07	15.66	43.28	5.07	89.64
4731	119.24	35.99	215.47	51.98	89.63
14718	38.97	27.26	103.83	29.32	89.63
818	4123.05	2816.44	2751.13	405.49	89.60
17545	74.49	49.29	192.85	48.58	89.59
17695	728.25	203.79	1236.56	236.71	89.59
5811	35.97	18.81	13.37	6.74	89.47

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TABLE SE: BEA			Atty. Docket No. 44921-5039WO		
Timepoint(s): 6, 24 hrs			Doc. No. 1793397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
3081	387.79	84.55	253.14	37.34	89.46
7895	997.72	308.71	1503.83	263.73	89.46
3924	183.13	68.64	101.62	16.04	89.34
24181	85.08	27.22	145.70	16.84	89.33
2752	405.86	139.92	593.99	60.88	89.33
1159	886.55	231.02	611.65	64.43	89.29
24388	188.48	72.47	251.08	30.81	89.29
3926	176.00	56.73	103.17	18.22	89.25
18981	231.55	65.64	189.11	9.52	89.21
7838	19.58	15.00	21.80	3.33	89.17
24537	528.52	104.62	396.25	38.65	89.08
2688	173.21	54.36	243.95	28.16	89.08
19484	184.45	70.04	320.46	37.72	89.03
22855	561.72	144.30	886.81	141.20	89.03
12979	391.37	216.96	627.81	88.47	88.94
7223	88.64	27.62	152.72	24.63	88.94
23159	416.48	85.49	537.44	47.74	88.91
13563	1028.27	255.15	1603.62	170.06	88.86
3696	42.57	32.72	106.32	10.80	88.86
2855	920.64	212.77	1412.67	261.05	88.77
3580	9.48	10.46	22.09	6.90	88.74
12629	65.11	30.82	27.44	7.55	88.61
18810	1188.71	319.49	906.85	60.20	88.52
18770	1131.01	331.57	887.70	58.94	88.48
19577	494.98	92.34	376.82	38.52	88.48
18891	1378.10	409.91	1823.58	193.46	88.48
7914	1537.05	507.11	1256.25	91.53	88.44

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TABLE 5F: CAPTOPRIL			Atty. Docket No. 44921-5089WO		
Timepoint(s): 336 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
23859	-10.09	17.25	58.28	12.00	99.70
1522	181.53	92.60	-79.60	14.77	99.40
24668	76.16	46.93	1110.08	605.52	99.10
19287	161.27	40.70	265.00	9.72	98.84
735	125.45	37.81	123.72	0.37	98.50
1348	29.21	17.75	0.23	1.09	98.12
16260	66.53	18.90	82.33	0.49	98.07
24696	69.96	48.08	-11.83	7.33	98.07
826	182.43	53.09	63.46	18.28	97.90
15851	203.67	153.22	36.02	16.84	97.69
19120	32.71	25.65	-8.80	2.19	97.43
1480	253.73	66.75	112.96	18.69	97.43
18659	51.26	29.25	80.08	1.30	97.43
15420	59.28	52.41	-14.25	3.04	97.39
2830	654.10	146.54	933.86	42.78	96.92
2858	891.04	236.04	443.07	41.79	96.88
17937	86.63	42.53	-12.26	22.60	96.83
10108	146.26	35.48	61.17	17.32	96.70
1223	191.43	47.65	289.39	15.78	96.66
16048	28.62	52.28	-8.09	3.07	96.66
10774	26.49	16.73	40.49	1.17	96.62
16944	848.22	191.45	550.56	29.83	96.58
546	173.90	50.96	271.42	13.74	96.53
12819	184.28	47.07	239.54	3.32	96.53
5735	56.51	21.12	63.63	0.57	96.45
7956	27.42	11.15	39.67	0.69	96.40
12332	567.22	177.99	328.76	21.43	96.32
18346	273.04	62.53	138.13	21.45	96.32
16425	20.91	30.81	-13.41	3.05	96.23
8426	54.76	23.35	27.91	1.50	96.19
9964	14.13	28.09	41.16	1.54	96.15
15395	797.12	155.79	610.46	12.19	96.02
21458	229.75	104.67	360.26	20.40	95.93
15259	227.63	56.54	154.42	4.47	95.93
11057	33.19	29.92	61.96	3.13	95.89
397	116.22	33.32	88.25	1.44	95.89
20429	108.55	34.07	193.71	39.16	95.85
12333	218.47	76.94	109.09	10.32	95.85
12629	64.58	30.66	134.34	14.35	95.76
20833	1255.87	351.77	1350.26	16.51	95.68
10673	62.50	35.24	48.56	1.93	95.63
9518	29.88	23.15	73.23	8.73	95.59
5630	77.86	48.50	150.84	8.45	95.59
16036	64.27	20.66	37.81	2.46	95.55
23773	214.43	85.23	94.48	13.72	95.51
11817	64.91	20.17	98.04	3.96	95.46
13976	459.29	377.97	122.98	19.90	95.46
14926	95.90	28.06	158.69	14.69	95.46
21633	302.73	119.13	151.23	11.45	95.42
910	58.30	22.93	35.87	1.63	95.42
11203	75.66	25.37	58.05	1.05	95.38
16562	188.78	45.14	125.67	5.83	95.29
6362	63.63	39.69	-15.88	19.50	95.25
23237	89.94	41.57	97.86	1.24	95.25
5384	41.70	44.55	1.71	2.18	95.25
22665	128.49	29.89	159.98	3.47	95.21

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TABLE 5F: CAPTOPRIL			Atty. Docket No. 44921-5089WO		
Timepoint(s): 336 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
6581	76.47	26.45	43.08	2.63	95.12
260	417.04	114.29	636.83	72.47	95.12
24814	171.82	33.74	127.03	5.19	95.12
13682	178.68	62.82	61.54	20.17	95.08
15028	346.53	107.46	569.31	126.83	95.08
17439	218.65	47.89	292.03	10.02	94.99
15797	20.60	17.76	-7.25	4.56	94.95
17549	1304.87	367.92	1416.98	24.18	94.95
17923	66.78	23.31	48.46	1.01	94.95
23360	178.74	46.59	218.52	2.99	94.91
20099	81.73	30.45	123.33	3.88	94.91
19327	89.68	29.52	50.76	3.50	94.86
5786	125.64	46.92	48.44	13.78	94.86
9929	531.71	124.53	680.04	14.58	94.82
2831	619.77	172.12	917.69	61.75	94.82
10477	88.24	37.19	51.43	2.96	94.82
21013	217.62	342.33	442.35	95.19	94.82
21651	32.33	26.35	2.01	3.21	94.78
19527	47.24	56.67	112.09	11.81	94.78
1921	178.67	59.48	97.23	10.49	94.73
8988	56.52	38.39	8.71	5.65	94.73
6766	481.24	157.08	653.99	16.43	94.73
18862	47.30	24.54	31.00	1.20	94.69
15470	328.11	71.27	198.29	29.91	94.69
3288	10.56	13.80	41.78	12.82	94.69
23109	2081.66	927.60	2211.62	60.64	94.61
7197	197.55	84.70	290.53	17.88	94.56
7279	201.88	88.54	108.84	9.39	94.52
19581	48.08	32.46	66.08	3.68	94.48

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TABLE 5G: CARBOPLATIN		Atty. Docket No. 44921-5089WO			
Timepoint(s): 6 hrs		Doc. No. 1798397.1			
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
6262	739.41	208.31	1532.53	76.80	99.61
24048	689.96	212.19	1411.28	55.30	99.36
17089	1547.81	626.59	4737.22	696.74	98.93
16081	115.61	379.88	645.20	213.95	98.54
25777	403.77	181.40	901.96	112.12	98.37
4933	134.08	204.01	525.52	82.57	98.20
7476	90.92	58.14	272.77	23.70	98.11
15171	241.90	97.44	403.05	21.96	98.03
24049	1518.47	439.97	2590.21	123.80	98.03
16080	44.66	251.23	378.60	161.27	97.99
10093	342.04	117.93	656.06	50.76	97.86
1069	1820.60	698.77	1513.87	16.71	97.64
25480	92.27	34.63	148.37	3.30	97.43
6647	510.34	159.21	1020.51	105.54	97.39
7247	504.54	113.43	793.61	51.11	97.34
18532	285.39	90.75	560.36	75.34	97.04
4067	123.93	59.98	232.57	36.85	96.92
23449	124.24	104.63	362.40	83.14	96.83
8314	95.89	403.64	202.84	47.87	96.79
14159	87.59	36.45	200.11	36.34	96.74
18280	584.52	131.77	819.56	51.87	96.70
23314	71.21	275.95	495.11	153.82	96.70
3816	326.31	77.12	471.75	21.93	96.66
17329	215.35	107.06	443.46	37.86	96.62
5461	193.57	116.65	442.55	77.30	96.57
22501	257.26	67.93	377.18	25.53	96.53
15277	900.30	154.78	1210.05	42.20	96.49
23538	101.09	71.79	256.02	74.72	96.44
8849	222.08	71.82	422.51	61.76	96.36
17779	1949.63	787.42	1501.46	41.41	96.36
23574	2277.50	970.11	1768.74	46.20	96.23
1127	1190.78	434.96	1227.98	24.14	96.14
4154	247.57	87.35	387.82	17.78	95.80
3471	80.41	35.57	126.92	4.34	95.78
22211	768.41	165.76	1038.58	34.89	95.72
21815	248.67	55.97	320.59	9.43	95.67
18597	521.69	183.32	851.48	104.45	95.63
2196	564.46	104.22	713.81	13.18	95.54
13598	350.22	110.18	570.66	47.31	95.46
16895	2022.10	903.47	1796.87	31.07	95.42
8522	571.58	153.62	693.92	15.58	95.42
8652	228.95	114.23	482.75	43.58	95.37
20026	64.36	24.25	120.87	11.23	95.33
15192	169.06	132.74	389.95	89.37	95.29
1622	2067.46	903.52	1573.48	71.56	95.29
3823	526.02	154.25	801.75	71.28	95.20
5989	269.96	71.53	419.90	36.98	95.12
3434	324.23	140.30	584.57	69.17	95.07
3156	1279.17	207.18	1810.46	187.54	95.03
10818	464.74	186.59	181.34	44.19	95.03
5575	86.94	36.56	34.41	8.85	94.99
11174	54.05	51.84	117.20	14.24	94.99
14425	213.74	79.18	349.63	37.59	94.94
16417	72.79	29.59	142.55	15.55	94.90
17771	769.30	306.35	1273.57	156.68	94.86
5208	1055.01	435.10	2101.50	490.32	94.82

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TABLE 5G: CARBOPLATIN					
Timepoint(s): 6 hrs					
Atty. Docket No. 44921-6039WO					
Doc. No. 1798397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
3431	1514.30	636.90	1297.11	34.77	94.82
21462	258.49	59.82	358.44	18.51	94.77
3822	921.02	284.55	1300.83	99.42	94.73
15190	1824.97	1183.78	2141.03	82.58	94.69
19111	1604.90	429.51	2027.13	89.10	94.64
14906	383.54	73.03	535.04	39.09	94.47
13144	-27.27	17.64	-54.47	5.38	94.43
18142	1995.09	839.14	1819.48	43.33	94.39
13634	827.03	282.41	1137.48	107.16	94.34
2350	646.60	103.17	832.07	60.88	94.30
1537	31.35	46.10	59.58	13.80	94.26
13239	110.05	49.12	151.36	7.79	94.17
20864	1582.67	662.32	1722.73	33.76	94.13
12402	540.97	155.59	755.78	32.87	94.13
2424	585.64	132.80	807.06	45.48	94.13
15106	1894.10	713.95	1463.01	37.13	94.09
12569	402.63	145.28	719.92	106.90	94.04
2022	270.40	55.81	378.75	24.92	93.83
13633	310.40	151.71	490.70	80.01	93.79
22197	123.97	52.28	217.39	36.02	93.79
13874	42.03	18.39	51.72	2.31	93.74
3533	212.11	64.89	298.00	11.86	93.74
5985	44.47	68.11	62.07	10.39	93.74
21643	1185.08	370.10	960.79	22.49	93.74
5089	70.77	28.48	123.98	19.48	93.74
17211	1445.11	555.30	1017.49	34.14	93.70
15772	28.16	13.60	23.47	26.74	93.66
25689	1435.28	508.41	1360.96	40.18	93.66
22545	252.03	89.09	444.84	127.61	93.62
11954	3134.66	1692.86	2572.78	105.71	93.57
8634	343.04	96.04	542.29	61.79	93.53
13771	91.36	32.90	152.72	14.45	93.53
14871	688.13	217.01	1066.71	67.36	93.53
25435	69.69	23.87	116.39	11.28	93.49
18076	2539.23	1190.89	2104.90	81.41	93.49
1660	6.16	20.59	24.43	41.71	93.44
20817	1076.80	681.07	1252.44	51.53	93.36
22923	57.85	40.50	3.36	7.47	93.32
20508	16.41	9.30	22.98	0.98	93.27
14304	95.81	30.28	138.83	9.76	93.23
23005	911.26	224.88	1191.71	45.14	93.23
18375	1004.76	291.14	1452.05	94.00	93.23
25754	73.97	20.01	103.72	4.72	93.19
820	2460.91	1164.05	2043.71	81.32	93.19

TABLE 51: CEPHALORIDINE			Atty. Docket No. 44921-5089WO		
Timepoint(s): 6, 24 hrs			Doc. No. 1798397.1		
Identifier	NonTexMean	NonTexSD	TexMean	TexSD	LDAScore
1698	72.61	72.54	355.15	57.50	98.88
25057	-16.00	13.42	28.61	15.15	98.84
23302	115.35	36.99	250.40	26.19	98.45
25098	44.75	40.56	161.77	39.01	98.45
7022	6.54	19.86	87.07	26.85	98.45
18005	16.30	11.61	71.95	28.31	97.64
16318	111.73	57.76	214.34	48.82	97.59
15849	181.68	73.50	381.77	34.83	97.29
23283	520.93	94.30	765.95	70.15	97.25
651	12.40	11.40	69.75	44.55	97.16
16112	56.89	23.53	146.28	35.70	97.12
25198	33.14	18.60	104.50	28.93	97.12
8879	109.65	35.18	198.92	13.77	97.03
19253	280.76	74.42	450.66	32.07	97.03
15376	140.99	45.51	267.24	27.71	96.90
21038	113.15	45.28	284.43	88.10	96.82
20917	114.76	34.55	219.65	37.89	96.69
650	17.69	13.01	74.86	36.83	96.47
11411	252.17	76.16	422.51	26.01	96.35
343	28.78	32.80	129.29	21.40	96.35
16248	128.59	52.73	293.26	99.85	96.30
20843	165.02	37.03	274.00	60.23	96.30
18995	61.26	23.28	126.99	20.34	96.17
7050	68.24	24.46	116.13	10.21	95.92
20753	128.41	31.77	231.50	37.70	95.83
18084	36.85	19.15	95.80	24.41	95.83
1764	97.37	32.56	181.11	28.78	95.83
22413	73.51	35.54	155.12	24.23	95.74
12162	313.72	69.35	466.55	53.66	95.57
9573	313.16	70.67	449.88	24.42	95.53
5458	521.55	111.52	766.69	82.52	95.49
23889	170.87	60.58	320.41	74.89	95.49
1623	84.54	20.77	130.31	10.23	95.44
19254	240.06	74.71	400.30	44.56	95.31
1828	13.93	10.20	37.44	6.38	95.27
672	-2.45	13.09	33.39	16.62	95.27
1855	13.51	8.02	32.00	4.11	95.18
3900	83.63	36.44	170.88	42.74	95.14
15281	172.53	45.57	282.14	34.03	95.10
1582	16.73	13.23	46.93	7.97	95.10
25589	154.39	37.33	240.89	33.81	95.10
627	63.31	19.85	119.93	25.90	95.06
17434	163.74	49.10	263.86	22.79	95.01
21063	75.00	25.88	144.62	27.06	94.97
14353	61.97	20.12	119.73	30.32	94.93
6850	87.12	29.12	157.80	23.31	94.93
2059	139.66	39.69	243.75	48.13	94.84
16333	132.19	38.88	212.16	19.97	94.71
25377	31.75	20.09	77.51	19.81	94.50
23282	277.48	51.59	385.61	37.11	94.50
12058	109.37	35.93	194.17	43.87	94.45
9952	163.81	35.63	235.14	38.00	94.37
22196	58.71	24.71	123.83	37.19	94.37
16121	110.03	60.28	208.77	16.39	94.33
24640	177.93	59.42	295.24	35.00	94.33
1946	46.78	14.37	67.25	3.13	94.28

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TABLE 5H: CEPHALORIDINE			Atty. Docket No. 44921-6089WO		
Timepoint(s): 6, 24 hrs			Doc. No. 1793397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
12259	-0.17	9.62	21.16	7.74	94.15
6790	62.58	24.20	118.33	27.25	94.07
21802	45.94	21.21	103.13	35.44	94.07
14125	128.30	50.32	211.96	15.22	94.07
18183	31.28	14.65	67.29	14.30	94.02
17225	162.76	46.10	264.51	40.73	93.94
20514	83.93	25.89	146.04	21.67	93.94
1342	31.31	15.65	72.08	26.80	93.81
16616	88.26	37.98	165.12	31.68	93.77
4386	55.88	26.02	117.38	28.79	93.77
13464	30.34	17.92	75.47	19.34	93.68
11358	82.35	33.88	151.50	27.12	93.59
7866	43.15	16.17	81.51	16.07	93.51
22967	163.95	54.65	241.59	15.86	93.47
8385	57.15	28.33	114.53	19.32	93.42
24748	-23.01	37.80	49.31	11.34	93.38
16059	50.12	14.86	84.72	17.27	93.38
16122	117.41	41.42	186.27	14.87	93.34
1350	143.74	30.94	209.15	28.63	93.34
8384	39.05	17.03	73.91	10.64	93.29
18259	216.96	155.49	545.75	138.45	93.28
20724	48.65	21.46	90.26	16.90	93.25
352	87.58	53.82	157.16	24.98	93.21
10740	26.94	24.94	69.61	15.31	93.12
1394	24.70	11.31	42.23	3.80	93.12
22466	462.31	92.72	638.40	68.34	92.99
13684	467.12	135.55	762.39	150.04	92.99
14768	85.99	47.21	225.50	66.59	92.98
13285	71.32	19.47	109.95	16.43	92.91
1537	29.82	40.75	245.05	131.87	92.90
18442	38.53	17.21	75.30	16.45	92.86
1183	52.85	29.47	214.38	101.63	92.85
127	19.05	14.19	48.31	9.93	92.73
1399	200.20	80.01	449.25	95.96	92.68
11203	75.19	24.99	127.88	16.58	92.65
870	22.03	9.87	40.53	4.22	92.61
4415	38.66	18.55	77.02	14.75	92.61
373	32.60	56.68	306.93	119.81	92.60
22524	112.62	47.12	195.09	26.00	92.56
6951	88.94	34.80	155.83	27.94	92.56
13023	176.39	400.42	1491.81	754.76	92.55
17636	102.26	27.02	156.20	28.41	92.48
7051	62.10	22.11	105.49	19.48	92.48
18749	115.18	42.04	202.78	33.94	92.39

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TABLE 5: CIDOFIVIR					
Timepoint(s): 120 hrs					
Atty. Docket No. 44921-5089WO					
Doc. No. 1796997.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
18609	203.96	70.15	541.22	19.78	99.70
20674	83.03	21.84	203.76	22.76	99.61
4312	76.73	35.26	365.78	59.40	99.57
24041	12.84	32.48	31.93	0.33	99.53
5733	10.73	30.54	617.55	122.19	99.44
2768	1962.14	417.45	933.17	95.15	99.32
2410	11.13	10.13	64.03	13.02	99.32
14289	62.53	19.54	95.56	0.76	99.27
5689	12.82	19.88	85.25	13.41	99.23
14594	-17.87	24.41	86.07	17.70	99.23
24000	64.13	33.98	157.59	7.48	99.19
8027	0.11	26.38	29.41	3.47	99.19
18322	2666.91	812.51	1165.22	99.03	99.06
7324	97.12	49.43	271.43	20.08	99.06
20903	70.06	46.59	288.96	29.37	99.06
20757	410.75	211.87	1571.32	228.32	98.97
1599	22.63	26.70	62.22	8.06	98.97
5183	215.17	70.24	445.78	24.68	98.97
4856	122.81	48.54	241.75	6.99	98.97
2655	42.27	39.82	529.96	152.39	98.97
10167	189.75	100.26	305.25	11.81	98.97
12175	225.36	80.40	666.87	94.23	98.93
22722	73.37	39.40	290.14	53.00	98.93
20082	75.76	32.27	258.55	44.96	98.93
912	474.15	83.63	764.00	33.56	98.84
8002	13.99	15.79	47.18	4.09	98.84
13158	463.87	106.89	360.87	1.60	98.80
10200	41.90	30.39	92.98	6.46	98.76
5572	332.45	146.31	611.55	14.40	98.67
410	1097.88	255.30	605.30	42.31	98.63
20755	145.36	116.99	986.50	562.94	98.63
23376	14.61	16.79	37.95	1.52	98.63
1600	44.38	66.08	114.35	13.26	98.63
25705	454.53	109.40	1132.56	152.81	98.59
13609	240.24	60.23	98.11	9.83	98.59
24219	315.68	82.27	692.16	77.33	98.59
26184	204.20	70.54	454.10	35.35	98.54
16081	117.80	381.49	136.30	8.26	98.54
7680	57.70	87.65	653.31	318.06	98.54
22681	222.75	194.18	580.89	50.39	98.54
9215	90.03	33.75	158.07	6.56	98.50
25699	137.08	68.59	-11.79	8.27	98.50
4048	-6.15	31.92	56.08	15.06	98.50
2729	640.63	170.18	328.03	37.57	98.50
15981	75.77	29.60	148.46	12.15	98.46
133	-43.58	39.29	55.82	20.14	98.37
24707	47.32	82.24	10.71	1.68	98.37
6193	192.02	179.55	250.16	3.55	98.37
3981	72.52	103.32	368.64	91.18	98.37
21893	51.03	33.90	172.83	32.83	98.37
16168	350.38	204.48	829.66	132.95	98.37
4262	43.72	51.67	193.22	27.67	98.33
10289	14.87	14.48	127.47	59.89	98.24
17161	1157.45	414.68	2144.64	136.59	98.24
26150	780.06	534.26	32.24	49.38	98.24

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TABLE 5i: CIDOFOVIR			Atty. Docket No. 44921-5039WO		
Timepoint(s): 120 hrs			Doc. No. 1798997.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
3916	737.83	188.48	383.68	38.35	98.24
5339	5.98	20.99	59.41	8.18	98.16
26084	113.22	92.96	448.40	70.70	98.16
21654	362.77	114.65	543.47	30.13	98.12
26119	124.48	46.50	204.85	9.09	98.12
17314	6.10	12.64	43.93	7.10	98.07
353	173.67	81.62	475.77	74.64	98.07
16756	177.77	53.62	345.26	28.00	98.07
11437	555.26	125.28	290.62	37.25	98.07
24433	35.92	17.39	77.13	4.05	98.03
5464	225.07	67.79	427.11	46.05	97.99
15416	49.65	20.05	91.41	3.94	97.99
21948	203.26	65.91	33.57	32.91	97.99
18361	460.95	159.60	865.38	68.10	97.95
4049	22.90	64.75	174.30	49.09	97.90
6765	788.37	204.50	462.53	19.08	97.90
17401	910.82	424.91	1651.59	134.17	97.90
20830	519.62	176.96	850.57	34.74	97.86
12908	40.69	40.63	135.60	42.31	97.86
19762	4.99	10.67	25.14	2.42	97.82
20457	382.89	90.62	215.96	13.41	97.82
5430	136.50	60.64	401.60	97.31	97.82
15300	137.15	130.99	496.58	110.00	97.73
11259	107.70	137.96	508.22	165.85	97.73
3808	168.07	57.61	297.97	55.59	97.73
22050	3164.11	929.00	1779.72	124.06	97.73
4451	290.06	65.29	164.79	13.86	97.73
16170	38.98	26.45	97.44	18.88	97.69
13332	420.04	95.61	169.12	30.12	97.69
15861	460.82	148.89	174.40	29.65	97.69
6606	251.17	124.12	178.93	1.98	97.65
19370	308.88	74.48	551.57	63.31	97.65
3874	883.32	205.24	530.31	28.27	97.65
20991	224.15	69.07	195.44	2.64	97.60
18811	46.63	26.47	80.60	1.75	97.60
5881	103.14	35.12	184.15	18.55	97.60
354	214.95	93.98	490.19	69.08	97.56
11454	238.74	78.96	470.27	65.91	97.56
12873	122.01	67.80	366.63	64.37	97.56
20829	813.56	302.89	1539.75	129.65	97.56
17807	753.81	228.33	1314.67	146.81	97.56
8585	289.56	118.65	190.91	6.78	97.56
8215	1680.14	394.54	881.26	110.65	97.56
14763	38.37	132.57	554.64	221.30	97.52

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TABLE 5J: CISPAN combined			Atty. Docket No. 44921-5089WO		
Timepoint(s): 6, 24 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
8990	276.73	75.18	522.76	68.28	96.93
1460	198.36	85.83	320.23	42.90	95.60
16853	67.12	22.69	121.67	21.69	95.08
13239	108.86	47.65	222.86	33.91	94.73
21355	373.47	117.15	627.82	92.43	94.89
6454	238.70	77.20	419.87	47.88	94.89
1247	1313.77	499.48	559.96	117.97	94.56
6506	233.04	59.13	375.55	54.15	94.34
1585	67.19	32.77	140.57	23.52	94.26
1962	33.04	26.70	76.49	11.48	94.17
18433	18.64	45.96	123.81	42.15	94.13
15050	638.79	181.52	459.28	26.53	94.04
17693	1261.20	375.03	651.01	91.79	93.87
4956	78.53	37.78	155.47	25.21	93.65
16233	68.67	88.34	117.42	12.47	93.18
11445	435.55	103.48	642.14	86.21	92.62
8004	125.10	43.16	255.80	43.43	92.37
1811	10.62	25.84	83.04	26.96	92.28
1542	929.09	263.76	560.16	66.12	91.97
16591	151.89	47.44	236.90	29.21	91.84
18694	52.90	48.32	176.24	47.08	91.68
11524	-14.63	24.06	46.43	29.33	91.59
19080	75.03	55.99	212.58	72.04	91.20
20514	83.88	26.10	127.69	12.79	91.19
15701	37.45	16.42	79.72	13.34	91.16
16122	116.73	39.95	217.85	62.09	90.99
2079	303.23	81.83	406.18	33.43	90.98
19327	88.79	28.83	152.22	21.27	90.86
335	95.54	44.88	191.73	23.12	90.86
14003	817.87	211.94	491.17	61.11	90.86
9104	138.43	38.55	221.59	41.76	90.69
25253	291.50	63.92	430.49	54.59	90.69
23322	1169.44	284.23	807.96	73.20	90.67
24696	68.34	46.61	180.46	53.14	90.60
1552	71.02	83.66	121.56	15.30	90.54
19120	31.87	24.91	90.61	26.26	90.51
17411	78.54	53.72	189.16	45.14	90.51
16121	109.00	58.08	258.63	87.07	90.47
1639	96.38	22.51	149.03	17.77	90.43
1622	2080.70	896.54	796.36	153.89	90.41
9882	487.60	181.11	245.48	60.74	90.41
23852	261.73	101.88	487.29	97.17	90.38
13684	465.64	134.08	778.77	108.34	90.38
7857	51.80	45.32	150.23	38.24	90.38
6281	232.74	67.04	343.63	49.82	90.34
15790	45.82	25.45	87.17	18.57	90.24
23884	40.55	32.64	101.67	19.55	90.21
17682	673.97	178.07	455.67	77.33	90.16
16581	39.15	19.04	83.46	15.21	90.12
24390	161.41	112.42	367.16	79.88	90.08
3886	57.66	28.30	124.53	24.81	90.08
13682	176.78	61.74	302.10	50.60	90.04
7262	1113.30	393.42	1879.06	245.81	90.00
11954	3158.62	1682.02	952.13	425.90	89.98
818	4151.32	2802.74	902.92	257.41	89.94

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TABLE 5J: CISPAN combined			Atty. Docket No. 44921-6089WO		
Timepoint(s): 6, 24 hrs			Doc. No. 1798327.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
819	3116.95	1659.72	925.18	255.80	89.90
16211	2269.84	1132.19	853.70	212.63	89.90
1521	20.42	50.86	117.89	40.21	89.78
23125	4625.10	2534.40	1935.15	332.35	89.77
9109	1022.92	338.20	736.62	48.42	89.77
10141	53.73	45.97	150.14	52.96	89.69
152	72.28	26.46	108.76	14.84	89.68
17154	198.73	57.61	281.13	33.91	89.59
6362	62.35	38.95	146.74	29.87	89.56
10540	19.51	18.83	64.08	25.25	89.52
651	12.58	12.76	33.89	11.18	89.52
17086	151.38	43.21	214.56	21.12	89.51
12020	167.06	60.45	260.26	34.23	89.51
4121	62.05	23.29	113.40	19.65	89.43
8211	2875.40	1605.55	956.21	247.45	89.38
20404	53.25	45.78	130.86	32.28	89.35
7522	31.59	18.74	75.54	18.10	89.30
20879	87.24	50.13	179.14	40.07	89.26
17550	1318.67	366.65	860.58	175.55	89.25
21950	727.03	149.84	534.23	70.97	89.21
25405	77.77	28.49	139.55	22.89	89.17
14125	127.72	49.56	229.81	40.28	89.17
1611	8.22	23.65	52.29	18.59	89.13
21685	122.94	42.72	207.33	33.76	89.13
17524	1176.52	284.08	761.61	160.07	89.09
10611	10.59	27.29	104.61	49.13	89.06
22849	197.26	50.25	298.83	40.93	89.00
1608	12.43	29.83	56.08	17.26	89.00
4312	76.57	37.18	172.28	72.36	88.97
1396	47.24	18.54	84.98	24.01	88.92
20871	52.42	25.81	108.86	22.74	88.92
10344	22.14	21.48	62.29	12.19	88.83
15587	38.29	19.07	66.30	11.60	88.82
9096	9634.12	6768.62	2697.48	901.04	88.82
4290	94.06	28.34	144.64	19.10	88.79
24143	192.56	96.48	385.57	70.47	88.74
12174	80.77	29.46	139.07	31.48	88.74
17336	65.85	21.84	107.99	13.40	88.74
25257	101.83	34.03	168.25	31.38	88.74
20350	154.58	49.68	245.00	41.28	88.70
11335	661.49	162.55	459.38	57.71	88.64
24146	219.42	50.91	370.23	55.30	88.63
16254	5.55	11.81	26.92	12.39	88.61
20876	1683.23	611.09	940.93	123.03	88.60
9312	31.90	15.15	74.64	21.22	88.58

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TABLE 5K: CISPLATIN					
timepoint(s): 169 hrs					
Atty. Docket No. 44921-5089WO					
Doc. No. 1795397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	UDAScore
14458	36.84	28.40	100.33	0.26	99.96
22385	106.64	51.70	345.64	8.69	99.87
11731	43.29	24.10	393.30	43.69	99.87
23745	201.94	65.06	823.60	110.42	99.83
12903	53.64	18.74	124.32	6.90	99.83
15503	124.27	37.32	319.29	21.43	99.79
8235	43.83	34.77	145.95	18.00	99.79
16756	177.83	53.82	327.44	3.02	99.74
16119	15.30	15.19	84.22	6.17	99.74
11967	1725.18	546.07	289.45	25.19	99.74
3608	333.84	110.50	62.62	5.74	99.70
18729	19.92	29.07	174.49	19.16	99.61
5891	-53.03	47.69	106.02	18.28	99.61
2048	31.69	20.74	125.19	16.43	99.61
4490	76.73	72.26	462.55	50.86	99.61
1743	29.35	16.21	72.89	1.22	99.61
1584	162.19	43.70	307.85	8.25	99.57
16137	6.75	397.82	87.49	8.36	99.53
23778	68.99	34.04	179.58	9.21	99.53
23261	1568.96	389.70	925.80	13.87	99.53
808	468.33	143.61	160.94	9.90	99.53
1962	33.33	26.74	101.07	4.72	99.53
21789	34.67	30.58	177.40	21.84	99.53
23769	-6.24	8.69	33.99	6.30	99.53
23070	125.37	31.23	218.44	4.95	99.49
12400	13.19	10.48	74.60	11.18	99.49
16676	38.33	26.96	110.79	5.32	99.49
23780	25.07	35.93	95.20	12.81	99.44
25545	94.29	48.16	306.94	34.66	99.44
15254	209.66	67.16	447.21	21.22	99.44
23992	5.39	7.25	34.45	3.17	99.44
14430	34.19	31.78	125.29	8.54	99.40
11969	96.84	38.48	303.71	38.83	99.40
4312	77.16	37.99	241.97	24.41	99.40
4967	33.46	19.94	94.30	3.72	99.36
2079	303.69	81.26	527.92	20.78	99.32
22816	23.12	15.17	89.33	8.69	99.32
3609	407.50	148.70	67.97	9.33	99.32
4361	90.16	30.77	193.28	10.19	99.32
13682	177.74	62.54	333.83	4.20	99.32
15504	129.02	50.62	447.33	63.50	99.27
633	271.13	101.41	110.07	15.08	99.27
21183	22.62	26.03	134.40	19.53	99.27
24222	101.20	52.50	460.48	61.63	99.27
8548	63.06	30.22	6.09	1.52	99.27
24301	109.26	35.74	248.67	13.48	99.27
18442	38.61	17.15	99.87	5.14	99.27
14370	32.54	45.58	189.80	11.25	99.23
21500	80.36	76.69	471.24	73.44	99.23
24211	148.45	87.73	552.73	49.74	99.23
770	798.02	219.52	248.56	33.80	99.23
21791	84.31	36.00	242.62	24.88	99.23
24651	100.74	23.52	203.14	12.02	99.23
17897	53.72	25.98	111.75	3.84	99.23
20890	101.09	46.35	342.52	50.55	99.19
712	1.36	9.08	60.25	14.12	99.19

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TABLE 5K: CISPLATIN Timepoint(s): 168 hrs. Att'y. Docket No. 44921-5039WO Doc. No. 173397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
18553	54.23	33.42	166.80	12.30	99.19
15884	183.00	57.89	383.85	23.01	99.19
19722	168.71	55.03	336.25	15.95	99.19
17481	26.11	28.66	137.39	13.89	99.19
5733	12.25	46.24	172.15	34.99	99.19
4895	232.18	95.74	44.77	8.48	99.14
15151	153.83	39.15	302.83	29.57	99.14
14759	21.72	15.86	78.25	9.50	99.14
15039	272.18	79.33	101.53	6.80	99.14
12782	20.00	43.24	135.93	6.16	99.14
23121	19.80	13.92	60.40	2.66	99.14
26292	22.82	12.83	85.01	11.49	99.14
2154	59.03	121.05	244.16	33.75	99.14
21583	125.87	40.62	270.04	27.65	99.14
3006	26.57	35.44	81.75	9.18	99.10
1203	5.08	18.58	86.62	14.26	99.10
24472	234.56	47.65	380.85	13.16	99.10
5729	87.49	38.35	274.95	40.90	99.10
132	-24.93	23.56	50.93	12.76	99.10
1801	97.64	29.41	197.50	14.44	99.10
1993	30.09	21.86	117.89	9.03	99.10
16675	33.74	34.04	112.81	11.29	99.10
1382	57.80	21.22	127.59	5.60	99.10
17586	115.18	35.27	246.61	21.48	99.06
21666	22.81	17.92	87.38	6.42	99.06
2125	76.55	80.69	345.60	72.31	99.06
21709	142.70	29.95	215.46	6.19	99.06
16538	132.96	36.43	245.73	9.25	99.06
2845	667.61	123.51	1098.14	42.15	99.02
753	42.04	16.33	120.03	23.17	99.02
21893	50.92	33.48	203.93	25.50	99.02
21836	29.24	16.81	91.95	8.44	99.02
21817	10.63	13.30	59.28	7.00	99.02
6517	231.85	156.64	721.49	128.57	99.02
1588	61.92	22.15	122.71	6.97	99.02
14564	48.33	23.27	104.89	3.20	99.02
3079	34.64	46.77	152.78	26.18	98.97
7602	193.69	43.89	364.34	31.12	98.97
20816	393.33	173.56	774.42	37.69	98.97
6322	18.88	17.54	122.95	22.89	98.97
17337	510.70	139.07	253.28	6.67	98.97
18161	114.11	43.86	244.42	22.79	98.97
4057	64.54	20.73	139.42	12.02	98.97
22552	314.43	92.85	696.18	70.05	98.93

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TABLE 5L: CISPLATIN			Atty. Docket No. 44321-5089WO		
Timepoint(s): 6, 24 hrs			Doc. No. 1793397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
20082	75.47	31.84	228.60	43.28	98.84
1598	47.75	56.92	133.89	25.63	98.58
15313	11.08	24.34	53.59	5.89	98.54
2655	43.13	48.31	177.30	66.12	98.20
14424	66.72	130.96	272.03	63.86	97.85
17314	5.89	11.89	63.70	27.83	97.85
21275	225.06	80.71	528.11	144.80	97.68
4047	85.85	50.33	190.04	23.02	97.60
20116	9.55	31.45	124.39	50.70	97.38
15382	122.93	203.50	341.43	85.17	97.34
1521	20.82	51.01	148.25	24.41	97.30
24146	220.17	51.83	396.31	40.61	97.30
8990	278.10	77.14	540.97	69.47	97.21
1884	178.33	37.79	272.14	18.27	97.17
4933	134.55	205.15	335.87	89.54	97.04
6506	233.65	59.50	415.92	45.52	97.04
4944	112.31	56.05	264.36	39.37	96.95
8004	125.79	44.06	271.11	40.68	96.95
1993	30.02	21.93	91.88	19.85	96.91
20506	21.57	7.97	46.99	7.30	96.82
21462	257.92	58.72	424.63	52.75	96.78
6974	129.50	46.90	236.12	28.32	96.78
11549	243.07	64.12	425.53	38.72	96.74
2905	245.79	107.78	488.69	56.33	96.74
1811	10.99	26.26	94.19	25.01	96.70
10839	313.60	67.83	533.54	83.77	96.70
2468	252.35	62.46	433.73	70.78	96.61
373	33.94	61.41	162.88	51.32	96.57
19040	186.25	107.25	258.19	19.20	96.57
15299	87.98	61.10	206.62	59.64	96.57
13684	467.21	135.45	831.58	69.76	96.52
910	57.76	21.93	136.53	45.93	96.35
4477	11.91	8.60	37.00	7.79	96.27
20871	52.68	25.99	122.97	14.46	96.22
16853	67.36	22.84	136.28	21.27	96.18
23473	156.94	56.94	338.21	73.37	96.18
2536	393.91	124.60	585.25	20.89	96.14
10015	232.29	77.80	340.64	28.00	96.14
18694	53.51	48.91	198.02	43.87	96.09
16284	40.93	27.58	129.79	27.84	96.09
18375	121.97	28.16	198.57	23.40	96.05
23314	70.46	275.32	498.55	211.58	96.05
651	12.67	12.78	40.79	8.43	95.97
3266	133.11	36.44	247.88	45.93	95.97
1460	198.97	85.95	340.15	49.64	95.97
20065	86.81	30.90	170.50	27.85	95.97
15301	38.37	68.10	96.58	21.67	95.92
23448	169.78	101.84	327.19	44.52	95.92
15003	36.27	96.97	63.65	10.34	95.88
26184	203.75	69.61	423.29	118.85	95.88
8336	26.96	37.28	139.71	61.60	95.79
6362	62.77	39.27	160.35	23.77	95.75
14003	815.94	212.81	484.61	51.19	95.67
9339	357.63	88.22	588.27	74.10	95.62
6384	60.88	59.65	127.67	27.22	95.54
15345	201.86	67.69	322.91	40.01	95.45

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TABLE 5L: CISPLATIN			Atty. Docket No. 44921-5089WO		
Timepoint(s): 6, 24 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LPAScore
22849	197.75	50.59	318.11	30.11	95.41
23868	178.04	289.84	277.77	47.28	95.41
16233	68.93	88.14	123.52	11.88	95.36
6454	239.80	78.37	418.57	35.68	95.36
21081	58.86	27.77	128.21	17.87	95.36
24143	193.56	97.20	413.12	53.39	95.32
15296	137.87	56.84	269.21	33.23	95.32
22374	148.45	41.20	247.50	28.04	95.28
13239	109.46	48.17	236.67	36.75	95.28
8768	64.97	26.90	141.33	30.56	95.28
1542	927.15	264.15	512.83	50.15	95.28
22352	156.66	103.69	254.35	25.00	95.24
14051	133.17	35.29	219.32	28.80	95.24
9343	189.65	67.21	349.25	44.44	95.24
1247	1309.30	501.39	550.55	103.22	95.19
7857	52.35	45.86	156.83	28.07	95.19
11727	230.50	78.02	409.08	59.02	95.19
1639	96.67	22.79	153.44	17.91	95.11
15374	138.74	36.97	231.57	31.99	95.02
3899	141.45	61.33	242.19	14.71	94.98
25405	78.08	28.73	149.92	18.38	94.98
23872	49.59	92.93	101.10	24.53	94.98
24368	244.08	80.76	439.99	52.18	94.98
10818	465.48	185.96	140.29	49.38	94.98
17693	1257.86	376.37	596.02	96.76	94.98
25253	292.22	64.49	449.51	58.18	94.89
11708	319.92	92.39	486.60	46.21	94.89
17908	63.14	60.90	124.23	27.40	94.89
24028	407.75	96.21	644.04	67.17	94.85
11455	115.78	48.10	202.56	32.14	94.85
20870	19.10	29.21	92.31	26.59	94.81
3931	94.55	29.06	155.45	15.94	94.68
6581	76.02	26.19	132.63	10.11	94.68
1447	208.86	37.67	272.57	11.93	94.64
22501	257.01	67.60	383.79	63.10	94.64
10720	153.08	43.55	217.97	97.98	94.64
20591	25.22	22.60	68.79	11.62	94.59
1292	62.12	24.60	116.95	15.58	94.55
21355	374.95	118.50	635.77	102.99	94.51
23852	262.89	102.86	519.85	100.21	94.51
18689	360.99	81.71	541.28	55.93	94.51
4426	222.88	38.63	305.45	29.97	94.51
23563	24.57	33.24	96.80	28.33	94.46

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TABLE 5M: CISPLATIN					
Timepoint(s): 0, 24, 168 hrs					
Att. Docket No. 44921-5083WO					
Doc. No. 1798297.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
1521	20.35	50.42	152.11	27.16	97.37
1884	178.00	37.40	272.68	21.76	97.03
16284	40.57	26.94	134.66	25.22	96.99
18694	52.96	48.08	203.55	35.96	96.77
10839	312.93	66.86	524.22	78.99	96.77
11549	242.48	63.43	420.82	36.27	96.73
8990	277.44	76.38	515.35	72.77	96.60
6362	62.37	38.73	167.05	23.05	96.60
1811	10.74	25.96	89.58	21.97	96.60
4477	11.83	8.50	36.45	6.35	96.55
4047	85.57	50.18	181.03	26.48	96.55
16853	67.12	22.50	136.44	18.16	96.55
3266	132.70	35.81	249.33	37.38	96.47
13684	466.14	134.44	811.93	63.86	96.47
2905	244.60	105.83	525.71	99.02	96.43
1460	198.53	85.75	335.50	43.05	96.38
23314	69.18	274.82	477.84	185.93	96.25
17693	1260.38	374.54	570.60	88.76	96.21
15301	38.18	68.12	96.20	20.88	96.12
17894	46.77	18.63	103.03	28.25	96.08
10015	231.48	76.52	389.17	82.89	95.99
19040	185.68	106.97	292.78	52.89	95.95
18375	121.75	27.96	193.24	20.67	95.74
4426	222.53	38.25	311.48	25.65	95.74
7857	51.97	45.46	159.10	25.13	95.65
6454	239.16	77.72	421.14	34.72	95.65
15296	137.17	55.52	295.99	61.04	95.56
10818	467.00	184.46	97.87	70.28	95.52
23852	261.84	101.45	536.68	85.55	95.52
1542	928.65	263.36	505.79	51.94	95.48
20090	122.37	27.65	178.94	11.38	95.31
1247	1312.52	499.20	486.71	136.84	95.31
13682	176.87	61.56	326.18	46.83	95.26
14003	817.40	211.66	451.12	81.85	95.26
12478	82.11	29.97	149.88	36.04	95.22
1585	67.31	32.78	148.67	23.18	95.22
9339	357.01	87.72	575.84	68.74	95.13
23868	177.77	290.29	269.73	44.26	95.09
20591	25.06	22.48	69.25	11.11	95.05
3352	439.29	115.94	757.04	153.95	95.00
6974	129.29	46.84	219.21	32.67	94.88
8888	58.70	29.09	133.86	26.30	94.88
21061	58.67	27.62	123.00	16.55	94.83
7262	1114.68	393.99	1942.97	210.00	94.83
24368	243.52	80.33	427.84	45.50	94.70
25253	291.81	64.18	436.10	53.03	94.53
20921	26.87	19.97	73.82	15.18	94.44
15438	65.27	31.97	154.80	42.05	94.36
12174	80.78	29.36	153.45	26.53	94.32
808	469.71	142.88	210.55	55.06	94.23
19667	34.63	16.92	74.26	11.91	94.19
3886	57.79	28.39	128.86	25.08	94.19
20082	75.08	31.10	214.13	47.37	94.08
14051	132.96	35.15	209.45	29.46	94.01
5073	188.58	69.99	346.14	69.21	93.93

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TABLE 5M: CISPLATIN			Atty. Docket No. 44921-5089WO		
Timepoint(s): 6, 24, 168 hrs			Doc. No. 1798397.1		
Identifir	NonToxMean	NonToxSD	ToxMean	ToxSD	LoAScore
10344	22.23	21.56	63.33	9.18	93.84
15386	93.23	133.87	380.59	101.27	93.76
9882	486.99	181.36	244.23	35.18	93.76
4443	259.36	71.87	429.91	75.00	93.76
16080	44.85	252.23	176.73	162.58	93.76
22005	63.42	50.09	187.23	39.58	93.71
15313	10.94	24.26	52.72	7.91	93.65
6384	60.76	59.71	117.04	26.05	93.63
15701	37.60	16.66	75.18	12.81	93.58
22257	33.56	15.61	61.03	7.13	93.54
2655	42.88	48.17	155.13	62.85	93.52
4198	698.17	161.70	448.59	56.51	93.50
6522	569.21	150.95	877.20	111.47	93.28
19128	112.63	38.66	180.82	19.01	93.15
17314	5.74	11.53	57.89	29.34	93.13
22871	101.59	29.83	165.82	22.84	93.11
21275	224.35	79.76	492.77	134.59	93.09
1727	43.38	60.84	96.90	23.97	93.07
19249	264.62	60.02	356.76	20.60	93.07
1993	29.72	21.35	101.33	20.81	93.04
4584	82.33	29.05	125.60	12.25	92.98
24162	523.84	133.30	788.13	85.20	92.94
7522	31.71	18.92	74.24	15.00	92.89
17713	134.82	29.04	191.13	21.86	92.85
1428	-7.27	15.96	40.03	18.58	92.83
14776	99.41	35.18	153.67	26.50	92.81
3418	333.44	86.68	495.74	46.58	92.81
4199	529.94	132.34	301.96	61.95	92.64
21685	123.15	42.92	207.52	32.56	92.64
7023	363.44	76.61	483.68	29.43	92.55
4420	40.76	32.16	92.81	27.98	92.48
4121	62.21	23.49	110.83	18.20	92.42
18995	61.31	23.53	109.28	20.56	92.42
14665	151.38	37.30	219.57	23.41	92.33
11404	134.16	54.82	304.44	53.63	92.14
910	57.47	21.40	138.17	38.81	92.10
24081	117.08	63.79	235.77	50.20	92.03
22351	45.44	32.53	86.73	20.28	91.99
16012	72.47	31.00	153.59	33.17	91.97
22211	766.80	164.47	1061.59	90.34	91.95
727	210.80	38.94	274.04	15.91	91.90
9104	138.35	38.03	253.38	40.14	91.88
10417	43.82	25.97	125.71	32.61	91.88
10611	10.74	27.42	115.20	49.23	91.84
1314	262.03	49.07	394.88	48.07	91.79

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TABLE 5N: CITRININ		Atty. Docket No. 44921-5089WO			
Timepoint(s): 6, 24 hrs		Doc. No. 1798397.1			
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
17541	622.47	209.71	2524.98	697.44	98.92
6108	533.46	112.70	1024.58	102.59	98.62
25064	962.08	317.37	2651.31	379.95	98.58
1698	70.27	55.64	598.98	232.89	98.49
8820	130.72	105.90	755.03	221.60	98.41
23917	725.54	174.69	1782.62	536.25	98.36
20817	1043.62	545.12	5020.35	2088.07	98.32
15391	756.64	170.28	1510.23	272.65	98.24
20864	1562.02	620.45	4051.37	596.98	98.19
24192	70.11	37.23	212.99	53.54	97.93
20818	665.29	354.08	2965.76	1254.63	97.93
1340	192.34	49.85	114.30	11.66	97.76
20035	180.50	107.18	446.34	61.98	97.72
25525	1057.73	339.31	2228.58	326.32	97.55
18989	782.09	261.73	1560.14	205.30	97.46
3431	1496.13	608.90	3517.88	499.00	97.42
13723	734.46	282.33	1643.16	339.11	97.29
353	173.42	82.57	323.18	43.00	97.25
15848	1318.65	418.94	2622.73	442.07	97.16
634	1135.42	374.65	2281.52	441.32	96.86
354	214.25	93.76	406.34	75.12	96.77
7681	101.15	43.91	212.89	41.46	96.64
13610	357.22	70.16	213.99	29.24	96.56
5601	970.57	259.22	473.69	102.75	96.47
3876	30.44	14.34	1.17	8.63	96.13
24375	115.03	40.98	208.88	57.88	96.04
8212	2232.57	1104.98	5289.94	717.26	95.96
15106	1878.08	698.66	3540.36	359.29	95.74
14670	1214.56	325.29	1917.56	318.04	95.70
15189	1735.59	1153.61	4557.38	1226.17	95.70
24496	122.73	40.31	47.99	15.89	95.57
20895	332.13	100.81	137.61	37.56	95.52
20876	1661.97	599.79	3113.86	382.39	95.52
18533	35.68	17.84	5.09	4.52	95.52
6630	1393.25	256.89	913.59	112.68	95.48
20844	837.88	286.57	1606.81	216.13	95.44
15850	1209.74	343.26	2046.05	316.40	95.44
7315	-13.72	19.65	37.49	20.35	95.44
9254	247.89	49.11	157.69	17.49	95.44
15363	443.12	132.07	716.96	123.62	95.31
18359	245.00	113.72	546.56	83.87	95.22
8211	2822.70	1582.68	6312.46	772.17	95.22
16831	42.34	13.79	13.06	7.30	95.22
18644	2209.11	1246.61	5017.03	698.10	95.14
15190	1803.71	1156.33	4453.59	1177.82	95.09
15201	1480.71	527.22	2864.67	616.92	95.09
18205	277.90	58.81	408.93	34.56	95.09
19094	1054.85	243.62	1623.72	219.27	95.05
17108	219.83	44.77	132.90	13.45	95.01
10464	131.59	35.74	68.61	13.81	94.84
9409	102.66	32.91	171.76	24.78	94.84
7586	795.05	201.44	401.14	109.74	94.79
18800	2701.84	1144.69	5340.05	791.36	94.79
25675	688.20	206.46	1130.86	172.21	94.75
2697	1222.06	354.81	1908.51	176.60	94.75
10267	2101.59	872.11	4127.29	650.25	94.71

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TABLE 5N: CITRININ		Atty. Docket No. 44921-5083WO			
Timepoint(s): 6, 24 hrs		Doc. No. 1798897.1			
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
22773	230.97	52.31	131.59	26.18	94.54
1651	880.31	240.55	631.98	31.80	94.19
17494	219.24	41.89	138.20	23.13	94.15
244	51.19	35.18	14.03	8.20	94.15
17693	1247.25	372.94	2027.18	231.36	94.10
6946	389.05	103.41	200.78	37.64	94.02
23783	436.13	76.56	298.50	28.57	93.93
19408	1997.30	674.69	2937.88	154.93	93.89
20088	383.97	79.45	244.56	32.48	93.89
16272	192.25	63.76	102.37	22.94	93.89
2866	642.47	211.99	276.00	84.07	93.85
16954	48.70	79.17	202.92	44.32	93.80
21685	124.50	43.36	59.69	10.37	93.72
1719	145.21	38.11	80.93	12.30	93.67
20810	1256.69	398.25	2088.75	313.45	93.63
5049	298.40	65.85	175.28	28.59	93.63
1814	172.31	47.40	99.15	13.17	93.63
16193	101.42	30.67	44.23	15.12	93.59
15017	1007.41	395.69	2150.20	484.37	93.58
17886	1014.59	265.55	1558.32	151.72	93.50
20803	432.89	100.25	912.31	140.76	93.49
1537	29.21	35.65	294.59	185.42	93.45
1399	198.89	71.28	576.63	288.99	93.45
22583	26.67	14.48	3.43	7.60	93.37
3091	784.77	186.23	457.77	105.80	93.37
9029	430.46	93.52	614.72	63.36	93.37
16849	114.53	44.11	44.12	13.14	93.33
22414	58.52	33.14	101.78	22.01	93.33
8283	122.89	43.92	338.56	122.17	93.32
20918	440.21	126.29	269.42	29.15	93.29
25069	131.62	55.06	390.27	136.77	93.28
19067	175.20	51.04	88.87	21.48	93.24
7022	6.12	16.94	127.93	68.30	93.24
723	32.80	15.28	8.05	5.98	93.20
2242	2295.34	607.45	1325.08	393.96	93.16
24390	165.35	113.57	-9.44	39.74	93.07
17211	1434.51	548.50	2482.85	274.87	93.03
22406	79.97	30.24	31.26	10.08	92.90
24469	1169.56	333.98	1827.58	165.96	92.86

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TABLE 50: COLCHICINE		Atty. Docket No. 44921-6083WO			
Timepoint(s): G, 24, 48 hrs		Doc. No. 1798397.1			
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
23166	132.81	58.53	371.64	112.54	97.29
4412	377.59	61.12	558.75	77.91	96.99
18151	1133.81	261.37	563.27	117.10	96.47
15964	1187.13	325.69	508.38	159.50	96.12
11618	419.37	129.59	119.80	80.64	96.12
16882	177.88	54.70	82.96	14.87	95.78
24321	722.16	202.93	318.04	123.60	95.43
9097	258.85	82.10	115.52	31.47	95.05
20001	1683.96	373.32	1059.37	114.06	94.92
16913	1386.59	297.09	894.57	81.02	94.75
17887	1461.63	317.71	838.24	208.19	94.70
16924	445.74	155.90	188.36	46.16	94.57
20988	1221.44	211.78	853.97	84.52	94.49
22271	275.62	66.08	156.87	37.40	94.32
2222	802.84	200.86	537.76	35.92	94.06
6806	1236.90	342.77	566.10	189.93	94.01
13855	22.06	28.83	139.05	42.55	93.95
20513	57.97	25.96	166.84	71.44	93.82
9296	1306.96	257.77	840.48	105.26	93.80
643	62.16	32.97	14.32	5.63	93.71
16982	128.17	257.40	1462.72	552.54	93.60
20312	405.72	95.10	209.02	92.75	93.58
4073	562.17	184.40	230.54	83.32	93.58
3925	477.10	119.06	265.65	66.28	93.45
2913	736.68	160.48	481.77	40.00	93.24
10984	2020.41	564.71	1032.75	348.86	92.98
22321	100.73	64.58	321.87	131.71	92.96
2767	44.79	40.13	182.37	66.23	92.91
4151	563.27	167.25	920.16	111.75	92.89
7615	90.46	40.50	169.26	27.71	92.81
17399	1980.57	449.65	1255.63	187.29	92.64
6552	1594.49	296.14	1077.60	126.50	92.64
13111	228.20	73.35	132.80	17.16	92.59
13727	124.04	53.37	38.71	19.99	92.55
18642	974.76	203.55	664.60	62.35	92.55
3050	91.21	49.08	313.78	134.78	92.53
6438	114.03	57.15	38.70	14.25	92.51
20405	33.56	28.74	132.47	64.39	92.48
14185	202.17	89.20	491.51	237.69	92.48
16849	114.55	44.14	48.23	13.11	92.46
12901	1626.70	415.03	1002.61	177.27	92.42
20697	1421.26	277.19	931.95	163.03	92.25
8837	359.37	91.36	235.96	24.61	92.25
17361	145.97	59.92	56.10	14.57	92.20
17329	213.41	103.82	524.01	86.38	92.18
15600	774.27	210.27	435.87	107.62	92.08
16879	1207.58	276.77	796.63	98.39	92.03
4330	500.26	160.51	241.64	84.25	92.03
22152	7.72	33.71	81.27	38.69	91.79
21053	105.50	59.69	39.98	16.30	91.69
17324	360.96	79.01	153.55	65.98	91.58
7540	155.81	94.07	328.58	92.44	91.58
16128	286.68	62.49	192.02	31.18	91.56
14790	165.31	84.94	49.50	20.48	91.52
23115	570.61	171.16	295.42	91.28	91.47

TABLE 50: COLCHICINE						Atty. Docket No. 44921-6083WO	
Timepoint(s): 6, 24, 48 hrs						Doc. No. 1798397.1	
Test ID	NonToxMean	NonToxSD	ToxMean	ToxSD	LDA Score		
11057	32.46	28.53	120.72	43.20	91.41		
7537	230.23	69.42	125.41	29.85	91.34		
19822	1596.44	410.54	942.00	210.50	91.26		
17386	303.88	93.74	128.16	41.06	91.02		
17248	2568.34	534.75	1704.94	295.46	91.00		
15191	2013.99	1219.17	2599.48	219.23	90.96		
1141	240.56	63.32	390.27	85.33	90.93		
3099	966.22	189.19	660.01	95.36	90.70		
21024	577.99	113.27	331.56	66.79	90.59		
8709	148.12	48.57	78.15	19.09	90.57		
19731	226.36	215.21	98.99	29.40	90.57		
6250	492.94	104.90	372.14	23.59	90.53		
117	21.16	17.56	-5.10	9.54	90.44		
17401	907.31	422.79	1550.66	328.51	90.42		
15377	25.87	15.51	55.07	8.41	90.42		
17326	22.55	24.06	93.51	28.61	90.42		
22697	59.78	40.38	12.83	13.23	90.35		
14595	87.77	36.04	175.49	38.60	90.29		
9223	150.65	64.81	54.19	23.82	90.27		
8785	209.90	55.55	288.76	24.92	90.22		
9339	360.32	89.43	226.70	47.31	90.22		
23253	624.10	163.49	380.42	78.17	90.09		
25907	19.74	25.13	47.86	14.93	90.09		
15893	1733.99	343.83	1225.85	165.26	90.05		
23514	407.55	167.53	162.38	70.14	89.97		
3875	510.89	136.65	232.91	81.51	89.90		
406	362.17	77.76	250.18	48.87	89.88		
18343	437.98	107.72	280.49	46.68	89.79		
25461	49.71	22.92	20.96	5.68	89.75		
10789	326.18	107.75	117.23	67.68	89.73		
23145	44.09	20.22	87.09	15.12	89.73		
4048	-7.14	26.09	121.21	153.77	89.66		
11174	53.20	50.67	171.90	46.40	89.64		
23709	2491.22	1205.88	2706.26	145.13	89.45		
23224	194.78	48.70	129.40	19.04	89.41		
11215	143.29	71.54	26.34	56.76	89.23		
19479	276.88	106.02	134.33	36.73	89.23		
15872	152.44	63.81	467.24	163.94	89.23		
10985	1146.00	265.29	633.75	164.98	89.17		
18451	1444.75	418.00	943.24	132.82	89.10		
812	157.19	35.17	88.26	32.94	89.04		

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TABLE 5P: CYCLOPHOSPHAMIDE			Atty. Docket No. 44921-5039WO		
Timepoint(s): 6 hrs			Doc. No. 179337.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
17089	1545.78	604.39	6128.97	335.19	99.53
16081	113.02	372.25	1532.22	184.12	99.40
23619	327.35	96.06	660.24	21.96	99.32
5393	-31.45	22.77	27.35	5.29	99.32
24049	1517.02	432.93	3280.45	348.50	99.10
22698	261.92	112.70	-415.61	188.19	99.06
26222	371.68	149.80	1265.79	372.61	98.76
18118	895.16	271.71	2268.31	465.94	98.67
16469	1143.78	291.23	1083.34	3.98	98.67
17056	37.10	19.82	-6.41	5.49	98.67
7084	123.08	117.51	622.25	118.49	98.59
24213	1604.12	394.78	3341.49	503.25	98.54
3470	143.86	59.86	458.18	196.11	98.54
23711	4518.75	2192.54	16927.73	3240.54	98.50
18831	4165.13	1320.79	10676.69	1466.84	98.50
108	289.68	144.40	164.86	3.48	98.46
1409	425.27	87.17	260.86	8.34	98.46
8815	664.61	111.50	420.20	41.92	98.46
12130	90.83	34.97	39.25	3.30	98.42
8213	3583.64	1528.59	10080.02	1528.73	98.42
109	556.91	312.14	239.04	32.06	98.42
21637	28.01	19.25	-16.57	5.06	98.29
15819	42.77	22.12	-47.81	46.21	98.16
44	34.58	17.78	-3.41	3.04	98.16
6154	256.83	383.44	-1506.42	1100.74	98.12
13412	28.40	24.99	148.78	61.50	98.12
6720	68.84	60.28	240.34	21.68	98.12
5117	162.84	78.90	364.60	35.27	98.07
5329	47.29	21.30	10.39	2.22	98.07
21866	109.05	73.32	379.42	172.12	98.03
14953	482.64	76.56	311.16	19.07	97.99
18350	90.05	49.29	301.03	46.70	97.99
2029	305.29	103.47	350.85	2.88	97.99
8837	358.84	91.24	173.81	19.49	97.95
25721	83.34	54.43	240.21	44.54	97.95
16272	191.69	64.06	131.07	3.08	97.95
5969	1516.76	347.22	2916.15	354.10	97.90
1689	4338.65	2126.09	15982.97	5400.06	97.90
4232	137.19	62.23	27.42	11.32	97.90
3049	202.76	101.21	529.19	69.46	97.86
18800	2711.70	1148.84	6417.82	556.95	97.86
14424	67.07	130.91	324.02	83.71	97.86
8849	222.06	71.45	477.43	62.77	97.77
25777	404.46	182.63	824.09	102.83	97.77
16902	66.96	91.89	-172.67	27.28	97.77
23078	147.27	46.50	55.48	8.60	97.77
5461	193.94	117.20	396.91	37.67	97.73
24814	171.74	33.51	92.18	13.93	97.73
10860	46.07	29.90	-6.09	2.93	97.69
1698	74.37	76.29	197.25	24.89	97.69
15408	193.87	58.16	69.92	11.05	97.69
17832	1948.88	851.66	5675.58	2032.21	97.65
7127	280.56	95.94	21.98	52.78	97.65
744	334.35	68.28	208.28	11.29	97.60
3081	387.30	84.71	227.05	31.49	97.56
18918	31.10	27.35	-32.80	10.09	97.56

TABLE 5P: CYCLOPHOSPHAMIDE			Atty. Docket No. 44921-5089WO		
Timepoint(s): 6 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
15154	267.93	62.29	131.15	21.56	97.52
17771	768.98	305.15	1490.79	130.43	97.52
20493	460.39	110.11	297.05	12.72	97.47
24437	68.49	25.43	175.35	41.14	97.47
8999	47.02	23.49	1.97	4.96	97.47
15382	122.71	202.12	570.78	188.00	97.47
8599	378.10	107.09	181.07	19.58	97.47
17682	672.30	178.35	399.02	29.34	97.43
22862	103.01	36.20	42.20	6.28	97.39
20920	626.34	183.56	421.78	11.19	97.39
17334	173.83	58.72	358.42	40.10	97.39
4067	123.98	59.95	245.14	32.72	97.39
17357	269.19	82.48	105.14	28.10	97.39
23314	72.17	276.94	318.28	105.05	97.35
19190	534.12	144.15	283.73	32.84	97.35
16943	2759.04	872.63	5041.36	392.40	97.35
16947	319.84	80.34	186.33	13.16	97.35
6405	380.95	93.60	241.49	11.37	97.35
9053	239.81	50.85	135.66	11.51	97.35
25253	293.83	65.17	155.93	16.09	97.30
1688	5256.94	3710.90	21824.32	7449.14	97.30
19993	2319.53	566.29	3763.82	221.97	97.30
20846	2377.64	663.94	3619.10	135.20	97.30
22142	32.37	17.29	0.24	3.37	97.26
17602	131.67	36.83	52.59	13.48	97.26
18274	300.34	63.28	159.26	25.71	97.26
15410	504.68	101.83	257.23	33.63	97.22
7299	181.01	153.33	372.36	39.71	97.22
6585	649.58	366.37	1390.92	91.78	97.17
17426	537.84	84.20	386.94	14.48	97.13
15190	1818.28	1175.28	4173.32	371.68	97.13
13598	349.78	108.22	755.01	165.06	97.09

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TABLE 59: DIFLUNISAL		Atty. Docket No. 44921-5089WO			
Timepoint(s): 24 hrs		Doc. No. 1798397.1			
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
15582	98.54	389.02	523.22	20.51	99.87
23699	325.81	88.09	984.09	67.68	99.79
1858	165.70	50.67	468.35	55.34	99.66
18687	415.65	168.60	1876.04	173.83	99.66
20810	1260.74	402.11	2154.96	30.08	99.44
23698	272.98	101.50	824.56	62.23	99.44
15906	73.43	105.60	328.56	63.09	99.40
21354	414.86	118.96	1273.64	189.63	99.36
16918	1181.89	410.28	2103.00	56.71	99.36
15048	861.35	213.04	1349.81	15.30	99.32
17758	126.22	53.45	567.25	114.93	99.14
23504	176.69	49.53	287.50	5.80	99.14
18686	468.60	214.77	2050.51	247.31	99.14
5351	711.19	145.06	979.89	15.97	99.06
18083	48.75	24.85	148.28	10.77	99.06
1977	142.19	40.33	293.78	26.17	98.97
20833	1254.24	350.22	1826.03	17.16	98.84
4012	650.38	267.26	1484.68	174.94	98.84
18250	1093.45	315.54	1684.15	30.30	98.80
26109	69.08	76.43	458.33	59.25	98.76
4049	23.28	65.36	63.64	6.15	98.76
23837	101.76	41.27	57.70	0.48	98.76
25679	901.31	261.02	1610.91	63.61	98.76
5887	79.37	88.10	285.80	15.29	98.63
23409	535.77	161.09	346.74	3.30	98.54
6380	135.92	123.74	459.26	82.61	98.54
2457	289.86	77.14	519.55	38.45	98.42
5687	744.60	177.74	1191.89	49.47	98.42
18293	770.57	235.09	1635.35	158.85	98.37
15579	32.24	115.84	189.18	29.09	98.33
18647	251.55	67.39	138.00	4.76	98.29
16849	114.09	44.40	66.30	1.36	98.20
15580	95.99	152.88	276.60	38.55	98.20
11205	594.93	193.66	371.24	5.25	98.20
17211	1440.25	553.34	2327.85	45.31	98.16
19244	1224.59	378.82	2305.53	135.95	98.16
1728	351.65	81.13	555.88	47.36	98.16
4010	965.06	407.94	2268.41	360.86	98.12
17563	1201.51	347.34	2039.09	80.83	98.07
19067	174.78	51.26	80.87	6.55	98.03
14763	38.55	133.68	500.64	63.55	98.03
17158	240.63	83.07	105.20	10.26	97.99
19727	1326.99	416.44	2052.69	41.43	97.90
2708	383.06	86.76	506.29	10.15	97.90
16204	755.43	187.45	1101.24	54.31	97.90
24748	-22.65	38.12	33.61	1.39	97.86
15239	567.21	132.24	803.19	32.26	97.82
22052	256.34	73.77	451.80	35.28	97.77
20715	135.54	60.66	373.16	45.27	97.73
19268	940.57	273.83	1595.25	83.86	97.73
17686	1016.62	266.11	1780.84	121.15	97.69
20986	36.18	25.28	113.63	23.08	97.65
3027	1127.48	331.63	1756.65	53.48	97.65
23849	287.19	137.85	391.28	6.74	97.60
4952	108.82	48.80	171.37	6.32	97.60

TABLE 50: DIFLUNISAL		Atty. Docket No. 44921-5089WO			
Timepoint(s): 24 hrs		Doc. No. 1798397.1			
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
1814	171.85	47.69	123.88	1.67	97.56
20839	1043.73	290.47	1565.67	42.99	97.52
16190	288.78	81.88	502.75	35.87	97.52
15875	1183.10	392.02	1973.54	86.87	97.35
16701	830.81	197.66	1528.91	267.69	97.35
15106	1887.41	709.31	3311.08	123.87	97.26
3434	326.00	140.86	131.21	15.66	97.26
21729	582.55	246.48	1512.04	499.79	97.26
19952	67.28	24.42	23.96	3.74	97.26
20818	681.56	422.22	1663.94	317.99	97.17
20149	1324.01	582.48	2795.60	215.42	97.17
14959	619.74	147.94	1010.98	113.74	97.13
16148	762.99	195.12	1313.23	188.91	97.13
24886	1263.69	371.87	2046.76	132.13	97.13
10878	952.87	253.83	1373.59	38.24	97.09
8946	207.89	87.83	74.88	7.06	97.09
19477	112.98	54.74	250.89	20.66	97.00
15468	734.22	179.64	1032.19	49.88	97.00
10109	1045.52	288.55	1597.93	74.73	96.96
3924	182.19	68.67	273.97	5.41	96.92
18918	31.02	27.50	-11.16	3.27	96.88
17729	878.67	224.12	1508.83	163.08	96.83
14695	1736.29	632.39	2885.22	95.16	96.79
9799	145.87	50.77	85.38	3.80	96.79
20925	337.86	103.37	649.53	101.58	96.79
25501	102.21	56.92	20.07	8.06	96.79
7062	686.14	173.76	1144.72	115.88	96.79
5398	0.40	12.35	33.62	24.14	96.75
20711	43.78	42.18	150.73	22.20	96.75
373	34.25	61.71	167.08	44.08	96.70
16929	956.64	234.98	1405.43	58.88	96.70
20817	1073.65	677.30	2215.68	400.07	96.70
4291	295.13	101.25	151.24	8.90	96.70
23336	141.91	43.60	268.14	38.59	96.66
23270	209.26	61.36	302.15	9.89	96.66
4259	700.25	158.48	1007.49	53.89	96.66
18509	418.06	82.28	584.02	27.38	96.62
1694	1145.19	337.82	1796.01	81.50	96.58
4011	459.62	198.95	896.31	148.45	96.53
6949	1.61	27.50	36.30	10.98	96.49
4713	107.84	37.11	71.04	3.04	96.40

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TABLE SR: HYDRALAZINE			Atty. Docket No. 44921-5083WO		
Timepoint(s): 6 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
23230	381.93	101.69	164.86	3.08	99.83
7299	180.37	151.55	684.70	26.37	99.66
11005	71.62	20.88	31.26	0.53	99.66
18715	190.60	53.82	312.84	2.17	99.66
18713	300.35	70.22	564.29	26.19	99.62
9306	45.76	18.52	121.89	7.27	99.62
19004	788.98	306.09	794.75	1.65	99.57
9525	5.08	44.31	64.20	2.12	99.57
19712	98.45	32.90	58.61	0.21	99.53
16203	66.52	16.97	45.27	0.17	99.53
20513	58.53	27.11	242.01	35.67	99.49
5918	26.70	40.82	72.84	4.20	99.44
14479	473.36	112.67	261.32	4.86	99.44
4194	34.33	17.04	74.46	0.76	99.40
8948	217.22	104.91	343.57	1.20	99.40
15015	503.71	91.72	339.92	3.82	99.36
22746	534.33	197.34	312.42	2.15	99.36
13235	16.43	13.42	75.50	8.64	99.32
90	93.87	50.03	147.79	0.44	99.32
16069	59.01	26.48	31.84	0.25	99.32
20523	549.70	152.39	1021.93	29.01	99.23
15872	155.66	71.91	53.38	1.82	99.23
3513	171.87	35.63	273.79	6.58	99.19
7452	8.04	13.04	37.85	2.68	99.19
15059	92.43	24.57	82.57	0.16	99.14
8597	241.04	57.82	387.68	12.70	99.14
20849	277.59	87.41	309.60	0.68	99.08
13298	101.48	29.62	51.68	1.68	99.08
11406	242.13	50.08	177.73	0.85	99.02
7071	133.86	64.50	98.99	0.88	99.02
23189	330.92	72.72	460.60	3.57	98.97
15411	303.87	90.07	657.96	59.65	98.97
8692	1045.40	309.78	638.87	9.02	98.97
22614	17.91	87.18	86.87	14.83	98.93
4969	-18.84	34.82	77.79	30.12	98.89
3081	387.16	84.82	227.51	15.73	98.89
15231	100.29	44.00	233.89	22.19	98.85
15942	230.65	65.79	294.11	1.11	98.85
18406	33.60	18.22	70.49	1.79	98.85
16024	239.14	63.32	487.33	52.09	98.85
2539	46.96	51.90	304.80	46.42	98.85
26119	124.62	46.64	176.21	1.26	98.80
6723	200.38	72.05	91.78	10.99	98.76
21878	144.05	35.94	106.39	0.58	98.76
8664	106.71	250.43	160.02	4.54	98.72
21014	155.47	80.73	369.94	37.53	98.72
14842	122.80	45.94	280.85	20.55	98.72
13093	700.37	165.48	367.14	36.76	98.72
20404	53.45	44.01	336.92	98.70	98.72
15126	792.34	224.59	1256.68	25.48	98.67
4948	153.55	61.38	307.30	11.57	98.63
6844	123.76	58.60	32.99	3.47	98.63
16025	150.51	42.20	268.08	8.85	98.59
7615	90.87	40.61	221.25	17.10	98.55
22575	20.61	15.66	10.19	0.32	98.50
23141	239.29	55.53	490.92	129.05	98.50

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TABLE 5R: HYDRAZINE			Atty. Docket No. 449241-5089WO		
Timepoint(s): 6 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LPAScore
15636	39.88	26.09	4.00	1.07	98.50
15885	93.27	28.63	182.42	15.91	98.46
5355	1164.75	345.23	1050.46	4.54	98.46
13151	711.00	343.67	1290.08	71.04	98.46
19195	1555.05	374.36	1121.86	8.23	98.42
6606	249.66	121.42	743.36	159.90	98.42
2888	2015.72	588.67	1201.76	29.67	98.42
20405	34.08	29.57	195.15	62.34	98.42
7197	197.58	84.65	309.34	7.55	98.42
1215	67.05	49.57	246.66	40.98	98.42
17479	157.69	34.71	89.24	4.57	98.37
22733	21.90	14.11	64.22	8.36	98.37
1920	426.50	112.57	740.10	44.20	98.37
8745	57.56	19.95	100.05	2.83	98.33
22915	171.30	47.15	114.08	2.66	98.33
25587	24.39	16.37	17.05	0.15	98.33
13259	68.80	25.82	161.38	28.29	98.33
17468	396.41	77.87	278.70	4.37	98.29
14405	465.44	308.54	1276.71	188.93	98.25
14861	48.74	17.37	75.52	1.15	98.25
3027	1129.44	333.52	1205.87	5.52	98.25
1214	165.46	52.58	424.14	92.45	98.20
11158	1023.54	302.35	1115.38	6.37	98.20
20202	624.37	196.92	959.56	18.31	98.20
18290	275.55	78.31	420.92	7.75	98.16
21527	239.85	60.68	369.29	12.50	98.16
24885	1107.60	334.53	1092.86	5.80	98.16
23689	0.64	11.77	22.99	3.94	98.16
8869	8.35	21.59	31.83	0.60	98.16
17502	147.76	53.99	264.34	13.12	98.16
13203	-15.66	28.87	51.81	11.94	98.12
25971	106.47	34.61	50.27	2.15	98.12
13095	60.49	15.80	32.26	1.41	98.12
26036	34.25	17.22	19.79	0.49	98.12
17570	230.73	71.54	273.93	2.11	98.08
22543	689.99	222.20	447.42	9.98	98.08
17312	26.98	34.41	42.60	0.40	98.08
16026	221.52	75.94	411.54	26.17	98.08
5684	333.75	76.46	482.85	10.21	98.03
15879	374.14	93.39	276.43	3.61	98.03

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TABLE 5S: IPOSFAMIDE					
Timepoint(s): 6, 24, 48, 144 hrs					
Atty. Docket No. 44921-5083WO					
Doc. No. 1798337.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
19252	647.94	142.98	520.93	34.13	89.74
16222	2071.83	907.04	1625.21	143.87	88.88
16148	767.65	197.63	575.47	57.95	86.32
17779	1952.57	790.85	1617.53	137.53	85.80
12932	153.85	49.70	108.04	13.75	85.63
11158	1027.66	302.42	759.65	56.80	85.37
10947	1800.32	754.28	1416.69	180.51	85.28
19408	2011.57	680.23	1580.63	160.66	85.24
16013	58.91	18.74	71.23	5.22	85.11
19254	241.32	76.35	239.54	14.43	85.06
17886	1504.90	495.37	1122.51	90.54	84.72
16895	2027.29	906.56	1603.00	189.71	84.63
18300	450.17	150.80	318.95	39.08	84.33
8211	2862.98	1618.85	2138.69	273.26	84.29
23710	1141.57	367.03	897.82	79.04	84.20
11954	3141.99	1699.73	2471.68	314.40	83.90
1853	2014.76	833.49	1614.19	220.80	83.90
14695	1746.72	637.07	1297.75	126.83	83.77
8212	2267.04	1143.40	1689.07	186.62	83.42
13976	453.36	377.22	783.29	266.52	83.38
14997	2596.32	1029.67	2216.17	249.47	83.20
23709	2500.59	1207.33	1994.07	261.44	83.16
22592	234.68	168.43	397.15	108.13	83.08
18142	2001.91	840.95	1479.52	180.12	82.99
9135	719.00	131.99	601.54	43.95	82.90
14694	2326.49	1072.07	1849.47	243.07	82.69
18810	1189.60	320.47	979.08	72.74	82.60
18077	2627.05	1191.54	1778.68	232.31	82.56
15125	1303.70	426.26	1007.41	95.34	82.55
20751	706.77	161.80	835.79	96.53	82.51
44	34.24	17.91	48.60	8.82	82.47
23544	1515.02	495.50	1325.70	110.75	82.17
19993	2320.17	574.10	2616.44	234.66	82.03
9942	443.45	98.80	518.47	38.50	81.95
17682	673.25	179.30	543.60	51.66	81.95
23574	2282.20	973.76	1808.58	200.84	81.82
6815	1138.28	344.89	837.60	73.20	81.65
11050	671.41	139.50	791.75	84.37	81.60
1247	1310.50	504.69	915.02	93.84	81.60
18078	1152.53	545.02	1014.06	139.87	81.56
1801	97.60	29.90	123.54	20.25	81.43
12901	1613.41	414.49	2126.00	326.75	81.39
20035	182.08	110.21	229.47	33.04	81.39
17118	53.61	19.28	66.07	6.68	81.30
17204	1733.32	660.21	1299.09	155.20	81.26
23847	47.46	36.72	90.72	17.29	81.21
10500	24.88	31.73	53.21	18.49	81.17
8347	76.96	46.62	110.08	23.49	81.13
3015	2318.93	997.42	1869.25	225.78	81.04
20832	722.84	197.13	591.89	72.43	81.00
18615	521.90	148.77	363.34	55.31	80.95
5989	269.37	71.43	354.20	68.39	80.91
19894	40.81	20.31	62.51	16.82	80.83
18076	2548.69	1193.37	1768.87	244.55	80.83
21423	1355.89	429.81	1080.04	115.43	80.78

TABLE 5S: IPOSFAMIDE					
Timepoint(s): 6, 24, 48, 144 hrs					
Att. Docket No. 44921-5089WO					
Doc. No. 1793397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
1523	89.47	23.47	100.14	7.66	80.70
11991	57.24	22.13	76.61	11.20	80.65
23109	2089.70	930.42	1566.07	197.88	80.44
19727	1331.92	420.23	1162.29	117.79	80.44
18451	1434.72	418.40	1801.12	268.28	80.39
23884	41.09	33.35	54.46	12.98	80.39
472	662.53	178.22	500.21	63.31	80.35
11153	1474.65	500.35	1320.86	134.33	80.35
23125	4577.67	2547.90	5632.15	1198.40	80.31
12598	545.25	95.85	644.01	73.00	80.31
915	30.40	17.20	53.68	14.78	80.26
6808	698.18	193.62	893.93	94.12	80.26
10260	85.57	33.38	94.71	10.64	80.18
25545	94.20	49.43	150.75	32.71	80.09
23660	1281.20	383.06	1072.18	89.30	80.09
15410	504.96	102.87	427.16	47.59	80.05
977	16.73	10.91	41.99	18.19	80.01
15137	1520.02	496.49	1254.30	128.20	80.00
26109	69.41	79.57	138.16	53.60	79.96
11136	1003.50	311.65	725.42	110.05	79.92
4217	519.77	126.27	592.35	45.95	79.92
13480	650.24	137.90	533.92	69.48	79.83
15535	448.65	83.59	358.13	46.40	79.79
15426	411.88	86.42	342.56	30.90	79.66
16012	73.15	32.18	78.40	10.56	79.65
4849	773.73	168.65	929.55	91.93	79.61
17765	1296.75	460.31	914.95	107.23	79.61
23967	383.11	92.35	484.27	65.27	79.53
9905	673.59	140.94	588.24	39.94	79.53
1583	30.08	18.99	43.08	7.71	79.53
1743	29.18	16.19	50.78	15.93	79.40
15446	370.71	93.07	266.06	61.63	79.40
18905	1363.50	302.26	1680.54	182.30	79.36
24049	1519.32	446.29	1776.05	182.78	79.31
24626	1504.58	431.27	1251.16	114.87	79.31
820	2467.06	1167.88	1920.44	339.35	79.22
1684	2833.17	1621.88	1212.60	870.83	79.22
21373	373.62	85.16	332.82	32.95	79.22
16211	2261.75	1141.46	1652.93	320.55	79.18
16521	285.41	90.61	359.56	55.31	79.14
22661	1309.12	421.45	1003.73	117.38	79.01

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TABLE 5T: INDOMETHACIN				Atty. Docket No. 44321-6033WO		
Timepoint(s): 48, 72 hrs				Doc. No. 179337.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore	
155	21.42	16.96	101.88	13.61	99.53	
154	112.29	36.99	249.23	25.25	99.27	
16173	14.63	13.08	179.81	66.16	99.18	
13614	340.21	88.42	786.72	118.82	99.01	
1850	46.85	347.25	309.01	159.03	98.93	
22499	8.20	11.83	58.62	9.91	98.88	
1893	29.44	20.17	163.67	70.52	98.84	
1221	0.23	15.84	193.08	98.35	98.80	
21445	0.99	14.21	203.14	86.78	98.75	
1854	43.31	289.94	282.61	143.16	98.67	
25517	38.27	31.10	173.50	50.20	98.58	
19710	43.43	20.81	132.45	42.06	98.54	
6431	51.07	32.99	209.15	53.95	98.50	
2457	288.90	75.46	543.74	54.46	98.45	
7299	177.44	143.66	797.13	276.35	98.41	
23964	12.50	18.01	63.92	17.10	98.37	
1943	31.78	14.21	86.66	15.03	98.15	
13615	253.23	68.59	560.03	77.71	98.15	
20713	215.61	108.00	606.67	98.17	98.11	
24237	56.39	37.15	281.98	103.56	98.07	
8565	31.85	16.10	105.94	38.19	98.02	
7540	154.84	89.44	535.02	179.10	98.02	
1845	-7.69	24.61	109.59	48.06	98.02	
18684	137.77	49.02	305.11	48.29	97.98	
7858	-4.71	7.47	47.48	40.75	97.98	
15408	192.19	56.59	376.55	44.39	97.98	
10281	172.58	185.66	567.51	296.37	97.94	
18867	103.82	49.82	263.24	51.22	97.94	
18353	112.33	68.84	349.21	48.50	97.94	
20715	134.85	59.63	354.19	34.91	97.90	
6551	576.57	201.46	1150.85	135.93	97.90	
7665	282.66	95.03	609.80	128.48	97.90	
20868	22.06	17.54	98.66	30.62	97.85	
343	28.72	32.40	151.55	21.38	97.85	
20869	21.84	21.14	111.52	32.81	97.85	
20711	43.08	40.65	197.85	41.42	97.77	
16521	283.95	85.02	655.14	127.79	97.59	
21444	19.93	43.02	180.28	49.29	97.51	
21683	33.96	22.93	127.35	39.46	97.47	
3180	309.65	80.63	524.23	45.30	97.47	
1942	17.90	24.48	99.74	38.19	97.47	
14184	113.17	49.05	251.46	48.41	97.42	
1894	202.61	73.39	421.42	64.64	97.42	
15851	200.88	151.27	525.10	94.05	97.38	
20700	85.68	416.32	391.89	193.02	97.38	
4749	234.65	200.18	431.09	62.04	97.38	
6094	138.21	54.26	356.45	88.21	97.38	
2555	96.41	46.12	235.98	52.95	97.34	
3260	193.81	71.46	443.67	108.75	97.34	
19012	483.92	149.86	930.52	98.29	97.21	
5887	77.25	81.17	491.60	169.72	97.16	
20041	192.79	82.66	490.91	119.03	97.16	
16007	26.63	17.31	92.50	26.48	97.04	
21653	236.04	61.07	399.34	79.22	97.04	
13004	142.59	42.21	275.32	36.65	96.99	

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TABLE 5T: INDOMETHACIN				Atty. Docket No. 44921-5039WO	
Timepoint(s): 48, 72 hrs				Doc. No. 1798397.1	
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
19387	667.36	146.95	1017.20	82.56	96.99
2554	53.34	18.18	111.59	20.52	96.99
4861	307.32	90.25	543.97	56.72	96.91
21467	13.64	131.26	140.69	60.68	96.86
18352	162.12	85.33	437.38	90.35	96.86
15191	2030.38	1211.92	434.31	67.70	96.86
24183	68.30	35.60	194.82	48.12	96.82
4748	110.39	127.49	266.50	52.38	96.82
19711	83.58	22.63	149.45	21.04	96.82
848	18.09	11.05	45.15	4.76	96.65
10015	231.63	76.39	422.68	89.46	96.65
11708	319.08	90.38	587.03	103.59	96.65
22321	101.90	68.06	234.02	51.42	96.61
1597	50.19	41.89	187.05	63.28	96.61
6120	511.17	159.69	914.08	108.73	96.52
20714	178.33	78.97	430.20	87.05	96.52
24200	421.16	141.29	847.55	177.88	96.52
3316	8.48	11.20	32.02	7.24	96.48
14595	87.99	36.42	175.31	16.47	96.39
21654	362.19	114.34	536.63	59.58	96.22
22479	433.07	146.06	846.76	137.55	96.18
18687	418.98	188.38	661.54	59.97	96.13
5572	330.93	144.21	692.30	98.63	96.09
3020	292.14	93.53	549.45	92.30	96.09
25366	52.69	46.59	140.27	34.35	96.01
11183	98.16	39.08	183.02	34.74	96.01
19145	363.77	71.33	513.30	38.33	95.96
15409	399.23	98.94	637.09	62.27	95.88
17950	64.06	23.04	112.35	10.61	95.79
16945	934.12	162.35	1222.61	66.01	95.79
16917	755.96	258.94	1351.72	135.35	95.75
9286	205.05	59.59	354.73	51.76	95.66
18217	15.31	19.01	63.19	16.35	95.62
14185	203.46	94.18	411.57	81.62	95.62
16646	28.33	20.91	71.67	15.31	95.58
23837	100.89	40.39	206.26	37.38	95.53
21066	43.85	16.28	90.93	15.15	95.53
18068	82.30	21.15	125.33	8.28	95.49
21410	183.82	61.54	326.34	61.71	95.45
18355	56.83	27.50	129.21	39.86	95.36
6044	327.15	91.24	520.74	70.39	95.36
23145	44.14	20.10	96.23	26.84	95.32
16859	122.48	51.26	241.14	54.89	95.27
15246	63.40	20.73	113.00	17.39	95.19
24019	27.09	25.66	86.45	18.38	95.19

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TABLE 5U: LITHIUM CHLORIDE					Att. Docket No. 44321-5089WO
Timepoint(s): 120 hrs					Doc. No. 1798397.1
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
24019	27.07	25.30	127.00	8.27	99.61
14421	418.40	87.55	639.64	12.93	99.57
13641	47.49	30.07	145.93	13.26	99.53
1463	619.17	296.16	1455.45	46.93	99.53
16300	61.51	20.88	147.76	15.29	99.49
13974	296.90	139.79	1260.41	77.75	99.49
3244	127.45	30.43	40.35	2.64	99.36
10464	131.43	35.68	41.70	2.59	99.36
1462	407.93	201.27	1216.38	60.80	99.36
18525	246.32	66.03	97.58	6.10	99.27
14227	72.35	65.02	265.04	34.60	99.23
25741	185.55	57.43	480.81	62.92	99.23
1224	3.70	11.53	50.50	8.69	99.23
13880	679.69	204.44	295.39	24.01	99.14
14261	39.73	17.42	113.90	16.40	99.14
18472	1551.82	378.09	827.52	66.71	99.10
15363	446.56	133.55	187.16	15.68	99.06
8598	139.25	41.61	362.49	73.57	99.01
5176	217.77	121.65	603.36	60.94	98.93
14754	99.93	24.11	228.47	44.23	98.93
20849	276.44	85.41	555.38	36.71	98.93
15955	750.17	198.73	371.84	30.56	98.89
14633	97.72	88.30	1.97	5.36	98.84
15371	378.04	55.30	593.66	40.88	98.80
17342	202.36	532.80	480.79	60.48	98.80
20809	317.42	60.81	558.00	56.79	98.80
16650	256.32	82.88	614.21	64.30	98.80
18109	19.25	21.24	92.33	9.99	98.76
18286	10.51	10.22	41.67	5.33	98.76
24049	1526.25	442.84	773.94	52.98	98.76
16245	386.32	115.78	64.71	31.63	98.76
23651	656.57	627.85	1600.29	142.54	98.76
574	335.41	164.90	679.82	42.41	98.71
20099	81.48	29.97	171.81	18.17	98.71
1876	24.82	21.34	269.98	118.48	98.71
23294	244.42	55.35	115.25	8.35	98.71
3733	340.43	153.36	790.69	47.48	98.67
23957	68.22	41.24	264.04	43.03	98.67
3348	496.09	130.59	245.12	25.78	98.67
20697	1418.84	278.90	908.67	36.86	98.67
260	415.71	110.33	903.01	137.68	98.63
19321	313.57	55.98	464.14	23.58	98.63
8597	240.21	54.94	523.47	111.57	98.63
17159	699.06	218.26	1124.72	53.18	98.63
18103	58.33	28.29	149.64	17.07	98.59
5698	1169.95	220.06	1885.00	141.61	98.59
24648	40.24	20.33	6.76	1.40	98.59
14020	277.14	68.14	152.09	12.77	98.54
15246	63.64	21.09	87.26	0.84	98.54
24115	68.51	36.48	345.37	126.46	98.54
21997	28.94	25.26	95.22	19.06	98.54
960	191.35	46.71	93.10	7.12	98.50
22321	100.55	58.87	629.47	166.32	98.50
20886	711.00	279.64	2114.90	382.05	98.50
16354	280.15	119.74	-118.26	64.76	98.50

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TABLE 5U: LITHIUM CHLORIDE					
Atty. Docket No. 44921-5083WO					
Timepoint(s): 120 hrs					
Doc. No. 1798397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDA Score
12376	19.26	124.98	83.39	19.10	98.50
17106	81.66	24.82	36.82	2.74	98.50
18473	2589.69	916.99	1318.66	52.24	98.50
9254	246.49	48.78	393.24	20.14	98.46
1340	191.26	49.84	289.47	26.83	98.46
17162	6.69	16.97	58.11	15.91	98.46
6806	1233.36	345.85	586.60	42.84	98.41
25840	-2.65	12.34	54.97	27.90	98.41
20887	784.36	296.51	2396.08	485.51	98.37
1372	199.45	51.98	391.46	35.86	98.33
18349	140.08	38.43	262.92	23.80	98.33
14989	500.38	106.29	910.22	99.63	98.33
4049	23.03	65.14	113.93	24.17	98.29
11483	65.04	45.49	132.25	10.90	98.29
9867	29.07	22.58	38.05	11.94	98.29
13411	789.51	324.70	239.08	27.46	98.29
25709	267.20	83.61	591.14	81.21	98.29
17160	1038.70	287.67	1872.62	168.15	98.24
12673	37.66	22.70	116.03	13.02	98.24
25306	27.76	21.91	-55.70	19.66	98.24
16349	47.04	14.11	94.68	13.74	98.24
13392	190.93	48.80	355.59	34.39	98.24
4048	-6.11	32.04	34.41	10.44	98.20
2915	87.49	36.50	176.88	18.22	98.20
15761	90.06	42.30	20.08	3.24	98.20
111	590.89	237.37	1115.91	164.07	98.20
24695	63.72	21.72	13.53	4.47	98.16
19152	164.93	52.20	401.36	74.04	98.16
24597	585.04	105.40	935.83	83.53	98.16
21527	239.33	59.62	438.09	50.65	98.16
3776	377.17	93.88	689.18	68.23	98.16
5626	26.84	18.16	84.22	9.81	98.11
3075	524.14	179.66	209.94	19.92	98.11
15511	214.84	128.36	897.69	308.94	98.11
6386	20.45	18.01	-5.75	1.87	98.07
134	69.84	33.24	7.05	4.13	98.07
19665	91.84	47.87	296.74	33.57	98.07
10984	2015.62	568.01	964.72	141.17	98.03
15247	637.80	190.94	1369.01	148.83	98.03
2905	246.54	108.85	410.67	11.79	98.03
13343	210.51	55.05	72.01	21.01	98.03

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TABLE 5V: MERCURIC CHLORIDE					
Timepoint(s): 3, 6, 24 hrs					
Atty. Docket No. 44921-5089WO					
Doc. No. 1798397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
8665	332.39	171.86	5197.14	2943.02	99.44
1475	136.94	103.32	3940.87	1974.36	99.18
20035	178.08	98.83	635.50	155.87	98.10
19723	74.87	55.61	273.03	109.44	98.02
15191	1988.23	1177.92	5041.11	935.19	96.55
14139	80.54	27.01	25.59	13.59	95.47
8664	86.42	70.91	2082.06	1352.81	95.23
12331	594.25	156.97	254.07	138.26	94.96
17734	119.63	75.92	566.88	280.56	94.84
23579	734.95	158.66	430.76	80.03	94.78
23983	544.27	150.95	220.82	131.74	94.46
14138	84.72	29.10	33.29	12.42	94.31
16518	826.45	273.09	2395.53	930.51	94.24
17635	651.30	148.78	358.62	92.32	93.79
7196	178.22	77.07	494.09	205.98	93.68
15850	1203.52	323.32	2507.97	545.30	93.68
24235	433.60	163.10	1038.60	349.80	93.55
21445	2.08	22.76	30.67	12.91	93.51
24649	122.93	28.55	76.77	12.19	93.49
5867	166.42	48.13	259.79	50.17	93.49
3348	497.46	129.58	259.25	78.88	93.45
15848	1313.68	402.72	2886.50	676.70	93.42
19768	706.30	166.91	1328.43	290.35	93.42
17161	1144.51	381.55	2737.15	723.56	93.33
1004	108.90	32.28	56.68	10.23	92.84
15190	1789.26	1124.32	5409.42	1117.57	92.73
14595	89.23	36.84	26.57	16.82	92.67
15189	1722.10	1120.12	5391.29	1462.09	92.60
15300	135.69	130.01	397.39	125.33	92.60
23314	67.33	271.41	622.50	259.52	92.43
15301	37.59	67.32	147.90	49.32	92.39
18944	202.65	68.48	458.00	181.57	92.30
6054	27.38	53.50	71.68	29.34	92.26
13642	209.02	74.04	85.92	29.90	92.24
23230	378.13	96.00	695.07	177.40	92.17
17211	1433.79	549.05	2380.95	279.33	91.85
3493	58.50	20.07	107.74	26.19	91.82
23825	283.86	49.04	166.00	50.35	91.78
18564	219.22	49.05	95.46	32.77	91.74
11680	360.19	81.92	233.52	34.79	91.68
17765	1277.82	438.77	2585.84	579.12	91.65
16982	138.22	290.89	380.00	223.17	91.57
13610	357.65	69.18	196.18	80.11	91.26
21993	76.47	25.96	129.83	18.36	91.26
8927	745.07	166.28	377.77	106.17	91.01
11871	55.24	129.01	197.33	57.60	90.91
11050	670.06	136.16	972.43	147.61	90.88
13507	422.59	99.12	659.30	138.95	90.83
9271	102.44	54.22	21.68	25.82	90.82
19031	59.98	47.58	145.41	39.97	90.79
24577	1168.59	364.98	2135.75	393.09	90.79
10182	2.45	99.29	78.59	59.67	90.75
18300	451.47	147.74	136.58	90.13	90.75
18259	207.76	78.23	1353.31	770.76	90.72
1928	485.55	106.87	208.21	110.11	90.66

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TABLE 5V: MERCURIC CHLORIDE					Atty. Docket No. 44321-6089WO
Timepoint(s): 3, 6, 24 hrs					Doe. No. 1793397.1
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
6632	171.87	58.89	288.22	64.66	90.53
13611	273.95	107.44	57.12	66.20	90.45
25098	43.26	30.01	276.68	179.66	90.37
22539	71.67	46.78	-27.28	37.71	90.36
20945	897.15	248.57	1469.22	277.42	90.32
19678	110.11	57.05	-19.38	53.40	90.32
23567	52.11	60.74	235.62	105.54	90.29
23868	159.82	189.43	1997.17	1212.75	90.24
812	157.29	34.98	83.70	36.70	90.19
23872	44.34	80.45	587.85	460.34	90.16
21372	276.72	65.43	134.32	44.54	90.10
18611	1409.94	446.15	2438.75	459.58	90.10
21306	126.88	54.43	52.78	18.76	90.09
3808	168.04	48.80	407.80	212.39	90.07
12031	145.86	38.78	225.16	30.38	90.06
23869	36.50	52.75	579.45	394.24	90.03
3015	2289.41	964.34	4534.92	1150.81	89.97
17908	60.79	49.95	325.35	238.47	89.90
25539	125.13	35.09	45.76	23.16	89.89
3473	120.74	34.02	69.52	20.97	89.83
2536	397.05	123.98	201.50	73.82	89.83
23826	344.12	55.78	225.14	47.99	89.80
9114	870.77	222.15	416.13	221.53	89.80
1639	97.37	22.99	62.34	12.37	89.70
20920	617.66	155.43	1397.16	623.36	89.60
20350	156.72	49.50	53.00	45.87	89.58
6615	279.24	84.15	96.62	96.14	89.50
19952	67.58	24.21	24.03	11.92	89.41
8237	102.59	36.73	179.81	51.98	89.37
11841	886.79	192.09	1632.36	479.53	89.34
2310	-47.82	40.85	36.34	37.62	89.32
15796	337.30	87.85	156.28	76.95	89.24
22681	216.80	177.12	918.02	459.53	89.21
22543	694.25	216.61	217.39	263.73	89.20
19433	110.29	59.85	445.41	230.04	89.17
22540	1828.95	538.43	794.41	586.09	89.07
17473	421.95	90.69	764.49	230.12	89.04
15875	1177.56	384.90	1982.41	472.79	88.98
18396	74.08	26.23	124.23	18.90	88.94
19	336.88	73.75	628.54	175.62	88.82
25567	456.18	167.99	922.98	373.29	88.65
20728	538.10	99.95	327.92	109.45	88.59
24351	-2.24	8.36	22.30	16.23	88.56
9053	240.22	50.14	146.06	39.78	88.55
18305	1364.98	457.67	2297.19	462.10	88.51

TABLE 5W: P-MIPRONATE			Atty. Docket No. 44921-508110		
Interim at 24 hrs			Doc. No. 1798897.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
439	55.65	23.09	35.13	0.15	99.49
381	23.05	20.96	4.85	0.20	98.80
1439	233.12	46.90	167.13	1.64	98.63
24501	526.65	117.76	477.38	1.09	98.50
815	1161.46	344.32	1840.91	46.72	98.50
21723	24.61	15.80	18.81	0.26	98.37
25907	19.98	25.22	27.99	0.55	98.33
4440	320.37	110.50	249.77	1.69	98.33
8950	91.09	33.83	64.54	0.45	98.29
1145	59.20	26.43	36.98	0.67	98.25
20257	130.93	45.11	78.91	1.23	98.20
12781	189.97	49.11	273.46	3.66	98.12
20427	796.69	192.75	1119.78	17.38	97.90
16938	1322.80	411.98	1887.43	31.46	97.90
1324	63.66	31.18	28.89	2.88	97.82
16584	115.91	45.04	161.39	2.19	97.73
17102	47.91	18.57	30.16	0.64	97.73
10227	447.34	108.01	244.96	13.58	97.69
1310	152.06	33.32	86.35	7.14	97.69
8476	3812.40	1012.46	4862.16	57.22	97.65
22051	151.18	44.26	223.47	4.06	97.65
5049	297.65	66.21	180.38	7.11	97.60
16323	68.35	35.92	36.63	1.47	97.56
6654	166.71	45.74	158.83	0.92	97.43
1651	678.67	240.75	692.24	5.18	97.39
16192	41.41	14.72	34.35	0.38	97.31
12343	50.68	18.55	31.84	0.83	97.31
691	133.51	42.32	62.52	3.81	97.26
17635	648.73	151.15	484.36	6.12	97.22
9286	205.78	60.59	319.19	10.41	97.22
14800	36.39	23.63	34.69	0.41	97.22
23888	105.90	50.58	91.90	1.08	97.13
5969	1521.63	357.02	1485.82	9.84	97.13
3475	384.13	98.77	465.98	4.26	97.05
11174	54.15	51.85	121.54	7.12	97.01
28119	124.47	45.67	234.96	195.06	97.01
18250	1094.73	316.96	1382.93	14.86	96.96
25069	133.97	60.97	77.32	2.29	96.88
18135	133.61	28.59	96.51	1.97	96.88
21742	33.31	18.06	25.78	0.33	96.83
25702	579.55	128.85	805.98	44.29	96.79
10936	207.62	43.60	191.02	1.12	96.79
12342	96.27	49.48	87.13	1.04	96.75
19976	47.03	15.83	30.77	0.70	96.75
9620	530.95	116.93	770.14	47.74	96.71
20810	1262.30	404.25	1842.66	50.26	96.71
24721	203.81	53.70	187.98	1.38	96.71
14967	49.34	21.65	19.69	1.41	96.58
1309	43.01	16.54	30.28	0.59	96.54
730	112.34	33.32	65.78	2.57	96.49
15876	1174.15	310.95	1565.93	37.98	96.49
16482	195.58	40.06	132.17	5.76	96.45
5654	41.42	24.77	86.94	5.20	96.45
15850	1216.75	351.89	1264.63	16.42	96.45
4259	700.70	159.00	935.48	29.71	96.36

TABLE 5W: PAMIDRONATE			Atty. Docket No. 44921-5089WO		
Timepoint(s): 24 hrs			Doc. No. 1798897.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
7010	309.13	55.63	255.94	3.25	96.36
18880	36.99	12.90	31.14	0.58	96.32
3007	126.64	42.37	192.91	7.32	96.28
1375	84.74	20.63	55.45	2.98	96.28
19244	1227.03	383.14	1715.96	64.01	96.28
6595	76.76	35.41	102.22	2.83	96.19
18126	701.66	166.62	548.76	14.64	96.19
10869	11.30	60.29	123.29	15.83	96.15
15239	567.46	132.45	783.53	43.73	96.11
4241	114.51	43.66	203.36	162.90	96.11
12360	55.02	27.32	35.03	1.44	96.11
11687	25.88	23.50	35.95	1.69	96.11
5492	97.03	47.49	24.35	5.81	96.11
9871	124.41	52.83	135.25	1.91	96.11
9410	62.57	24.27	60.98	0.84	95.98
13105	64.62	26.94	43.02	1.19	95.98
10659	132.22	90.74	258.54	43.13	95.94
106	59.79	20.18	35.91	1.62	95.89
2697	1226.39	358.41	1822.86	80.35	95.85
10217	310.63	90.28	201.72	7.38	95.85
22658	275.00	67.48	237.14	2.73	95.85
3417	445.05	113.12	533.98	7.67	95.81
15446	369.04	93.58	428.95	2.94	95.81
2847	62.77	31.28	81.96	1.81	95.81
2469	1383.42	482.22	963.09	26.57	95.81
17175	619.05	156.40	867.90	59.01	95.77
4386	56.38	26.60	45.57	0.72	95.77
21491	110.61	27.92	90.43	1.09	95.77
20844	843.25	294.01	1309.53	64.24	95.72
9370	773.72	201.87	676.25	8.78	95.72
15130	274.69	83.28	262.79	4.56	95.64

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TABLE 5X: PAN		Atty. Docket No. 44921-6089WO				
Timepoint(s): 168 hrs		Doc. No. 1798697.1				
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore	
6100	-24.28	62.27	70.39	19.04	99.79	
2048	31.63	20.68	119.91	5.57	99.79	
24024	32.82	21.87	144.74	15.76	99.79	
14722	658.73	219.20	1717.84	115.16	99.74	
21651	31.52	24.04	198.29	19.08	99.74	
15401	75.65	26.38	220.16	14.55	99.70	
15503	124.16	37.19	305.20	27.55	99.70	
7090	16.70	14.04	114.99	16.69	99.70	
10893	-30.66	62.67	46.11	19.29	99.70	
23780	24.98	35.81	102.35	16.07	99.66	
16726	944.95	205.53	460.40	16.03	99.61	
14430	33.41	27.29	289.33	65.58	99.61	
15434	132.29	53.11	374.76	31.01	99.53	
17198	812.71	267.14	249.19	36.68	99.53	
15437	38.33	22.07	168.45	19.74	99.53	
225	123.21	34.21	276.57	21.70	99.49	
3584	64.34	31.89	290.58	28.71	99.49	
9084	46.92	17.70	134.77	13.50	99.49	
20736	331.77	100.84	748.89	43.21	99.49	
19374	-8.73	12.21	63.84	14.49	99.44	
20699	94.34	231.80	255.20	18.42	99.44	
22818	23.08	15.16	83.31	4.90	99.44	
23297	384.07	96.58	840.46	53.16	99.44	
15002	140.16	98.17	338.90	19.21	99.44	
3269	75.61	36.41	385.17	72.48	99.44	
23773	212.24	81.04	629.63	48.29	99.40	
23992	5.27	6.59	56.95	14.22	99.36	
17682	673.28	176.72	223.65	27.55	99.36	
3079	34.49	46.53	164.24	20.61	99.36	
23778	68.50	31.99	270.34	37.08	99.36	
19006	642.56	208.65	1445.68	75.63	99.31	
20887	793.69	313.68	218.40	48.36	99.31	
6039	310.04	86.04	693.54	28.37	99.27	
15003	35.50	95.84	254.52	23.59	99.27	
17227	873.36	191.79	476.74	33.25	99.27	
1801	97.51	29.11	207.98	12.46	99.27	
10015	231.53	75.18	560.75	25.13	99.27	
12683	60.85	40.62	505.60	124.63	99.23	
16675	33.50	33.48	151.49	16.04	99.23	
1809	36.19	128.09	267.84	32.82	99.23	
15981	75.09	25.95	290.62	83.27	99.23	
2637	124.84	42.73	270.38	22.27	99.23	
2284	99.14	37.28	252.45	25.44	99.23	
11338	39.20	31.91	342.99	92.86	99.19	
16425	19.78	26.43	256.34	69.36	99.19	
9212	1017.57	301.78	2309.86	189.18	99.19	
13977	281.63	142.69	1144.78	134.21	99.19	
3572	33.77	17.83	169.37	47.47	99.19	
22079	78.37	356.23	216.47	49.64	99.19	
13974	288.69	149.15	842.98	65.09	99.19	
24564	568.47	175.61	176.63	24.26	99.14	
18603	-45.88	67.13	192.24	18.99	99.14	
2010	33.66	315.34	180.93	36.19	99.14	
17501	31.72	17.98	94.02	6.17	99.14	
23376	14.35	15.90	95.17	30.08	99.14	

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TABLE SX: PAN		Atty. Docket No. 44921-5089WO			
Timepoint(s): 168 hrs		Doc. No. 1798897.1			
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
6517	231.39	155.95	730.29	101.68	99.14
20599	22.90	12.70	74.26	5.67	99.14
23377	61.42	52.07	359.41	62.64	99.14
14405	459.81	287.63	2264.76	369.05	99.14
1564	38.78	169.92	459.31	64.11	99.10
16676	38.17	26.57	134.01	11.56	99.10
21695	59.83	35.43	188.55	18.05	99.10
20886	719.56	292.49	116.56	44.10	99.10
17151	16.05	62.27	445.34	138.38	99.06
770	798.22	219.65	310.69	35.90	99.06
7262	1116.47	390.83	2517.22	160.89	99.06
23981	809.28	155.43	1417.26	153.29	99.06
22552	314.65	94.11	570.75	29.08	99.06
20709	162.15	69.62	483.04	60.17	99.06
7585	-91.46	37.80	142.97	84.57	99.01
15853	5.82	59.90	258.64	131.89	99.01
22592	233.64	160.86	1028.66	111.76	98.97
4445	514.32	117.31	988.03	63.78	98.97
4086	14.01	16.98	152.91	75.32	98.97
21509	88.80	92.91	448.20	56.16	98.97
24651	100.64	23.29	204.63	19.93	98.97
7101	389.56	671.41	1218.47	165.33	98.93
15851	200.60	148.70	784.83	83.88	98.93
23769	-6.25	8.68	29.51	10.78	98.93
15504	128.87	50.45	417.46	77.64	98.93
1613	-7.12	28.04	117.88	29.33	98.93
15438	65.66	32.54	171.12	14.45	98.93
1460	198.26	83.19	563.02	70.47	98.93
13976	449.17	351.62	2551.95	498.75	98.93
20903	69.41	42.80	397.90	116.45	98.89
23123	310.66	118.21	861.54	70.50	98.89
15790	45.93	25.16	134.46	10.51	98.89
21391	213.21	127.55	742.74	58.03	98.89
455	137.60	153.63	269.32	29.16	98.89
20772	149.52	40.53	313.83	28.96	98.89
19275	726.18	191.87	1580.61	140.07	98.84
17149	81.87	40.60	328.14	60.26	98.84
19243	76.71	48.71	359.48	105.52	98.84
17197	1903.25	828.79	668.38	83.11	98.84
11891	-15.63	11.78	25.77	9.49	98.84
4640	80.30	30.25	184.62	15.77	98.80
4569	0.89	6.39	34.18	10.37	98.80
2629	25.55	23.81	70.08	4.98	98.80
18529	202.36	80.95	572.14	48.95	98.80

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TABLE 5Y: PAN					
Timepoint(s): 6, 24 hrs					
Att'y. Docket No. 44921-5089WO					
Doc. No. 1798397.1					
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LPAScore
410	1099.85	252.82	487.89	71.66	99.01
1137	58.38	18.64	128.72	40.53	97.55
18322	2669.23	812.57	1422.54	109.34	97.47
15433	67.21	32.38	147.81	13.69	97.04
8990	278.32	77.85	504.55	67.10	96.35
23115	565.35	169.43	1013.53	113.02	96.22
1460	199.21	86.34	300.32	24.45	95.97
335	96.10	45.37	194.53	15.33	95.92
2866	637.05	212.44	1020.97	43.03	95.75
15701	37.69	16.68	82.72	11.76	95.75
16853	67.54	23.29	107.06	8.27	95.58
17693	1257.20	377.49	705.99	42.86	95.41
6250	490.36	103.66	731.52	54.23	95.36
19327	89.22	29.33	144.42	10.71	95.28
21977	88.79	52.26	163.28	17.00	95.11
1962	33.32	26.88	74.11	7.81	95.08
19080	75.82	57.08	219.58	56.51	95.06
13598	349.80	109.75	578.05	60.94	95.02
11524	-14.25	24.65	43.36	19.72	95.02
729	90.40	35.70	171.30	19.74	94.98
15552	175.81	40.06	237.25	9.67	94.98
4312	77.28	38.83	150.22	19.98	94.94
16996	137.86	44.69	250.58	35.37	94.85
17411	79.24	54.48	184.11	25.15	94.76
20752	13.07	11.34	26.51	2.40	94.76
11445	436.52	103.96	686.40	101.03	94.42
17755	393.23	102.51	214.27	40.93	94.42
19077	208.94	51.22	306.89	24.65	94.25
21355	375.05	118.77	619.86	88.05	94.21
6454	239.78	78.25	421.17	60.75	94.16
21092	392.44	225.02	575.95	55.98	94.12
11618	414.89	130.79	694.32	108.18	94.03
18338	72.29	20.32	112.46	9.87	94.03
15050	637.68	181.55	464.30	24.18	94.03
1608	12.70	29.99	54.74	9.39	93.99
24539	613.90	163.40	344.65	53.69	93.99
5900	265.48	65.87	137.54	40.46	93.99
13239	109.63	48.60	209.05	26.39	93.99
5163	20.12	13.08	44.33	7.38	93.82
21130	78.12	26.32	110.79	5.99	93.73
2236	140.10	38.70	215.23	16.78	93.69
5967	1225.74	339.49	1876.92	202.57	93.65
9799	145.09	50.35	241.50	35.40	93.56
16205	940.52	264.48	668.73	24.99	93.56
456	869.99	317.52	515.38	44.20	93.56
25097	4.68	10.99	25.79	8.52	93.52
12020	167.47	60.50	285.05	31.13	93.52
5924	162.21	46.91	256.59	29.67	93.52
4716	156.93	40.11	238.10	25.26	93.48
8339	432.55	130.90	704.91	90.15	93.43
5561	167.91	55.87	283.83	41.10	93.39
15112	1549.68	531.98	736.99	111.89	93.39
7278	1467.27	341.78	1077.40	67.94	93.35
7108	53.62	29.56	116.16	20.84	93.30
4956	79.01	38.21	153.60	24.20	93.30
20404	53.75	46.18	126.25	22.59	93.26

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TABLE 57: PAN						Atty. Docket No. 44921-5089WO	
Timepoint(s): 6, 24 hrs						Doc. No. 1798897.1	
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore		
6049	621.00	123.14	541.13	9.05	93.22		
9109	1021.28	337.87	723.36	26.27	93.22		
4393	1268.21	369.74	824.30	42.57	93.18		
18541	1081.46	298.74	758.66	24.93	93.13		
15556	208.38	83.99	333.56	45.17	93.09		
4589	1213.38	369.83	790.80	42.48	93.09		
22271	273.68	65.98	411.42	75.15	93.05		
21423	1355.28	427.17	786.98	56.19	93.05		
6506	234.14	60.71	335.18	21.90	93.05		
4290	94.34	28.53	147.53	19.36	93.05		
20350	155.10	50.13	248.15	31.72	93.05		
714	46.67	31.34	115.67	27.05	93.05		
1485	93.58	57.35	198.96	32.55	93.00		
18433	19.39	46.95	105.10	24.21	93.00		
17567	1185.38	364.09	750.70	33.02	93.00		
24615	817.72	230.83	583.06	24.71	92.96		
15742	33.17	14.60	56.07	3.60	92.96		
20766	56.29	20.07	93.49	10.52	92.92		
15209	164.94	33.20	220.88	12.45	92.92		
20879	87.79	50.58	180.08	38.06	92.88		
19408	2011.27	675.11	1014.96	97.93	92.88		
1247	1309.18	501.52	569.36	138.91	92.83		
15299	88.50	61.88	119.48	12.69	92.83		
11377	116.76	30.96	177.28	17.37	92.79		
9037	22.39	16.20	56.28	11.77	92.79		
24390	162.85	113.82	331.70	49.97	92.79		
1550	30.09	69.61	60.64	8.26	92.79		
1300	156.68	44.76	234.60	19.19	92.75		
1585	67.71	33.38	128.60	16.01	92.70		
25599	56.14	20.41	91.99	8.79	92.66		
17524	1173.79	285.74	801.36	115.86	92.62		
15122	420.86	89.65	588.05	45.81	92.58		
25369	18.36	10.68	38.74	6.19	92.58		
3886	58.10	28.84	117.74	22.59	92.53		
643	61.37	32.91	119.52	18.91	92.53		
14003	815.86	212.90	497.74	73.28	92.49		
18164	1083.28	283.92	680.99	54.84	92.49		
20864	1587.98	660.11	798.40	87.84	92.45		
17742	1066.26	308.06	723.12	37.02	92.45		
23248	37.67	17.23	53.27	3.03	92.45		
17204	1732.06	656.42	888.59	86.53	92.45		
24501	525.70	117.48	664.66	34.25	92.40		
14125	128.41	50.32	217.38	25.88	92.36		
5968	962.02	263.60	1474.27	231.26	92.36		

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TABLE 52: PAN			Atty. Docket No. 44921-5089WO		
Time period: 6. 24. 168 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
15433	66.69	31.46	164.15	24.65	97.20
1962	33.08	26.68	80.19	11.69	95.26
16122	116.83	40.09	224.79	57.88	94.96
1247	1312.82	499.50	526.34	127.30	94.87
16853	67.23	22.82	120.51	22.86	94.83
17693	1260.09	375.71	656.50	74.07	94.78
13239	108.92	47.30	236.00	58.32	94.57
15112	1553.39	530.07	717.14	110.65	94.35
18433	18.80	46.13	126.18	39.27	94.35
16121	109.21	58.36	264.16	84.47	94.18
15701	37.56	16.60	76.48	12.40	94.05
19077	208.57	51.01	301.25	21.97	94.01
4723	1721.81	624.78	922.60	68.61	93.58
25097	4.60	10.95	24.13	7.34	93.23
7278	1469.82	340.27	993.59	122.75	93.23
1159	888.08	229.69	532.18	82.33	93.19
15184	-80.88	50.16	76.70	82.34	93.07
456	871.69	317.12	499.51	56.17	92.97
1608	12.56	29.97	50.60	9.98	92.93
15437	38.06	21.84	118.82	46.29	92.69
225	122.71	33.55	235.76	49.22	92.51
14997	2605.00	1019.08	1218.22	195.95	92.46
15401	75.23	25.84	175.78	44.88	92.39
19408	2015.21	673.87	1049.53	100.77	92.20
18076	2552.08	1185.85	1116.73	165.36	91.90
18077	2630.74	1183.04	1067.76	130.98	91.72
15434	131.68	52.58	292.95	80.76	91.61
16211	2268.34	1131.65	761.93	145.25	91.51
11208	322.94	110.75	642.87	141.37	91.48
24651	100.37	23.09	169.86	33.73	91.48
16012	72.52	31.21	141.73	32.89	91.35
1542	928.57	263.76	548.27	84.14	91.34
14722	656.51	217.90	1314.74	367.97	91.31
4589	1215.64	368.99	748.52	72.66	91.21
17886	1506.14	491.91	843.64	96.88	91.16
17829	2232.91	1111.68	900.83	138.88	91.16
15673	804.12	164.51	1076.89	78.92	91.16
4312	76.92	38.49	154.79	22.22	91.09
2079	303.47	81.98	400.13	28.12	90.99
18694	53.10	48.50	177.05	53.91	90.96
18322	2673.81	811.21	1499.15	181.85	90.79
16168	350.70	206.64	479.34	84.79	90.78
17779	1958.43	783.05	911.49	158.95	90.73
8990	277.74	77.38	465.89	83.79	90.57
3434	322.35	138.05	614.67	136.42	90.57
18729	19.67	29.33	96.11	37.87	90.57
14003	817.64	211.58	458.34	85.08	90.53
22816	22.96	15.10	59.89	23.04	90.49
9799	144.50	49.47	258.44	54.08	90.49
1521	20.40	50.29	136.10	71.19	90.49
15886	302.74	61.73	436.98	44.28	90.45
16155	1084.95	423.63	632.04	54.95	90.43
1485	92.98	56.73	213.05	31.14	90.36
17204	1735.18	656.07	938.01	109.72	90.30
1203	4.95	18.70	44.90	22.64	90.27

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TABLE 52: PAN		Atty. Docket No. 44921-5089WO			
Timepoint(s): 6, 24, 168 hrs		Doc. No. 1798897.1			
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
19080	75.38	56.65	202.18	64.18	90.27
1822	2078.05	898.00	838.34	144.28	90.26
17712	858.75	187.72	604.46	57.40	90.26
19407	1533.63	471.44	919.83	109.37	90.26
4280	1275.34	435.07	698.85	97.31	90.22
635	1254.34	431.22	723.36	97.99	90.17
22554	544.56	150.27	343.47	69.26	90.17
11524	-14.44	24.49	37.71	21.53	90.14
21703	16.32	12.14	42.83	13.13	90.10
14125	127.72	48.99	246.62	72.21	90.06
17480	119.30	33.27	190.90	31.79	90.01
23322	1169.31	283.61	760.72	114.86	89.96
8234	49.37	21.69	92.92	31.52	89.93
13682	176.92	61.79	309.18	50.37	89.89
11321	175.44	50.38	286.20	55.16	89.89
25253	291.91	64.62	414.09	38.27	89.71
23852	262.19	102.61	480.31	78.92	89.71
20781	57.13	21.07	88.06	13.32	89.70
1582	16.87	13.15	45.26	13.10	89.67
24696	68.64	47.19	170.78	42.12	89.67
818	4144.91	2804.50	980.91	271.23	89.66
9109	1022.78	337.79	702.34	58.34	89.66
21708	36.51	16.01	73.22	15.22	89.63
17549	1309.92	366.25	854.17	88.86	89.61
16591	151.86	47.16	253.45	36.23	89.54
17154	198.88	57.70	280.48	33.03	89.53
14694	2332.83	1063.34	1038.43	256.02	89.48
23109	2093.27	924.06	1002.79	195.59	89.48
2236	139.93	38.69	200.68	21.94	89.48
22661	1310.36	418.55	756.78	88.01	89.48
7857	51.98	45.43	149.29	46.95	89.45
20876	1681.76	611.63	958.77	99.56	89.44
25468	2183.54	1132.38	823.42	189.02	89.44
23215	106.03	29.48	169.54	21.53	89.41
5900	265.96	65.56	144.68	40.70	89.41
1811	10.93	26.49	65.20	23.39	89.37
23709	2507.78	1197.86	1088.40	231.11	89.35
495	135.24	83.30	303.90	57.27	89.32
20998	161.29	73.65	276.37	48.32	89.32
17194	46.75	27.72	107.07	19.66	89.32
19327	88.98	29.10	144.83	20.18	89.28
18101	81.85	27.96	121.65	14.02	89.27
819	3112.24	1661.98	1015.34	283.90	89.27
3015	2325.38	988.40	1058.04	289.77	89.22
21355	374.22	118.21	598.37	91.02	89.20

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TABLE SAA: SEMUSTINE			Atty. Docket No. 449241-5089WO		
Timepoint(s): 168 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
23830	-3.74	14.74	24.13	2.44	98.46
2655	43.68	49.43	103.83	13.87	98.07
22547	15.31	164.20	55.98	7.70	97.99
21893	51.15	34.39	119.77	15.62	97.86
7806	52.07	19.62	68.71	1.17	97.73
7785	1830.12	494.30	1054.17	67.70	97.69
25705	455.94	115.83	867.36	30.91	97.64
22050	3163.82	930.45	2122.73	41.59	97.47
21443	103.90	53.37	35.53	5.08	97.26
23981	812.67	160.21	626.66	12.41	97.13
5733	12.64	47.16	51.31	11.73	97.13
8494	276.36	53.17	213.99	3.26	97.13
8901	25.65	33.31	2.82	0.93	97.13
7023	364.88	77.19	291.07	3.81	97.09
18353	113.25	70.77	275.16	28.92	97.04
3027	1129.65	333.83	1127.48	12.54	97.04
8177	3894.73	1495.61	2320.07	89.57	96.92
19398	4332.61	2167.49	2566.57	72.18	96.83
23626	71.43	37.20	159.26	19.40	96.83
18650	804.69	246.36	518.86	13.70	96.74
15627	5054.50	1946.06	3041.20	96.69	96.62
20757	413.88	222.48	607.95	51.66	96.53
2410	11.25	10.57	25.63	2.99	96.49
7274	576.90	150.70	364.54	16.30	96.44
26147	1030.83	225.21	645.26	49.87	96.32
3359	119.66	57.61	290.85	65.10	96.27
11994	104.13	23.52	63.18	4.39	96.06
7867	64.06	34.54	163.76	30.00	96.02
3701	90.19	44.20	111.89	2.06	95.93
23800	32.07	18.29	77.92	15.10	95.84
1684	2810.78	1628.26	2548.66	84.69	95.84
19162	2230.57	613.60	1498.90	55.20	95.84
14958	138.49	48.09	181.53	4.13	95.80
11454	238.93	79.65	379.87	38.25	95.76
7764	6.68	15.73	27.19	3.33	95.76
19993	2327.93	570.40	1514.68	94.53	95.76
9407	350.93	216.90	167.34	16.19	95.76
15600	772.34	211.63	480.10	25.98	95.76
22662	137.98	35.08	116.24	1.67	95.72
18142	1994.46	839.22	1965.70	25.18	95.63
7278	1466.77	341.68	1037.78	55.91	95.59
1685	9177.09	7104.79	4192.02	442.45	95.59
15136	720.68	229.89	618.26	7.44	95.50
17248	2563.75	537.86	1741.86	94.90	95.46
15301	38.66	68.20	52.95	4.33	95.46
24627	5024.80	1714.05	3187.73	133.28	95.46
16678	192.60	90.16	295.43	9.43	95.37
21798	2088.65	441.72	1574.36	40.27	95.37
3582	396.47	105.41	299.17	10.26	95.29
22618	28.62	11.98	54.72	9.80	95.24
20295	23.12	13.39	-1.42	5.25	95.20
10269	1868.08	422.77	1408.13	42.28	95.16
7975	744.31	175.27	709.93	7.00	95.12
3090	308.90	80.19	389.68	9.44	95.07
8163	105.92	55.18	246.10	47.62	95.03

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TABLE 5AA: SEMUSTINE			Atty. Docket No. 44921-5089WO		
Timepoint(s): 168 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
7337	130.17	35.83	72.98	11.19	95.03
5689	12.93	20.23	44.79	8.55	94.99
22737	204.61	104.35	375.42	54.48	94.94
4640	80.47	30.73	144.33	17.03	94.82
10819	1187.21	363.05	1125.76	18.01	94.82
3269	76.54	40.97	147.76	18.49	94.77
18468	90.58	33.19	99.23	1.85	94.77
6204	39.16	12.29	53.01	1.67	94.77
19372	61.97	54.00	9.74	2.20	94.73
21628	116.51	45.00	204.96	26.35	94.69
3075	523.79	180.19	291.98	21.30	94.69
8015	52.45	36.45	80.79	2.30	94.64
20105	80.00	53.71	27.37	3.94	94.64
18830	5928.33	2277.75	3404.34	229.07	94.60
12639	1231.40	359.71	1328.85	25.82	94.60
2697	1227.29	359.86	1375.72	25.94	94.56
2326	1442.32	399.30	866.19	98.10	94.56
9180	82.53	35.16	153.13	21.13	94.47
22838	1383.85	399.86	912.16	54.21	94.47
23509	2234.19	462.51	1771.07	42.02	94.47
23709	2494.50	1202.87	2200.91	59.43	94.34
2912	2618.16	709.02	1838.26	100.99	94.34
20944	1191.93	395.05	1322.96	34.77	94.30
25589	154.92	38.08	184.54	2.96	94.30
18800	2730.47	1166.13	1296.14	149.09	94.26
2311	22.96	16.01	54.56	12.04	94.17
410	1097.48	256.27	795.24	44.26	94.17
17885	246.73	58.07	148.75	13.01	94.13
21458	229.64	104.63	360.82	32.46	94.13
22069	689.12	145.53	514.75	17.18	94.13
3584	65.13	35.08	106.58	9.75	94.13
5968	966.61	265.81	609.81	49.16	94.04
19525	27.97	21.00	56.08	10.20	94.04
18757	250.38	72.47	327.68	9.19	94.00
19768	711.98	179.77	874.96	22.13	94.00
7392	29.06	15.76	62.61	15.61	94.00
10267	2119.14	891.88	2056.03	48.77	94.00
23190	70.87	28.52	103.79	5.80	93.96
25676	218.79	80.22	97.09	19.62	93.96

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TABLE 5Bb: SUFLADIAZINE					
Timepoint(s): 24 hrs					
Att'y. Docket No. 44921-5089WO					
Doc. No. 1798397.1					
Identifier	NonIoxMean	NonIoxSU	IoxMean	IoxSU	LLAScore
13158	464.71	105.53	185.18	11.81	99.53
2010	31.95	313.46	578.42	46.88	99.79
15535	445.86	80.88	792.83	41.28	99.74
1564	34.77	147.30	1395.56	106.27	99.70
4452	989.99	248.64	328.14	43.97	99.70
4450	282.32	50.39	113.73	16.34	99.61
20700	81.27	404.57	1604.45	209.39	99.61
20481	208.68	44.26	81.56	7.25	99.57
25686	666.44	155.98	1348.56	47.39	99.53
5695	1559.28	402.43	636.16	43.80	99.53
6477	13.20	160.91	187.40	49.13	99.53
17101	352.23	77.89	621.28	16.27	99.49
15175	318.83	49.56	153.62	12.70	99.49
20699	90.33	220.48	1192.64	109.71	99.49
6478	22.55	383.52	251.88	88.78	99.44
725	117.71	45.62	14.15	2.76	99.44
645	151.16	54.99	17.82	6.85	99.44
3987	192.50	47.15	465.13	55.22	99.44
21947	752.67	136.25	319.39	29.30	99.40
17291	1389.57	412.30	482.86	101.58	99.40
238	227.68	51.22	496.72	69.45	99.36
20887	794.18	312.69	103.79	42.68	99.36
1558	203.57	58.77	553.28	64.74	99.36
17661	255.29	58.73	540.05	70.79	99.36
16947	320.42	79.17	77.47	19.86	99.36
16204	752.56	177.92	1702.82	145.45	99.36
18906	255.45	83.89	55.16	8.36	99.36
17357	269.77	81.23	2.53	12.73	99.31
17514	859.90	174.50	359.55	37.03	99.31
16416	22.83	18.51	84.23	3.30	99.27
2085	688.34	191.75	339.59	20.82	99.27
7101	380.51	644.25	3330.36	683.13	99.27
18278	1896.72	507.81	639.93	108.91	99.27
25718	392.38	80.21	851.19	103.08	99.23
1478	352.13	79.44	88.92	22.22	99.23
9621	292.01	59.49	563.88	51.66	99.23
23596	1491.59	375.55	487.23	90.69	99.23
20884	637.92	256.49	19.93	9.59	99.23
10016	207.78	73.01	590.63	39.54	99.23
7685	282.42	91.44	861.31	113.78	99.19
472	661.53	177.31	345.51	23.33	99.19
18597	521.43	162.83	914.02	31.92	99.19
4222	545.41	102.20	1014.25	79.67	99.19
20866	719.84	291.88	50.84	41.81	99.19
1884	178.24	37.12	331.54	22.95	99.19
1422	297.77	88.40	75.68	10.49	99.19
17104	449.21	107.90	1060.31	149.95	99.14
17907	1319.66	300.38	623.40	49.85	99.14
17284	229.07	60.08	77.02	16.01	99.14
8981	142.60	87.32	716.17	136.32	99.14
4451	290.54	64.21	76.77	27.51	99.14
15955	751.14	196.31	146.28	35.67	99.10
16419	306.72	58.43	562.97	56.12	99.10
16627	97.46	34.41	213.43	14.92	99.10
22592	234.18	163.38	903.10	59.07	99.10
19824	224.78	67.21	32.81	20.42	99.10

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TABLE 5Bb: SUFLADIAZINE					
Att'y. Docket No. 44921-5089WO					
Timepoint(s): 24 hrs					
Doc. No. 1798997.1					
Identifier	NonItoxMean	NonItoxSD	ItoxMean	ItoxSD	LOAScore
9905	674.04	138.26	279.49	36.23	99.10
15002	139.13	94.64	580.42	72.97	99.10
812	157.04	34.99	39.35	14.07	99.10
15193	172.71	60.15	463.80	40.10	99.10
11205	596.04	192.04	155.98	25.86	99.10
17535	246.41	64.45	529.14	76.63	99.06
4360	330.80	65.83	138.60	23.78	99.06
5667	742.84	172.36	1513.63	136.63	99.06
20056	309.09	59.92	81.20	26.34	99.06
11081	352.98	113.10	740.48	49.43	99.06
3916	738.87	186.54	212.10	43.88	99.06
1801	97.49	29.02	212.29	21.51	99.06
25317	15.28	68.43	72.14	39.26	99.06
24501	524.69	114.42	955.66	83.01	99.06
19508	100.97	41.09	11.48	5.01	99.06
19769	63.82	80.07	487.54	129.83	99.01
25546	473.54	139.58	193.05	34.65	99.01
10878	951.05	250.12	1714.95	105.09	99.01
10819	1183.30	358.76	2036.62	53.76	99.01
18507	701.19	159.97	1396.26	108.52	98.97
2915	87.36	36.13	206.79	19.36	98.97
15003	34.41	91.73	507.05	83.25	98.97
2583	369.08	148.55	848.08	90.80	98.97
9620	529.25	111.98	1071.29	125.35	98.97
19298	364.57	96.71	819.01	116.31	98.97
6614	478.70	150.19	97.33	35.20	98.97
15986	320.13	83.84	46.97	24.78	98.97
13646	727.39	191.95	1634.83	174.87	98.93
240	184.44	53.70	394.90	58.94	98.93
16675	33.18	31.66	226.87	74.32	98.93
11968	297.46	82.47	94.28	17.16	98.93
17540	561.49	199.04	1583.99	230.39	98.93
19161	1068.85	309.26	2020.78	120.96	98.93
23924	208.78	62.50	465.78	53.25	98.93
4482	227.17	73.35	67.19	17.67	98.93
5199	611.50	182.04	158.54	39.19	98.93
117	21.06	17.59	-12.77	2.61	98.89
22536	1715.17	473.49	3319.42	278.50	98.89
17100	819.32	235.74	1519.10	85.28	98.89
14332	537.23	133.39	1143.62	152.21	98.89
5232	365.72	93.58	160.50	9.58	98.89
10561	78.49	36.71	188.47	14.45	98.89
15098	185.41	66.49	32.78	6.96	98.89
3401	14.24	21.17	144.41	52.94	98.89

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TABLE 6CC: SULFADIAZINE					Atty. Docket No. 44921-5089WO
Timepoint(s): 3, 6 hrs					Doc. No. 179837.1
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
2459	327.82	133.31	1186.99	180.16	99.44
985	18.91	23.49	435.93	226.01	99.36
6054	24.46	35.46	463.67	144.11	99.18
21546	-60.81	78.07	461.08	143.78	99.14
11259	101.27	105.67	1117.26	304.40	99.05
223	10.81	16.39	121.57	31.76	99.05
13745	27.17	26.30	236.39	104.08	99.05
8304	263.66	68.46	104.04	18.52	99.05
2154	54.19	102.13	766.15	271.93	98.93
6585	635.65	314.22	2778.88	622.70	98.80
17506	33.02	28.55	170.00	54.28	98.80
2153	179.20	124.41	1217.91	474.19	98.75
23872	47.29	87.73	387.10	112.80	98.71
15301	35.41	55.60	466.69	146.16	98.67
15192	164.68	117.96	858.98	208.00	98.67
17327	209.40	86.17	531.34	65.50	98.62
15300	131.96	108.91	967.46	264.07	98.62
7700	80.97	38.43	377.20	103.65	98.58
13930	128.33	69.33	520.74	123.87	98.54
10659	128.90	79.62	602.71	192.55	98.54
7197	195.08	78.35	557.25	113.13	98.37
19060	150.81	79.81	399.19	134.24	98.32
15299	86.11	52.88	422.06	161.10	98.28
355	10.95	13.39	102.92	40.18	98.28
7196	178.85	80.11	517.52	81.96	98.28
25730	196.00	64.30	513.70	106.95	98.24
5356	-12.88	18.58	46.77	19.05	98.19
19657	3.19	17.88	84.23	34.61	98.15
25084	-12.38	22.65	46.65	25.44	98.11
1501	58.67	53.51	250.18	120.56	98.02
17908	62.13	58.89	240.27	66.39	97.98
16314	43.27	38.63	240.75	61.16	97.94
2555	95.85	44.10	292.92	71.25	97.94
21682	-35.82	31.41	50.22	26.54	97.89
5384	40.19	41.73	218.67	41.90	97.89
22626	83.22	71.71	465.98	192.17	97.85
11483	64.30	44.10	197.71	47.03	97.85
16053	229.00	93.51	658.28	200.15	97.81
4045	93.63	47.19	244.15	46.42	97.81
804	454.28	182.83	934.61	83.33	97.76
8874	118.37	60.25	305.67	73.98	97.76
23314	62.72	247.80	1403.77	543.62	97.76
21	69.73	31.90	161.45	47.41	97.76
22681	218.11	182.12	981.97	310.38	97.72
7471	219.05	63.97	421.52	40.74	97.72
13240	475.09	362.91	2390.71	790.75	97.68
1340	192.32	49.81	108.32	15.13	97.64
16312	54.74	33.76	197.76	42.24	97.59
11876	107.52	40.42	242.85	40.07	97.46
20161	38.17	33.28	150.28	32.80	97.46
15996	49.41	38.61	170.53	42.38	97.42
12978	105.07	45.80	334.16	95.16	97.42
14179	49.88	26.28	132.84	24.19	97.38
12534	87.91	36.00	223.28	65.14	97.38
21779	147.51	35.16	262.54	35.74	97.29

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TABLE 5CC: SULFADIAZINE			Atty. Docket No. 44921-5089WO		
Timepoint(s): 3, 6 hrs			Doc. No. 1798397.1		
Identifier	NonToxMean	NonToxSD	ToxMean	ToxSD	LDAScore
11979	210.67	69.55	85.98	17.52	97.25
17161	1152.09	406.69	2288.34	334.10	97.25
11434	326.14	103.27	663.21	132.01	97.12
6844	124.34	58.18	17.91	11.06	97.12
22	53.08	46.64	206.89	59.81	97.12
3464	165.60	53.31	329.80	63.59	97.08
3434	322.01	136.13	755.72	108.22	97.08
22248	243.91	118.15	625.27	179.46	97.03
9423	937.34	251.31	1765.27	274.26	97.03
21683	34.05	23.48	105.62	26.60	96.95
16527	51.16	16.84	24.15	3.25	96.90
4512	1.04	32.53	73.93	19.11	96.86
4725	81.40	55.94	245.03	66.25	96.78
21239	114.57	59.35	258.57	37.93	96.78
17329	213.88	104.30	531.44	105.41	96.65
13487	37.67	24.44	111.98	36.87	96.56
15089	179.58	77.35	389.68	58.33	96.56
3454	86.52	35.67	198.35	31.79	96.47
20523	547.69	149.96	965.84	112.80	96.43
15058	197.84	70.39	377.22	46.94	96.35
14492	613.89	164.78	1076.44	162.75	96.35
12999	128.09	33.18	203.14	17.45	96.30
22967	163.84	54.49	255.51	13.19	96.26
18008	1.51	16.75	42.22	12.38	96.26
24640	177.45	57.95	357.46	73.86	96.26
7913	55.20	20.69	108.16	18.70	96.17
2625	141.92	31.66	87.09	9.03	96.17
3049	201.89	100.36	461.30	105.24	96.17
18011	31.95	28.60	105.17	25.57	96.13
23834	71.40	23.40	137.38	25.69	96.09
19818	32.37	21.21	85.97	15.20	96.04
12673	37.51	22.58	99.74	25.41	96.04
15377	25.91	15.53	56.38	6.78	96.00
12745	330.67	112.37	623.69	81.74	96.00
14111	150.33	66.27	327.97	47.79	96.00
11157	681.75	178.91	356.49	80.44	96.00
23166	134.04	62.51	266.66	54.48	95.96
3519	375.54	125.21	690.15	176.36	95.87
16124	420.65	131.40	193.12	32.21	95.83
17800	204.49	42.25	108.97	22.01	95.79
8639	368.08	97.97	620.44	125.57	95.79
25090	83.00	43.32	203.07	48.58	95.79
15191	2005.55	1208.87	3819.43	343.39	95.74
7469	286.95	67.51	149.39	36.61	95.70
21238	-17.22	39.01	55.57	20.45	95.70

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## WE CLAIM:

1. A method of predicting at least one toxic effect of a compound, comprising:
  - (a) preparing a gene expression profile of a tissue or cell sample exposed to the compound; and
  - 5 (b) comparing the gene expression profile to a database comprising at least part of the data or information of Tables 1-5.
2. A method of claim 1, wherein the gene expression profile prepared from the tissue or cell sample comprises the level of expression for at least one gene.
- 10 3. A method of claim 2, wherein the level of expression is compared to a Tox Mean and/or NonTox Mean value in Tables 5-5CC.
4. A method of claim 3, wherein the level of expression is normalized prior to  
15 comparison.
5. A method of claim 1, wherein the database comprises substantially all of the data or information in Tables 5-5CC.
- 20 6. A method of predicting at least one toxic effect of a compound, comprising:
  - (a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of at least one toxic effect.
- 25 7. A method of predicting the progression of a toxic effect of a compound, comprising:
  - (a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of toxicity progression.
- 30 8. A method of predicting the renal toxicity of a compound, comprising:
  - (a) detecting the level of expression in a tissue or cell sample exposed to the

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compound of two or more genes from Tables 1-5; wherein differential expression of the genes in Tables 1-5 is indicative of renal toxicity.

9. A method of identifying an agent that modulates the onset or progression of a  
5 toxic response, comprising:
- (a) exposing a cell to the agent and a known toxin; and
  - (b) detecting the expression level of two or more genes from Tables 1-5;  
wherein differential expression of the genes in Tables 1-5 is indicative of toxicity.
10. A method of predicting the cellular pathways that a compound modulates in a  
cell, comprising:
- (a) detecting the level of expression in a tissue or cell sample exposed to the  
compound of two or more genes from Tables 1-5; wherein differential expression of the  
genes in Tables 1-5 is associated the modulation of at least one cellular pathway.
11. The method of any one of claims 6-10, wherein the expression levels of at least 3  
genes are detected.
12. The method of any one of claims 6-10, wherein the expression levels of at least 4  
20 genes are detected.
13. The method of any one of claims 6-10, wherein the expression levels of at least 5  
genes are detected.
14. The method of any one of claims 6-10, wherein the expression levels of at least 6  
25 genes are detected.
15. The method of any one of claims 6-10, wherein the expression levels of at least 7  
genes are detected.
16. The method of any one of claims 6-10, wherein the expression levels of at least 8  
30 genes are detected.

17. The method of any one of claims 6-10, wherein the expression levels of at least 9 genes are detected.
- 5 18. The method of any one of claims 6-10, wherein the expression levels of at least 10 genes are detected.
19. A method of claim 6 or 7, wherein the effect is selected from the group consisting of nephritis, kidney necrosis, glomerular and tubular injury, and focal  
10 segmental glomerulosclerosis.
20. A method of claim 8, wherein the renal toxicity is associated with at least one kidney disease pathology selected from the group consisting of nephritis, kidney  
necrosis, glomerular and tubular injury, and focal segmental glomerulosclerosis.  
15
21. A method of claim 10, wherein the cellular pathway is modulated by a toxin selected from the group consisting of cephaloridine, cisplatin, puromycin aminonucleoside (PAN), bromoethylamine hydrobromide (BEA), gentamicin, ifosfamide, cyclophosphamide, carboplatin, AY-25329, indomethacin, acyclovir, citrinin,  
20 mercuric chloride, diflunisal, cidofovir, pamidronate, lithium, hydralazine, colchicine, sulfadiazine, and adriamycin.
22. A set of at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 1-5.  
25
23. A set of probes according to claim 22, wherein the set comprises probes that hybridize to at least 3 genes.
24. A set of probes according to claim 22, wherein the set comprises probes that  
30 hybridize to at least 5 genes.
25. A set of probes according to claim 22, wherein the set comprises probes that

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hybridize to at least 7 genes.

26. A set of probes according to claim 22, wherein the set comprises probes that hybridize to at least 10 genes.

5

27. A set of probes according to any one of claims 22-26, wherein the probes are attached to a solid support.

28. A set of probes according to claim 27, wherein the solid support is selected from the group consisting of a membrane, a glass support and a silicon support.

10

29. A solid support comprising at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 1-5.

30. A solid support of claim 29, wherein the solid support is an array comprising at least 10 different oligonucleotides in discrete locations per square centimeter.

15

31. A solid support of claim 29, wherein the array comprises at least about 100 different oligonucleotides in discrete locations per square centimeter.

20

32. A solid support of claim 29, wherein the array comprises at least about 1000 different oligonucleotides in discrete locations per square centimeter.

33. A solid support of claim 29, wherein the array comprises at least about 10,000 different oligonucleotides in discrete locations per square centimeter.

25

34. A computer system comprising:

(a) a database containing information identifying the expression level in a tissue or cell sample exposed to a renal toxin of a set of genes comprising at least two genes in Tables 1-5; and

30

(b) a user interface to view the information.

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35. A computer system of claim 34, wherein the database further comprises sequence information for the genes.
36. A computer system of claim 34, wherein the database further comprises  
5 information identifying the expression level for the set of genes in the tissue or cell sample before exposure to a renal toxin.
37. A computer system of claim 34, wherein the database further comprises  
10 information identifying the expression level of the set of genes in a tissue or cell sample exposed to at least a second renal toxin.
38. A computer system of any of claims 34-37, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.
- 15 39. A computer system of claim 38, wherein the external database is GenBank.
40. A method of using a computer system of any one of claims 34-37 to present information identifying the expression level in a tissue or cell of at least one gene in  
20 Tables 1-5, comprising:  
    comparing the expression level of at least one gene in Tables 1-5 in a tissue or cell exposed to a test agent to the level of expression of the gene in the database.
41. A method of claim 40, wherein the expression levels of at least two genes are  
25 compared.
42. A method of claim 40, wherein the expression levels of at least five genes are compared.
- 30 43. A method of claim 40, wherein the expression levels of at least ten genes are compared.

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44. A method of claim 40, further comprising the step of displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level when exposed to a toxin.
- 5 45. A method of claim 9, wherein the known toxin is a renal toxin.
46. A method of claim 42, wherein the renal toxin is selected from the group consisting of cephaloridine, cisplatin, puromycin aminonucleoside (PAN), bromoethylamine hydrobromide (BEA), gentamicin, ifosfamide, cyclophosphamide, carboplatin, AY-25329, indomethacin, acyclovir, citrinin, mercuric chloride, diflunisal, cidofovir, pamidronate, lithium, hydralazine, colchicine, sulfadiazine, and adriamycin.
- 10 47. A method of any one of claims 6-10, wherein nearly all of the genes in Tables 1-5 are detected.
- 15 48. A method of claim 47, wherein all of the genes in at least one of Tables 5-5CC are detected.
49. A kit comprising at least one solid support of any one of claims 29-33 packaged with gene expression information for said genes.
- 20 50. A kit of claim 49, wherein the gene expression information comprises gene expression levels in a tissue or cell sample exposed to a renal toxin.
- 25 51. A kit of claim 50, wherein the gene expression information is in an electronic format.
52. A method of any one of claims 6-10, wherein the compound exposure is *in vivo* or *in vitro*.
- 30 53. A method of any one of claims 6-10, wherein the level of expression is detected by an amplification or hybridization assay.

54. A method of claim 53, wherein the amplification assay is quantitative or semi-quantitative PCR.
- 5 55. A method of claim 53, wherein the hybridization assay is selected from the group consisting of Northern blot, dot or slot blot, nuclease protection and microarray assays.
56. A method of identifying an agent that modulates at least one activity of a protein encoded by a gene in Tables 1-5 comprising:
- 10 (a) exposing the protein to the agent; and  
(b) assaying at least one activity of said protein.
57. A method of claim 56, wherein the agent is exposed to a cell expressing the protein.
- 15 58. A method of claim 57, wherein the cell is exposed to a known toxin.
59. A method of claim 58 wherein the toxin modulates the expression of the protein.